

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 ; Search time 12.4614 Seconds

(Without alignments)  
1003.251 Million cell updates/sec

Title: US-09-674-752-23

Perfect score: 688  
Sequence: 1 QVQLVQSGAEAKKRGSSVKV.....EPREDALDINGGTMVSS 130

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 761.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	515	74.9	128	2 PH0952	Ig heavy chain V r
2	509.5	74.1	133	2 C33548	Ig heavy chain V-1
3	509.5	74.1	627	2 S14683	Ig mu chain precu
4	502.5	73.0	135	2 PH0953	Ig heavy chain V r
5	501	72.8	116	2 PH0959	Ig heavy chain V r
6	498	72.4	120	2 PH0962	Ig heavy chain V r
7	498	72.4	122	2 PH0958	Ig heavy chain V r
8	498	72.4	132	2 S46394	Ig heavy chain V r
9	497.5	72.3	119	2 PH0961	Ig heavy chain V r
10	496	72.1	132	2 PH0954	Ig heavy chain V r
11	496	72.1	136	2 PH0960	Ig heavy chain V r
12	494.5	71.9	129	2 A33548	Ig heavy chain V-1
13	490.5	71.3	125	2 PH0957	Ig heavy chain V r
14	488.5	71.0	127	2 PH0955	Ig heavy chain V r
15	486	70.6	126	2 B33548	Ig heavy chain V-1
16	481	69.9	135	2 B32274	Ig heavy chain V r
17	456.5	66.4	133	2 PH1663	Ig heavy chain pre
18	452.5	65.8	121	2 A49590	Ig heavy chain V r
19	451	65.7	108	2 PH1664	Ig heavy chain V r
20	451	65.6	98	2 S26915	Ig heavy chain V r
21	451	65.6	116	2 S31698	Ig heavy chain V r
22	451	65.6	116	2 S36261	Ig heavy chain pre
23	451	65.6	123	2 S44108	Ig heavy chain V r
24	450	65.4	124	2 S19655	Ig heavy chain V-1
25	450	65.4	136	2 S31600	Ig heavy chain V r
26	447.5	65.0	122	2 B49590	Ig heavy chain V r
27	447	65.0	98	2 S24680	Ig heavy chain V-1
28	447	65.0	119	2 S44106	Ig heavy chain V-1
29	446.5	64.9	142	2 A32483	Ig heavy chain V r

30	446	64.8	118	2 S36265	Ig heavy chain V r
31	442.5	64.3	122	2 C49590	Ig heavy chain V r
32	442	64.2	171	2 S23623	Ig heavy chain V r
33	437.5	63.6	160	2 PLO105	anti-PR2 erythrocy
34	436.5	63.4	109	2 PH1671	Ig heavy chain V r
35	435.5	63.3	129	2 S36260	Ig heavy chain V r
36	435	63.2	135	2 S49530	Ig heavy chain V r
37	434	63.1	98	2 S46463	anti-Sm antibody V
38	430.5	62.6	127	2 S34014	Ig heavy chain V-1
39	428.5	62.3	129	2 S46393	Ig heavy chain V r
40	428	62.2	98	2 A30523	Ig heavy chain V-1
41	426	61.9	97	2 PH0870	Ig heavy chain V r
42	422.5	61.4	122	2 S36271	Ig heavy chain V r
43	420.5	61.1	117	2 G1H8U	Ig heavy chain V-1
44	420.5	61.1	121	2 S20783	Ig heavy chain V r
45	417	60.6	116	2 S31667	Ig heavy chain V r

#### ALIGNMENTS

##### RESULT 1

PH0952

Ig heavy chain V region (G6+ CIL-SMI) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

C/Accession: PH0952

R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kippes, T.J.

J. Exp. Med. 175, 983-991, 1992

A/Title: Evidence for somatic selection of natural autoantibodies.

A/Reference number: PH0952; PMID:92202880; PMID:1552291

A/Accession: PH0952

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-128 <MAR>

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-30/Region: framework 1

F/15-98/Domain: immunoglobulin homology <IMM>

F/31-35/Region: complementarity-determining 1

F/36-50/Region: framework 2

F/51-67/Region: complementarity-determining 2

F/68-98/Region: framework 3

F/99-116/Region: complementarity-determining 3

Query Match

Best Local Similarity 74.9%; Score 515; DB 2; Length 128;

Matches 103; Conservative 7; Mismatches 18; Indels 2; Gaps 1;

QY 1 QVQLVQSGAEAKKRGSSVKVSCKASGDTFNSPISWROAPGQGLBWMGGIPIFGSTKY 60

DB 1 QVQLVQSGAEAKKRGSSVKVSCKASGDTFNSPISWROAPGQGLBWMGGIPIFGSTKY 60

QY 61 AOKFQGRVITLADKSTAYMEISLSBDPAIYCCARQNGGMYEGPILPEPDALDIW 120

DB 61 AOKFQGRVITLADKSTAYMEISLSBDPAIYCCARQNGGMYEGPILPEPDALDIW 118

QY 121 GGGTMTVSS 130

DB 119 GGGTMTVSS 128

##### RESULT 2

C33548

Ig heavy chain V-1 region (783) - human

C/Species: Homo sapiens (man)

C/Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996

C/Accession: C33548

R/Kippes, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.

Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989

A/Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr.

A/Reference number: A33548; PMID:89345575; PMID:2503826

A/Accession: C33548

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tree  
 A/Molecule type: DNA  
 A/Residues: 1-133 <KIP>  
 A/Experimental source: the sequence was determined from the differentiated gene  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/15-98/Domain: immunoglobulin homology <IMV>

Query Match 74.1%; Score 509.5; DB 2; Length 133;  
 Best Local Similarity 72.7%; Pred. No. 4,76-39;  
 Matches 101; Conservative 10; Mismatches 13; Indels 15; Gaps 3;

QY 1 QVOLVSGAEAKKPGSSVSVKSCASGDTFNSPFIWVROAPGQGLEWNGIIPFGSTKY 60  
 DB 1 QVOLVSGAEVKKPGSSVSVKSCASGDTFNSPFIWVROAPGQGLEWNGIIPFGTANY 60  
 QY 61 AOKFGQRYVTITADGSTSTAYMELNSLRSEDTAYVYCAKGTGLGPISSGWY-----PNSD 114  
 DB 61 AOKFGQRYVTITADGSTSTAYMELNSLRSEDTAYVYCAKGTGLGPISSGWY-----PNSD 114  
 QY 116 ----ALDIWGQGTMTVSS 130  
 DB 115 YYYGMDVWGQGTMTVSS 133

## RESULT 3

S14683

Ig mu chain precursor, membrane-bound (clone 201) - human

C/Species: Homo sapiens (man)

C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999

C/Accession: S14683; S08047

R/Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.

Nucleic Acids Res. 18, 4278, 1990

A/Title: Complete nucleotide sequence of the membrane form of the human Igm heavy chain.

A/Reference number: S14683; MUID:90332450; PMID:2115996

A/Accession: S14683

A/Molecule type: mRNA

A/Residues: 1-627 &lt;PRI&gt;

A/Cross-references: EMBL:X17115; NID:933450; PID:CA34971.1; PID:933451

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: immunoglobulin; membrane protein

F/1-15/Domain: signal sequence; status predicted &lt;SIG&gt;

F/16-627/Product: Ig mu chain #status predicted &lt;MAT&gt;

F/34-117/Domain: immunoglobulin homology &lt;IMV&gt;

Query Match 74.1%; Score 509.5; DB 2; Length 627;  
 Best Local Similarity 72.7%; Pred. No. 2,56-38;  
 Matches 101; Conservative 10; Mismatches 13; Indels 15; Gaps 3;

QY 1 QVOLVSGAEAKKPGSSVSVKSCASGDTFNSPFIWVROAPGQGLEWNGIIPFGSTKY 60  
 DB 20 QVOLVSGAEVKKPGSSVSVKSCASGDTFNSPFIWVROAPGQGLEWNGIIPFGTANY 79  
 QY 61 AOKFGQRYVTITADGSTSTAYMELNSLRSEDTAYVYCAKGTGLGPISSGWY-----PNSD 115  
 DB 61 AOKFGQRYVTITADGSTSTAYMELNSLRSEDTAYVYCAKGTGLGPISSGWY-----PNSD 133  
 QY 116 ----ALDIWGQGTMTVSS 130  
 DB 134 YYYGMDVWGQGTMTVSS 152

## RESULT 4

PH0953

Ig heavy chain V region (G6+ CIL-SIC) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

C/Accession: PH0953

R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A/Title: Evidence for somatic selection of natural autoantibodies.

A/Reference number: PH0953; MUID:92202880; PMID:1552291

A/Accession: PH0953

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-135 &lt;MAR&gt;

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology &lt;IMV&gt;

F/31-35/Region: complementarity-determining 1

F/36-50/Region: complementarity-determining 2

F/51-67/Region: complementarity-determining 3

F/68-98/Region: complementarity-determining 3

F/99-123/Region: complementarity-determining 3

Query Match 73.0%; Score 502.5; DB 2; Length 135;  
 Best Local Similarity 75.2%; Pred. No. 26-38;  
 Matches 103; Conservative 8; Mismatches 17; Indels 9; Gaps 2;

QY 1 QVOLVSGAEAKKPGSSVSVKSCASGDTFNSPFIWVROAPGQGLEWNGIIPFGSTKY 60  
 DB 1 QVOLVSGAEVKKPGSSVSVKSCASGDTFNSPFIWVROAPGQGLEWNGIIPFGTANY 60  
 QY 61 AOKFGQRYVTITADGSTSTAYMELNSLRSEDTAYVYCAKGTGLGPISSGWY-----PNSD 113  
 DB 61 AOKFGQRYVTITADGSTSTAYMELNSLRSEDTAYVYCAKGTGLGPISSGWY-----PNSD 118  
 QY 114 PDALDIWGQGTMTVSS 130  
 DB 119 EDALDIWGQGTMTVSS 135

## RESULT 5

PH0959

Ig heavy chain V region (G6+ T-L26) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

C/Accession: PH0959

R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A/Title: Evidence for somatic selection of natural autoantibodies.

A/Reference number: PH0952; MUID:92202880; PMID:1552291

A/Accession: PH0959

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-116 &lt;MAR&gt;

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-30/Region: framework 1

F/31-35/Region: immunoglobulin homology &lt;IMV&gt;

F/36-50/Region: complementarity-determining 1

F/51-67/Region: complementarity-determining 2

F/68-98/Region: complementarity-determining 3

F/99-104/Region: complementarity-determining 3

Query Match 72.8%; Score 501; DB 2; Length 116;  
 Best Local Similarity 76.2%; Pred. No. 2,46-38;  
 Matches 99; Conservative 8; Mismatches 9; Indels 14; Gaps 2;

QY 1 QVOLVSGAEAKKPGSSVSVKSCASGDTFNSPFIWVROAPGQGLEWNGIIPFGSTKY 60  
 DB 1 QVOLVSGAEVKKPGSSVSVKSCASGDTFNSPFIWVROAPGQGLEWNGIIPFGTANY 60  
 QY 61 AOKFGQRYVTITADGSTSTAYMELNSLRSEDTAYVYCAKGTGLGPISSGWY-----PNSD 120  
 DB 61 AOKFGQRYVTITADGSTSTAYMELNSLRSEDTAYVYCAKGTGLGPISSGWY-----PNSD 106  
 QY 121 GQGTMTVSS 130  
 DB 107 GQGTMTVSS 116

## RESULT 6

PH0962



Ig heavy chain V region (G6+ T-142) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
 C/Accession: PH0962  
 R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
 J. Exp. Med. 175, 983-991, 1992  
 A>Title: Evidence for somatic selection of natural autoantibodies.  
 A/Reference number: PH0952; MUID:92202880; PMID:1552291  
 A/Accession: PH0962  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: DNA  
 A/Residues: 1-120 <MAR>  
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F:1-30/Region: framework 1  
 F:15-98/Domain: immunoglobulin homology <IMM>  
 F:31-35/Region: complementarity-determining 1  
 F:36-50/Region: framework 2  
 F:51-67/Region: complementarity-determining 2  
 F:68-98/Region: framework 3  
 F:99-108/Region: complementarity-determining 3

Query Match 72.4%; Score 498; DB 2; Length 120;  
 Best Local Similarity 77.7%; Pred. No. 4.6e-38;  
 Matches 101; Conservative 8; Mismatches 11; Indels 10; Gaps 3;

QY 1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPGGLEMMGGIIPFGSTKY 60  
 1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPGGLEMMGGIIPFGSTKY 60  
 DB 1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPGGLEMMGGIIPFGSTKY 60  
 QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPPDLDIW 120  
 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPPDLDIW 120  
 DB 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPPDLDIW 120  
 QY 121 GGGTMTVSS 130  
 121 GGGTMTVSS 130  
 DB 111 GGGTMTVSS 120

RESULT 7  
 PH0958  
 Ig heavy chain V region (G6+ CLJ-HUM) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
 C/Accession: PH0958  
 R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
 J. Exp. Med. 175, 983-991, 1992  
 A>Title: Evidence for somatic selection of natural autoantibodies.  
 A/Reference number: PH0952; MUID:92202880; PMID:1552291  
 A/Accession: PH0958  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: DNA  
 A/Residues: 1-122 <MAR>  
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F:1-30/Region: framework 1  
 F:15-98/Domain: immunoglobulin homology <IMM>  
 F:31-35/Region: complementarity-determining 1  
 F:36-50/Region: framework 2  
 F:51-67/Region: complementarity-determining 2  
 F:68-98/Region: framework 3  
 F:99-110/Region: complementarity-determining 3

Query Match 72.4%; Score 498; DB 2; Length 122;  
 Best Local Similarity 76.9%; Pred. No. 4.6e-38;  
 Matches 100; Conservative 8; Mismatches 14; Indels 8; Gaps 2;

QY 1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPGGLEMMGGIIPFGSTKY 60  
 1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPGGLEMMGGIIPFGSTKY 60  
 DB 1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPGGLEMMGGIIPFGSTKY 60  
 QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPPDLDIW 120  
 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPPDLDIW 120

DB 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARVFN-----PLF--FAVGMQVW 112  
 QY 121 GGGTMTVSS 130  
 DB 113 GGGTMTVSS 122

## RESULT 8

S46394  
 Ig heavy chain V region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
 C/Accession: S46394  
 R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.  
 J. Mol. Biol. 239, 68-78, 1994  
 A>Title: In vitro assembly of repertoires of antibody chains on the surface of phage by  
 A/Reference number: S46390; MUID:94254092; PMID:8196048  
 A/Accession: S46394  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-132 <Fig>  
 A/Cross-references: EMBL:231681; NID:9509788; PIDN:CA63486.1; PID:G1335147  
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.4%; Score 498; DB 2; Length 132;  
 Best Local Similarity 75.9%; Pred. No. 5.1e-38;  
 Matches 101; Conservative 11; Mismatches 17; Indels 4; Gaps 2;

QY 1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPGGLEMMGGIIPFGSTKY 60  
 1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPGGLEMMGGIIPFGSTKY 60  
 DB 1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPGGLEMMGGIIPFGSTKY 60  
 QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPPDLAL 117  
 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPPDLAL 117  
 DB 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPPDLAL 117  
 QY 118 DIMGGTMTVSS 130  
 118 DIMGGTMTVSS 130  
 DB 120 DIMGGTMTVSS 132

## RESULT 9

PH0961  
 Ig heavy chain V region (G6+ T-133) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
 C/Accession: PH0961  
 R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
 J. Exp. Med. 175, 983-991, 1992  
 A>Title: Evidence for somatic selection of natural autoantibodies.  
 A/Reference number: PH0952; MUID:92202880; PMID:1552291  
 A/Accession: PH0961  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: DNA  
 A/Residues: 1-119 <MAR>  
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F:1-30/Region: framework 1  
 F:15-98/Domain: immunoglobulin homology <IMM>  
 F:31-35/Region: complementarity-determining 1  
 F:36-50/Region: framework 2  
 F:51-67/Region: complementarity-determining 2  
 F:68-98/Region: framework 3  
 F:99-107/Region: complementarity-determining 3

Query Match 72.3%; Score 497.5; DB 2; Length 119;  
 Best Local Similarity 76.2%; Pred. No. 5e-38;  
 Matches 99; Conservative 9; Mismatches 11; Indels 11; Gaps 2;

QY 1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPGGLEMMGGIIPFGSTKY 60  
 1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPGGLEMMGGIIPFGSTKY 60

Db 1 QVOLVOSGAELKPKGSSVKVSCKASGDTFSSVAISWRQAPGQGLEWGGIIPFGTANY 60  
 QY 61 AOKFOGRVTMTADGSTSTAYMEINLSRSEDTAIYYCARQONGWEGPLLEPRDALDI 120  
 Db 61 AOKFOGRVTMTADGSTSTAYMEINLSRSEDTAIYYCARQONGWEGPLLEPRDALDI 120  
 QY 121 GGGTMTVSS 130  
 Db 110 GGGTMTVSS 119

## RESULT 10

PH0954

Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

C/Accession: PH0954

R/Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A/Title: Evidence for somatic selection of natural autoantibodies.

A/Reference number: PH0952; PMID:92202880; PMID:1552291

A/Accession: PH0954

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-132 &lt;MAR&gt;

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-30/Region: framework 1

F/15-98/Domain: immunoglobulin homology &lt;IMM&gt;

F/31-35/Region: complementarity-determining 1

F/36-50/Region: complementarity-determining 2

F/51-67/Region: complementarity-determining 3

F/68-98/Region: framework 3

F/99-120/Region: complementarity-determining 3

Query Match 72.1%; Score 496; DB 2; Length 132;  
 Best Local Similarity 71.4%; Pred. No. 7.7e-38;  
 Matches 100; Conservative 10; Mismatches 12; Indels 18; Gaps 3;  
 QY 1 QVOLVOSGAELKPKGSSVKVSCKASGDTFSSVAISWRQAPGQGLEWGGIIPFGTANY 60  
 Db 1 QVOLVOSGAELKPKGSSVKVSCKASGDTFSSVAISWRQAPGQGLEWGGIIPFGTANY 60  
 QY 61 AOKFOGRVTMTADGSTSTAYMEINLSRSEDTAIYYCARQONGWEGPLLEPR 114  
 Db 61 AOKFOGRVTMTADGSTSTAYMEINLSRSEDTAIYYCARQONGWEGPLLEPR 114  
 QY 115 D-----ALDINGGGTMTVSS 130  
 Db 113 NYYTGMVWGGTMTVSS 132

## RESULT 11

PH0960

Ig heavy chain V region (G6+ T-L30) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

C/Accession: PH0960

R/Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A/Title: Evidence for somatic selection of natural autoantibodies.

A/Reference number: PH0952; PMID:92202880; PMID:1552291

A/Accession: PH0960

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-136 &lt;MAR&gt;

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-30/Region: framework 1

F/15-98/Domain: immunoglobulin homology &lt;IMM&gt;

F/31-35/Region: complementarity-determining 1

F/36-50/Region: complementarity-determining 2

F/68-98/Region: framework 3  
 F/99-124/Region: complementarity-determining 3

Query Match

Best Local Similarity 72.1%; Score 496; DB 2; Length 136;

Matches 99; Conservative 10; Mismatches 11; Indels 26; Gaps 2;

QY 1 QVOLVOSGAELKPKGSSVKVSCKASGDTFSSVAISWRQAPGQGLEWGGIIPFGTANY 60  
 Db 1 QVOLVOSGAELKPKGSSVKVSCKASGDTFSSVAISWRQAPGQGLEWGGIIPFGTANY 60  
 QY 61 AOKFOGRVTMTADGSTSTAYMEINLSRSEDTAIYYCARQONGWEGPLLEPR 104  
 Db 61 AOKFOGRVTMTADGSTSTAYMEINLSRSEDTAIYYCARQONGWEGPLLEPR 104  
 QY 105 YEGPLLEPRDALDINGGGTMTVSS 130  
 Db 121 Y-----GMDVWGGTMTVSS 136

## RESULT 12

A33548

Ig heavy chain V-1 region (NET) - human

C/Species: Homo sapiens (man)

C/Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996

C/Accession: A33548; PH0956

R/Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffly, S.; Chen, P.P.; Carson, D.A.

Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989

A/Title: Developmentally restricted immunoglobulin heavy chain variable region gene ex

A/Reference number: A33548; PMID:89345575; PMID:2503826

A/Accession: A33548

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-129 &lt;KIP&gt;

R/Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A/Title: Evidence for somatic selection of natural autoantibodies.

A/Reference number: PH0952; PMID:92202880; PMID:1552291

A/Accession: PH0956

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-129 &lt;MAR&gt;

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-30/Region: framework 1

F/15-98/Domain: immunoglobulin homology &lt;IMM&gt;

F/31-35/Region: complementarity-determining 1

F/36-50/Region: complementarity-determining 2

F/51-67/Region: complementarity-determining 3

F/68-98/Region: framework 3

F/99-117/Region: complementarity-determining 3

Query Match 71.9%; Score 494.5; DB 2; Length 129;  
 Best Local Similarity 73.4%; Pred. No. 1e-37;  
 Matches 102; Conservative 8; Mismatches 10; Indels 19; Gaps 4;  
 QY 1 QVOLVOSGAELKPKGSSVKVSCKASGDTFSSVAISWRQAPGQGLEWGGIIPFGTANY 60  
 Db 1 QVOLVOSGAELKPKGSSVKVSCKASGDTFSSVAISWRQAPGQGLEWGGIIPFGTANY 60  
 QY 61 AOKFOGRVTMTADGSTSTAYMEINLSRSEDTAIYYCARQONGWEGPLLEPR 111  
 Db 61 AOKFOGRVTMTADGSTSTAYMEINLSRSEDTAIYYCARQONGWEGPLLEPR 111  
 QY 112 PRPDALDINGGGTMTVSS 130  
 Db 116 -----FDYMGGTLVTVSS 129

## RESULT 13

PH0957

Ig heavy chain V region (G6+ CLL-BRA) - human (fragment)

C/Species: Homo sapiens (man)

C:Date: 17-Apr1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C:Accession: PH0957  
R:Martin, T., Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
U. Exp. Med. 175, 983-991, 1992  
A:Title: Evidence for somatic selection of natural autoantibodies.  
A:Reference numbers: PH0952; PMID:92202880; PMID:1552291  
A:Accession: PH0957  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-125 <MAR>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-30/Region: framework 1  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:36-50/Region: framework 2  
F:51-67/Region: complementarity-determining 2  
F:68-98/Region: framework 3  
F:99-113/Region: complementarity-determining 3

Query Match	71.3%;	Score 490.5;	DB 2;	Length 125;
Best Local Similarity	71.5%;	Pred. No. 2.3e-37;		
Matches 98;	Conservative 10;	Mismatches 10;	Indels 19;	Gaps 3;

**Qy**

1 QVQLVQSGAEAKKPGSSVKVSKASGDTFNSFIISWRQAPEGLEMMGGIIIPFGSTKY 60  
||| ||| ||| ||| ||| : : ||| ||| ||| ||| ||| : |  
||| ||| ||| ||| ||| ||| : : ||| ||| ||| ||| ||| : |

**Db**

1 QVQLVQSGAEVKKPGSSVKVSKASGDTFSSYAINWVRQAPEGLEMMGGIIPFGTANY 60  
||| ||| ||| ||| ||| ||| : : ||| ||| ||| ||| ||| : |  
||| ||| ||| ||| ||| ||| ||| : : ||| ||| ||| ||| ||| : |

```

Oy      61 AQRQGRVTMTADGGSTSTAYMELNSRSEDAIYYCARQ--ONG----GWYEGPLLEPR 113
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 AQRQGRVTITADESTNTAYMELSSLRSEDAVYYCARDCSGGSCYFWGMF----- 112

```

QY	114	PDALDIWGQGTMTVSS	130
		:	
Db	113	----DPWGQGTLYTVSS	125

## RESULT 14

Ig heavy chain V region (GG + CLL-AND) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
 C/Accession: PH0955  
 R/Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.  
 J. Exp. Med. 175, 983-991, 1992  
 A>Title: Evidence for somatic selection of natural antibodies.  
 A/Reference number: PH0952; M0ID:92202880; PMID:1552291

A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>  
F;31-35/Region: complementarity-determining 1

F;51-67/Region: complementarity-determining 2  
F;68-98/Region: framework 3  
F;99-117/Region: complementarity-determining 3

Query Match	Score
71.0%	488.5

Query Match	71.0%;	Score 488.5;	DB 2;	Length 127;
Best Local Similarity	71.0%;	Pred. No. 3.5e-37;		
Matches 98; Conservative	10;	Mismatches 11;	Indels 19;	Gaps 2

```
QY      1 QVQLVSGAEAKKPGSSVKVSCASGDTFNSFPISWVRQAPEGLEMMGGIIPFGSTKY    60  
       ||||| | : : ||||| | : ||||| |  
DB      1 QVQLVSGAEVKKPQGSVKVSCASGDTFSYALSWVRQAPEGLEMMGGIIPIFYTANY    60
```

```

QY      61 AOKFOGRVTMTADGSTSTAYMELNLSRESDTAIYYCARQONG-----WYEGPLIEP 112
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 AOKFOGRVTMTADESTSTAYMELNLSRESDTAIYYCARVSIPOVQHHYYYYY----- 113

```

QY	113	RPDALDIWGQGTMTVSS	130
		: : :	
Db	114	---MDVWGKGTVTVSS	127

RESULT 15  
B33548

C:Species: Homo sapiens (man)  
C:Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996

R. Kippes, T. J. Tomhave, E. J. Pratt, L. F. J. Duffy, S. Chen, P. V. Caisson, U. A. Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989

A:Reference number: A33548; PMID:89345575; PMID:2503826  
A:Accession: B33548  
A:Status: Unpublished, nucleic acid sequence not shown, not compared with consensual

A. Molecule type: DNA  
A. Residues: 1-126 <KIP>  
A. Experimental source: the sequence was determined from the differentiated gene

C:Keywords: heterotetramer; immunoglobulin C:Suprafamily: immunoglobulin V region; immunoglobulin E-15-98/Domains: immunoglobulin homologs<IMM>

Query Match	70.6%	Score 486;	DB 2;	Length 146;
Best Local Similarity	71.5%;	Pred. No. 5.8e-37;		
Matches 98;	Conservative 9;	Mismatches 12;	Indels 18;	Caps 2;

```
QY      1 QVQLVQSGLAEKKKPGSSVKVSKCSKASGDTFNSPISWVQAQPGLGLEMMGGIIPIIGSTIKY 60
        |||||
DB       1 QVQLVQSGLAEVKKKPGSSVKVSKCSKASGDTFSSIAISWVAQAPGQGLEMMGGIIPITGTANY 60
```

```

Oy      61 AQAQFGKRVMTADGSGTSTAYMELNSLRSEDAIYYCARQNGG-----WEGPLLEPR 113
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 AQAQFGKRVITADESTSTAYMELSSLRSEDAIYYCARVSLFGVQVHHYYYY----- 112

```

```
QY      114 PDALDIWGQGTMTVSS 130
          :|:| | | | | | |
Db      113 ---MDVWGLGTTVTSS 126
```

Search completed: December 30, 2003, 11:03:13  
Job time : 13.4614 secs

```

Db      1  QVQLVSGAEVKKRGSSSVKSCSKASGDTFSSVAISWVROAPGQGLEWMGGIIPFGTANY 60
QY      61  AOKFGGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGMYEPPLEPPDALDIY 120
Db      61  AOKFGGRVTMTADGSTSTAYMELNSLRSEDTAVYYCARGYY-----MDVW 109
QY      121  GQGTMTVSS 130
Db      110  GQGTMTVSS 119

RESULT 10
PH0954
Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C/Accession: PH0954
R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A/Title: Evidence for somatic selection of natural autoantibodies.
A/Reference number: PH0952; MUID:92202880; PMID:1552291
A/Accession: PH0954
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-132 <MAR>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-30/Region: framework 1
F/15-98/Domain: immunoglobulin homology <IMM>
F/31-35/Region: complementarity-determining 1
F/36-50/Region: framework 2
F/51-67/Region: complementarity-determining 2
F/68-98/Region: framework 3
F/99-120/Region: complementarity-determining 3

Query Match      72.1%; Score 496; DB 2; Length 132;
Best Local Similarity 71.4%; Pred. No. 7.7e-38;
Matches 100; Conservative 10; Mismatches 12; Indels 18; Gaps 3;

QY      1  QVQLVSGAEVKKRGSSSVKSCSKASGDTFNSPISWVROAPGQGLEWMGGIIPFGSTKY 60
Db      1  QVQLVSGAEVKKRGSSSVKSCSKASGDTFSSVAISWVROAPGQGLEWMGGIIPFGTANY 60
QY      61  AOKFGGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQON-----CGWEGGLEPPR 114
Db      61  AOKFGGRVTMTADGSTSTAYMELNSLRSEDTAVYYCARPHASIDDFWSGY-----P 112
QY      115  D----ALDIWQGTMTVSS 130
Db      113  NYYYGMDVWGQGTMTVSS 132

RESULT 11
PH0960
Ig heavy chain V region (G6+ T-L30) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C/Accession: PH0960
R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A/Title: Evidence for somatic selection of natural autoantibodies.
A/Reference number: PH0952; MUID:92202880; PMID:1552291
A/Accession: PH0960
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-136 <MAR>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-30/Region: framework 1
F/15-98/Domain: immunoglobulin homology <IMM>
F/31-35/Region: complementarity-determining 1
F/36-50/Region: framework 2
F/51-67/Region: complementarity-determining 2

```

```

F/68-98/Region: framework 3
F/99-124/Region: complementarity-determining 3

Query Match      72.1%; Score 496; DB 2; Length 136;
Best Local Similarity 67.8%; Pred. No. 7.9e-38;
Matches 99; Conservative 10; Mismatches 11; Indels 26; Gaps 2;

QY      1  QVQLVSGAEVKKRGSSSVKSCSKASGDTFNSPISWVROAPGQGLEWMGGIIPFGSTKY 60
Db      1  QVQLVSGAEVKKRGSSSVKSCSKASGDTFSSVAISWVROAPGQGLEWMGGIIPFGTANY 60
QY      61  AOKFGGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQON-----CGW 104
Db      61  AOKFGGRVTMTADGSTSTAYMELNSLRSEDTAVYYCARGRTRVSVSTLYDSSGYDFPSGY 120
QY      105  YEGPLEPPDALDIWQGTMTVSS 130
Db      121  Y-----GMDVWGQGTMTVSS 136

RESULT 12
A33548
Ig heavy chain V-1 region (NB1) - human
C/Species: Homo sapiens (man)
C/Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C/Accession: A33548; PH0956
R/Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A/Title: Developmentally restricted immunoglobulin heavy chain variable region gene exp
A/Reference number: A33548; MUID:89345575; PMID:2503826
A/Accession: A33548
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-129 <KIP>
R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A/Title: Evidence for somatic selection of natural autoantibodies.
A/Reference number: PH0952; MUID:92202880; PMID:1552291
A/Accession: PH0956
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-129 <MAR>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-30/Region: framework 1
F/15-98/Domain: immunoglobulin homology <IMM>
F/31-35/Region: complementarity-determining 1
F/36-50/Region: framework 2
F/51-67/Region: complementarity-determining 2
F/68-98/Region: framework 3
F/99-117/Region: complementarity-determining 3

Query Match      71.9%; Score 494.5; DB 2; Length 129;
Best Local Similarity 73.4%; Pred. No. 1e-37;
Matches 102; Conservative 8; Mismatches 10; Indels 19; Gaps 4;

QY      1  QVQLVSGAEVKKRGSSSVKSCSKASGDTFNSPISWVROAPGQGLEWMGGIIPFGSTKY 60
Db      1  QVQLVSGAEVKKRGSSSVKSCSKASGDTFSSVAISWVROAPGQGLEWMGGIIPFGTANY 60
QY      61  AOKFGGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONG-----WYEGPLE 111
Db      61  AOKFGGRVTMTADGSTSTAYMELNSLRSEDTAVYYCAR-----GPRLLADVLLWF-GEISE 115
QY      112  PRPDALDIWQGTMTVSS 130
Db      116  -----FDYWGQGTMTVSS 129

RESULT 13
PH0957
Ig heavy chain V region (G6+ CLL-BRA) - human (fragment)
C/Species: Homo sapiens (man)

```

```

Query Match      72.4%; Score 498; DB 2; Length 122;
Best Local Similarity 76.9%; Prid. No. 4,6e-38;
Matches 100; Conservative 8; Mismatches 14; Indels 8; Gaps 2;

      1 QVQLVSGAELKAPKPGSSVYKSCVASGDTNFPISWVRAQPGGLEEMGGLIPPESTCY 60
      1 QVQLVSGAEVKKPQGSVKVSCVASGDTSSVAISVRAPQGLEEMGGLIPPESTIY 60
      61 AAKFQQRVMTADGSGTAYMEINLSRSDTALYYCARQONGWYEGPLLEPRPDALDI 120
      |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

	Query Match	72.3%	Score 497.5;	DB 2;	Length 119;
	Best Local Similarity	76.2%;	Pred. No. Se-38;		
	Matches	99;	Conservative	9;	Mismatches 11; Indels 11; Gaps 2;
Dy		1 QVQLVSGAELAKPPSSYKVCCKAGDPTFNSPRLISWNRQARPGCLGIEWMGGITLPFGSKTY			60          ::: :

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A/Molecule type: DNA  
 A/Residues: 1-133 <RIP>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMV>

Query Match 74.1%; Score 509.5; DB 2; Length 133;  
 Best Local Similarity 72.7%; Pred. No. 4.7e-39;  
 Matches 101; Conservative 10; Mismatches 13; Indels 15; Gaps 3;

OY 1 QVOLVSGAEAKKPGSSSVKSCASGDTFNSPISWROAPGQGLEMMGIIPIFGSTKY 60  
 |||||  
 1 QVOLVSGAEVKKPGSSSVKSCASGDTFSSVAISWROAPGQGLEMMGIIPIFGTANY 60  
 |||||  
 OY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCAR-----QONGWYEGPLLEPRD 115  
 |||||  
 61 AOKFQGRVTITADESTSTAYMELSLRSEDTAYYCAKTGILGYPSSGMY-----PNSD 114  
 |||||  
 OY 116 ----ALDIWGQGTMTVSS 130  
 :|||  
 DB 115 YYYGMDVMWGQGTMTVSS 133

## RESULT 3

Ig mu chain precursor, membrane-bound (clone 201) - human

C/Species: Homo sapiens (man)

C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999

C/Accession: S14683; S08047

R/Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.

Nucleic Acids Res. 19, 4278, 1990

A/Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.

A/Reference number: S14683; MUID:90332450; PMID:2115996

A/Accession: S14683

A/Molecule type: mRNA

A/Residues: 1-627 <PPI>

C/COB8-reference: EMBL:X17115; NID:g33450; PIDN:CAA4971.1; PID:g33451

C/Supertfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: immunoglobulin; membrane protein

F:1-15/Domain: signal sequence #status predicted <SIG>

F:16-627/Product: Ig mu chain #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMV>

Query Match 74.1%; Score 509.5; DB 2; Length 627;  
 Best Local Similarity 72.7%; Pred. No. 2.5e-38;  
 Matches 101; Conservative 10; Mismatches 13; Indels 15; Gaps 3;

OY 1 QVOLVSGAEAKKPGSSSVKSCASGDTFNSPISWROAPGQGLEMMGIIPIFGSTKY 60  
 |||||  
 20 QVOLVSGAEVKKPGSSSVKSCASGDTFSSVAISWROAPGQGLEMMGIIPIFGTANY 79  
 |||||  
 OY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCAR-----QONGWYEGPLLEPRD 115  
 |||||  
 60 AOKFQGRVTITADESTSTAYMELSLRSEDTAYYCAKTGILGYPSSGMY-----PNSD 133  
 |||||  
 OY 116 ----ALDIWGQGTMTVSS 130  
 :|||  
 DB 134 YYYGMDVMWGQGTMTVSS 152

## RESULT 4

Ig heavy chain V region (G6+ CLF-SIC) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

C/Accession: PH0953

R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A/Title: Evidence for somatic selection of natural autoantibodies.

A/Reference number: PH0952; MUID:92202880; PMID:1552291

A/Accession: PH0953

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-135 <MAR>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMV>

F:11-35/Region: complementarity-determining 1

F:16-50/Region: framework 2

F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3

F:99-123/Region: complementarity-determining 3

Query Match 73.0%; Score 502.5; DB 2; Length 135;  
 Best Local Similarity 75.2%; Pred. No. 2e-38;  
 Matches 103; Conservative 8; Mismatches 17; Indels 9; Gaps 2;

OY 1 QVOLVSGAEAKKPGSSSVKSCASGDTFNSPISWROAPGQGLEMMGIIPIFGSTKY 60  
 |||||  
 1 QVOLVSGAEVKKPGSSSVKSCASGDTFSSVAISWROAPGQGLEMMGIIPIFGTANY 60  
 |||||  
 OY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONG-----GWYEGPLLEPR 113  
 |||||  
 61 AOKFQGRVTITADESTSTAYMELSLRSEDTAYYICAR--NGYCGDCYSRWELLRFDS 118  
 |||||  
 OY 114 PDALDIWGQGTMTVSS 130  
 |||||  
 DB 119 EDAPDIMGQGTMTVSS 135

## RESULT 5

Ig heavy chain V region (G6+ T-L26) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

C/Accession: PH0959

R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A/Title: Evidence for somatic selection of natural autoantibodies.

A/Reference number: PH0952; MUID:92202880; PMID:1552291

A/Accession: PH0959

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMV>

F:31-35/Region: complementarity-determining 1

F:36-50/Region: framework 2

F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3

F:99-104/Region: complementarity-determining 3

Query Match 72.8%; Score 501; DB 2; Length 116;  
 Best Local Similarity 76.2%; Pred. No. 2.4e-38;  
 Matches 99; Conservative 8; Mismatches 9; Indels 14; Gaps 2;

OY 1 QVOLVSGAEAKKPGSSSVKSCASGDTFNSPISWROAPGQGLEMMGIIPIFGSTKY 60  
 |||||  
 1 QVOLVSGAEVKKPGSSSVKSCASGDTFSSVAISWROAPGQGLEMMGIIPIFGTANY 60  
 |||||  
 OY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRDADIW 120  
 |||||  
 61 AOKFQGRVTITADESTSTAYMELSLRSEDTAYYICARQNG--WF-----DPM 106  
 |||||  
 OY 121 GQGTMTVSS 130  
 |||||  
 DB 107 GQGTMTVSS 116

## RESULT 6

PH0962

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 30, 2003, 10:47:09 : Search time 12.4614 Seconds  
(without alignments)  
1003.251 Million cell updates/sec

Title: US-09-674-752-23

Perfect score: 688

Sequence: 1 QVQVVGSGAEKKRGGSSVKV.....EPRPDALDINGQGMVTSS 130

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:\*

1: PIR1:.\*  
2: PIR2:.\*  
3: PIR3:.\*  
4: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	515	74.9	128	2	PH0952 Ig heavy chain V r
2	509.5	74.1	133	2	C33548 Ig heavy chain V-1
3	509.5	74.1	627	2	S14683 Ig mu chain precur
4	502.5	73.0	135	2	PH0953 Ig heavy chain V r
5	501	72.8	116	2	PH0959 Ig heavy chain V r
6	498	72.4	120	2	PH0962 Ig heavy chain V r
7	498	72.4	122	2	PH0958 Ig heavy chain V r
8	498	72.4	132	2	S46394 Ig heavy chain V r
9	497.5	72.3	119	2	PH0961 Ig heavy chain V r
10	496	72.1	132	2	PH0954 Ig heavy chain V r
11	496	72.1	136	2	PH0960 Ig heavy chain V r
12	494.5	71.9	129	2	A33548 Ig heavy chain V-1
13	490.5	71.3	125	2	PH0957 Ig heavy chain V r
14	488.5	71.0	127	2	PH0955 Ig heavy chain V r
15	486	70.6	126	2	B33548 Ig heavy chain V-1
16	481	69.9	135	2	B32274 Ig heavy chain pre
17	456.5	66.4	113	2	PH1663 Ig heavy chain V r
18	452.5	65.8	121	2	A49590 Ig heavy chain V r
19	452	65.7	108	2	PH1664 Ig heavy chain V r
20	451	65.6	98	2	S26915 Ig heavy chain V r
21	451	65.6	116	2	S31698 Ig heavy chain pre
22	451	65.6	116	2	S36261 Ig heavy chain V r
23	451	65.6	123	2	S44108 Ig heavy chain V-D
24	450	65.4	124	2	S19665 Ig heavy chain V r
25	450	65.4	136	2	S31600 Ig heavy chain V r
26	447.5	65.0	122	2	B49590 Ig heavy chain V r
27	447	65.0	98	2	S24680 Ig heavy chain V1
28	447	65.0	119	2	S44106 Ig heavy chain V-D
29	446.5	64.9	142	2	A32483 Ig heavy chain V r

30	446	64.8	118	2	S36265 Ig heavy chain V r
31	442.5	64.3	122	2	C49590 Ig heavy chain V r
32	442	64.2	171	2	S23623 Ig heavy chain V r
33	437.5	63.6	160	2	PL0105 anti-PR2 erythrocy
34	436.5	63.4	109	2	PH1671 Ig heavy chain V r
35	435.5	63.3	129	2	S36260 Ig heavy chain V r
36	435	63.2	135	2	S49530 anti-5m antibody V
37	434	63.1	98	2	S46463 Ig heavy chain V1
38	430.5	62.6	127	2	S34014 Ig heavy chain V r
39	428.5	62.3	129	2	S46393 Ig heavy chain V r
40	428	62.2	98	2	A30523 Ig heavy chain V-1
41	426	61.9	97	2	PH0870 Ig heavy chain V r
42	422.5	61.4	122	2	S36271 Ig heavy chain V r
43	420.5	61.1	117	1	G1HUB3 Ig heavy chain V-1
44	420.5	61.1	121	2	S20783 Ig heavy chain V r
45	417	60.6	116	2	S31667 Ig heavy chain V r

#### ALIGNMENTS

```
RESULT 1
PH0952
Ig heavy chain V region (G6+ CTL-SWI) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0952
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kippes, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0952
A:Status: nucleic acid sequence not shown
A:Residues: 1-128 <MAR>
A:Molecule type: DNA
C:Keywords: heterotetramer; immunoglobulin
F:11-30/Region: framework 1
F:115-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-116/Region: complementarity-determining 3

Query Match 74.9%; Score 515; DB 2; Length 128;
Best Local Similarity 79.2%; Pred. No. 1.4e-39;
Matches 103; Conservative 7; Mismatches 18; Indels 2; Gaps 1;

QY 1 QVQVVGSGAEKKRGGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGCIPIFGSTKY 60
DB 1 QVQVVGSGAEKKRGGSSVKVSCKASGDTFNSFPISWVRQAPGQGLEWMGCIPIFGTANY 60
QY 61 AOKFGQRTMTADGSTTAAYVELNSLRSEDTAIYYCARQOQGVGEGLLEPRPDALDIW 120
DB 61 AOKFGQRTMTADGSTTAAYVELNSLRSEDTAIYYCARQOQGVGEGLLEPRPDALDIW 118
QY 121 GQGTMTVSS 130
DB 119 GQGTMTVSS 128

RESULT 2
C33548
Ig heavy chain V-1 region (783) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: C33548
R:Kippes, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene exp
A:Reference number: A33548; MUID:89345575; PMID:2503826
A:Accession: C33548
```

```
US-09-880-748-1190
; Sequence 1190, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 1190
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1190

Query Match      73.9%; Score 525.5; DB 11: Length 255;
Best Local Similarity 78.0%; Pred. No. 2,4e-42;
Matches 103; Conservative 8; Mismatches 18; Indels 3; Gaps 2;

QY      1 0VQLLOSATEVKKPKGASMKVSCMASGYPTSYDISMVRQAPGQGLEMMGMISYSGNTDY 60
DB      1 0VQLVSGAEVKKPKGASVAVSCASGYTTTSTGISMVRQAPGQGLEMMGMISAVNGNTNY 60
QY      61 AOKFOGRVTMTTDTSRRTAYMELRSLRSDDTAVVYCCARDGGGAYEDVWSGEYPEYYAM 120
DB      61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVVYCCARD--PSPYVDILTGYFLPY--MD 117
QY      121 VWGQGTIVTVSS 132
DB      118 VWGKGTLTVSS 129

RESULT 3
US-10-041-860-31
; Sequence 31, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 127
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-31

Query Match      73.8%; Score 524.5; DB 12: Length 127;
Best Local Similarity 78.9%; Pred. No. 1,4e-42;
Matches 105; Conservative 6; Mismatches 15; Indels 7; Gaps 3;
```

```
QY      1 0VQLLOSATEVKKPKGASMKVSCMASGYPTSYDISMVRQAPGQGLEMMGMISYSGNTDY 60
DB      1 0VQLVSGAEVKKPKGASVAVSCASGYTTTSTGISMVRQAPGQGLEMMGMISAVNGNTNY 60
QY      61 AOKFOGRVTMTTDTSRRTAYMELRSLRSDDTAVVYCCARDGGGAYEDVWSGEY--PEYYAM 119
DB      61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVVYCCARD---HYYD--SSDYLYYYGL 114
QY      120 DWGQGTIVTVSS 132
DB      115 DWGQGTIVTVSS 127

RESULT 4
US-10-041-860-243
; Sequence 243, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 243
; LENGTH: 127
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-243

Query Match      73.8%; Score 524.5; DB 12: Length 127;
Best Local Similarity 78.9%; Pred. No. 1,4e-42;
Matches 105; Conservative 6; Mismatches 15; Indels 7; Gaps 3;

QY      1 0VQLLOSATEVKKPKGASMKVSCMASGYPTSYDISMVRQAPGQGLEMMGMISYSGNTDY 60
DB      1 0VQLVSGAEVKKPKGASVAVSCASGYTTTSTGISMVRQAPGQGLEMMGMISAVNGNTNY 60
QY      61 AOKFOGRVTMTTDTSRRTAYMELRSLRSDDTAVVYCCARDGGGAYEDVWSGEY--PEYYAM 119
DB      61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVVYCCARD---HYYD--SSDYLYYYGL 114
QY      120 DWGQGTIVTVSS 132
DB      115 DWGQGTIVTVSS 127

RESULT 5
US-10-041-860-325
; Sequence 325, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Peng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; FILE REFERENCE: ABGENIX.051A
```





CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumor necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.

SO Sequence 257 AA:

Query Match 71.5%; Score 508.5; DB 23; Length 257;  
 Best Local Similarity 73.7%; Pred. No. 2.1e-39;  
 Matches 98; Conservative 13; Mismatches 19; Indels 3; Gaps 2;

OY 1 QVOLLQSATVEKKPGASMKVSCMASGYPTSYDISWVRQAPQGLEMMGMIISYGNTDY 60  
 DB 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPQGLEMMGMIISYNGNTNY 60  
 OY 61 AOKFGQRYMTTDTSRRTAYMELRLSRSDPTAVVYCARDDGGGAYE--DVMSGEYPEYYA 119  
 DB 61 AOKLQGRVMTTDTSTSTAYMELRLSRSDPTAVVYCAR--GRLSYDILTGYYARDYQGM 118  
 OY 120 DVMSGQGTIVTVSS 132  
 DB 119 DVMSGRTMTVTSN 131

RESULT 15  
 ID ABP45394 standard; Protein; 254 AA.

AC ABP45394;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1405.

KM Blys: B Lymphocyte stimulator; TNF superfamily; human; cytotatic;  
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 DR WPI; 2002-114799/15.

XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 PS Claim 1; Page 2079-2080; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumor necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.

SO Sequence 254 AA:

Query Match 71.4%; Score 508; DB 23; Length 254;  
 Best Local Similarity 74.6%; Pred. No. 2.3e-39;  
 Matches 100; Conservative 12; Mismatches 14; Indels 8; Gaps 3;

OY 1 QVOLLQSATVEKKPGASMKVSCMASGYPTSYDISWVRQAPQGLEMMGMIISYGNTDY 60  
 DB 1 EVQLVQSGAEVKKPGSSVVSCKASGYTFTSYGISWVRQAPQGLEMMGMIISYNGNTNY 60  
 OY 61 AOKFGQRYMTTDTSRRTAYMELRLSRSDPTAVVYCARDDGGGAYE--DVMSGEYPEYYA 118  
 DB 61 AOKLQGRVMTTDTSTSTAYMELRLSRSDPTAVVYCAR---AREYDILTGYY-HHDA 114  
 OY 119 DVMSGQGTIVTVSS 132  
 DB 115 FDIWKGRTIVTVSS 128

Search completed: December 30, 2003, 10:54:30  
 Job time : 43.5464 secs

CC the antibodies and fragments of the antibodies described in the method  
CC of the invention.  
XX  
SQ Sequence 251 AA;  
Query Match 71.8%; Score 510.5; DB 23; Length 251;  
Best Local Similarity 76.5%; Pred. No. 1.3e-39;  
Matches 101; Conservative 7; Mismatches 17; Indels 7; Gaps 2;  
QY 1 QVQLQSGATPEVKKPKGASMKVSCNAGSYPTSYDISWVRQAPGGGLEMMGMISITSGNTDY 60  
DB 1 QVQLVSGAEVKKPKGASVKKVSCASGYFTSYGISWVRQAPGGGLEMMGMISITSGNTDY 60  
QY 61 AOKFQGRVTMTTDSRTAYMELRSRSDDTAVYCARGGGAYEDVWSGEYPERYAMD 120  
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSRSDDTAVYCAR-----MEYDILGYGGYF--D 113  
QY 121 WVGQGTIVTVSS 132  
DB 114 WVGQGTIVTVSS 125  
RESULT 13  
ID ABP45441 standard; Protein; 259 AA.  
XX  
AC ABP45441;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 1452.  
XX  
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN MO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US19110.  
XX  
PR 16-JUN-2000; 2000US-212210P.  
PR 17-OCT-2000; 2000US-240816P.  
PR 16-MAR-2001; 2001US-276248P.  
PR 21-MAR-2001; 2001US-277379P.  
PR 25-MAY-2001; 2001US-293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX  
DR WPI; 2002-114799/15.  
XX  
PT Antibodies against B lymphocyte stimulating polypeptides, useful for  
XX the diagnosis and treatment of cancers and immune disorders -  
XX  
XX Claim 1; Page 2135-2136; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in

CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and actively such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent  
CC the antibodies and fragments of the antibodies described in the method  
CC of the invention.  
XX  
SQ Sequence 259 AA;  
Query Match 71.8%; Score 510.5; DB 23; Length 259;  
Best Local Similarity 73.9%; Pred. No. 1.4e-39;  
Matches 99; Conservative 12; Mismatches 20; Indels 3; Gaps 2;  
QY 1 QVQLQSGATPEVKKPKGASMKVSCNAGSYPTSYDISWVRQAPGGGLEMMGMISITSGNTDY 60  
DB 1 QVQLVSGAEVKKPKGASVKKVSCASGYFTSYGISWVRQAPGGGLEMMGMISITSGNTDY 60  
QY 61 AOKFQGRVTMTTDSRTAYMELRSRSDDTAVYCARGGGAYEDVWSGEY--PERYA 118  
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSRSDDTAVYCARGGGAYEDVWSGEY--PERYA 119  
QY 119 MDVWQGTIVTVSS 132  
DB 120 FDIWGRGTIVTVSS 133  
RESULT 14  
ID ABP45343 standard; Protein; 257 AA.  
XX  
AC ABP45343;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 1354.  
XX  
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN MO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US19110.  
XX  
PR 16-JUN-2000; 2000US-212210P.  
PR 17-OCT-2000; 2000US-240816P.  
PR 16-MAR-2001; 2001US-276248P.  
PR 21-MAR-2001; 2001US-277379P.  
PR 25-MAY-2001; 2001US-293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX  
DR WPI; 2002-114799/15.  
XX  
PT Antibodies against B lymphocyte stimulating polypeptides, useful for  
XX the diagnosis and treatment of cancers and immune disorders -  
XX  
XX Claim 1; Page 2018-2019; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to

Db 61 AOKLGRVTMTDTSTSTAYMELRSLRSDPTAVVYCAR---CGNV-DILTG---YIIGA 112  
 QY 119 MDVWGQGTIVTVSS 132  
 Db 113 FDIWGQGTIVTVSS 126  
 RESULT 11  
 ABP45565 standard; Protein; 257 AA.  
 ID ABP45565 standard; Protein; 257 AA.  
 AC ABP45565;  
 DT 19-AUG-2002 (first entry)  
 DE Human Blys binding scFv SEQ ID 1576.  
 XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 OS Homo sapiens.  
 XX MO200202641-A1.  
 XX 10-JAN-2002.  
 XX 15-JUN-2001; 2001MO-US19110.  
 PR 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 PT WPI; 2002-114799/15.  
 DR 2002-114799/15.  
 XX  
 XX  
 PT Antibodies against B lymphocyte stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 PS Claim 1; Page 2283-2284; 3148pp; English.  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antineumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 SQ Sequence 257 AA;  
 Query Match 72.1%; Score 512.5; DB 23; Length 257;  
 Best Local Similarity 75.9%; Pred. No. 9e-40;

Matches 101; Conservative 8; Mismatches 21; Indels 3; Gaps 2;  
 QY 1 OVQLLOSATEVKKPKGASMKVSCASGYPTSYDISMVRAPQCGLEMGWISYSGNDY 60  
 Db 1 OVQLVSGAGAEVKKFGASVSCSASGYTTSIGISWVRAPQCGLEMGWISTYNGNRY 60  
 QY 61 AOKFGCRVTMTDTSTSTAYMELRSLRSDPTAVVYCARDCGCGAYEDVWGEYP-EYYAM 119  
 Db 61 PQKLGRVTMTDTSTSTAYMELRSLRSDPTAVVYCARDC--GRLSYDILUTGYARDYGM 118  
 QY 120 DVWGQGTIVTVSS 132  
 Db 119 DDMGRGTMTVTVSS 131  
 RESULT 12  
 ABP45551  
 ID ABP45551 standard; Protein; 251 AA.  
 AC ABP45551;  
 DT 19-AUG-2002 (first entry)  
 DE Human Blys binding scFv SEQ ID 1562.  
 XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 OS Homo sapiens.  
 XX MO200202641-A1.  
 XX 10-JAN-2002.  
 XX 15-JUN-2001; 2001MO-US19110.  
 PR 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 PT WPI; 2002-114799/15.  
 DR 2002-114799/15.  
 XX  
 XX  
 PT Antibodies against B lymphocyte stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 PS Claim 1; Page 2267-2268; 3148pp; English.  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antineumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent

DT 19-AUG-2002 (first entry)  
 XX Human Blys binding scFv SEQ ID 1610.  
 DE  
 XX Blys: B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200202641-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 15-JUN-2001; 2001WO-US19110.  
 XX  
 PR 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 PI Ruben SM, Baraeh SC, Choi GH, Vaughan T, Hilbert D;  
 XX  
 DR WPI; 2002-114799/15.  
 XX  
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for  
 XX the diagnosis and treatment of cancers and immune disorders -  
 XX  
 PS Claim 1; Page 2324-2325; 3148pp; English.  
 XX  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antineumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX  
 SO Sequence 257 AA;  
 XX  
 Query Match 72.4%; Score 514.5; DB 23; Length 257;  
 Best Local Similarity 77.0%; Pred. No. 5.9e-40;  
 Matches 104; Conservative 6; Mismatches 18; Indels 7; Gaps 3;  
 XX  
 QY 1 OVQLLOSATEVKKPKGASMKVSCMASGYPTSTYDISWVRQAPGQLEMMGWISYSGNTDY 60  
 DB 1 OVQLLOSAGEVKKPKGASVSVCKASGYTFTSYGISWVRQAPGQLEMMGWISAYGNKTY 60  
 QY 61 AOKFOGRVTMTDTTSRTAYMELRLSRDDTAIVYVCARDGGGAAVEDVWSEGEYB-YY 117  
 DB 61 ADELQGRVTMTDTTSRTAYMELRLSRDDTAIVYVCARDTIG--YDLITG-TPPPYYTY 116  
 QY 118 AMDVWGGGTTVYSS 132  
 DB 117 DMDVWGRGLTVVSS 131

RESULT 10  
 ABP45414  
 ID ABP45414 standard; Protein; 249 AA.  
 AC  
 XX ABP45414;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human Blys binding scFv SEQ ID 1425.  
 XX  
 KW Blys: B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200202641-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 15-JUN-2001; 2001WO-US19110.  
 XX  
 PR 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 PI Ruben SM, Baraeh SC, Choi GH, Vaughan T, Hilbert D;  
 XX  
 DR WPI; 2002-114799/15.  
 XX  
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for  
 XX the diagnosis and treatment of cancers and immune disorders -  
 XX  
 PS Claim 1; Page 2103-2104; 3148pp; English.  
 XX  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antineumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX  
 SO Sequence 249 AA;  
 XX  
 Query Match 72.2%; Score 513; DB 23; Length 249;  
 Best Local Similarity 76.9%; Pred. No. 7.8e-40;  
 Matches 103; Conservative 8; Mismatches 13; Indels 10; Gaps 4;  
 XX  
 QY 1 OVQLLOSATEVKKPKGASMKVSCMASGYPTSTYDISWVRQAPGQLEMMGWISYSGNTDY 60  
 DB 1 OVQLVSGAEVKKPKGASVSVCKASGYTFTSYGISWVRQAPGQLEMMGWISAYGNKTY 60  
 QY 61 AOKFOGRVTMTDTTSRTAYMELRLSRDDTAIVYVCARDGGGAAVEDVWSEGEYBYY--A 118

XX 10-JAN-2002.  
PD  
XX  
PF 15-JUN-2001; 2001WO-US19110.  
XX  
XX 16-JUN-2000; 2000US-212210P.  
PR 17-OCT-2000; 2000US-240816P.  
PR 16-MAR-2001; 2001US-276248P.  
PR 21-MAR-2001; 2001US-277379P.  
PR 25-MAY-2001; 2001US-293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for  
PS the diagnosis and treatment of cancers and immune disorders -  
XX Claim 1; Page 2522-2523; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method  
CC of the invention.  
XX  
SQ Sequence 253 AA;  
Query Match 73.1%; Score 520; DB 23; Length 253;  
Best Local Similarity 75.8%; Pred. No. 1.8e-40;  
Matches 100; Conservative 12; Mismatches 18; Indels 2; Gaps 2;  
QY 1 QVOLLQSGATEYKRGKAGSMKVCMAAGYPFTSYDISWTRQAPGQGLEWGMGISYSGNTDY 60  
Db 1 EVOLVOSGAIEVKRKGASVIVSCKASGYTFSTYGIWTRQAPGQGLEWGMGISYNGDNTY 60  
QY 61 AOKFQGRVTMTTPTSRRTAYMELRSLSDDTAYYYCARDDGGAGYEDWNGEYPEYAMD 120  
Db 61 AOELOGRVMTTDTSTSTAYMELRSLSRSDDTAYYYCAR-GDFQDY-DILTYGYPYVYGM 118  
QY 121 VMGGGTTVTYSS 132  
Db 119 VMGGGTMVTYSS 130  
RESULT 8  
ABP45767  
ID ABP45767 standard; Protein; 248 AA.  
XX  
XX ABP45767;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
XX Human Blys binding scFv SEQ ID 1778.  
DE  
XX  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
OS Homo sapiens.  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US19110.  
XX  
XX 16-JUN-2000; 2000US-212210P.  
PR 17-OCT-2000; 2000US-240816P.  
PR 16-MAR-2001; 2001US-276248P.  
PR 21-MAR-2001; 2001US-277379P.  
PR 25-MAY-2001; 2001US-293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX WPI; 2002-114799/15.  
XX  
XX  
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for  
PT the diagnosis and treatment of cancers and immune disorders -  
XX Claim 1; Page 2524-2525; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method  
CC of the invention.  
XX  
SQ Sequence 248 AA;  
Query Match 72.4%; Score 514.5; DB 23; Length 248;  
Best Local Similarity 75.8%; Pred. No. 5.6e-40;  
Matches 100; Conservative 9; Mismatches 16; Indels 7; Gaps 2;  
QY 1 QVOLLQSGATEYKRGKAGSMKVCMAAGYPFTSYDISWTRQAPGQGLEWGMGISYSGNTDY 60  
Db 1 EVOLVOSGAIEVKRKGASVIVSCKASGYTFSTYGIWTRQAPGQGLEWGMGISYNGDNTY 60  
QY 61 AOKFQGRVTMTTPTSRRTAYMELRSLSDDTAYYYCARDDGGAGYEDWNGEYPEYAMD 120  
Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAYYYCAR-----SYDILTYGYP--FGMD 113  
QY 121 VMGGGTTVTYSS 132  
Db 114 VMGGGTMVTYSS 125  
RESULT 9  
ABP45599  
ID ABP45599 standard; Protein; 257 AA.  
XX  
XX ABP45599;  
XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D,  
 XX WPI: 2002-114799/15.  
 DR  
 XX  
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 PS  
 XX  
 PS Claim 1, Page 2693-2694; 3148pp; English.  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX  
 SQ Sequence 251 AA:  
 Query Match 73.6%; Score 523; DB 23; Length 251;  
 Best Local Similarity 74.6%; Pred. No. 9.3e-41;  
 Matches 103; Conservative 5; Mismatches 14; Indels 16; Gaps 2;  
 QY 1 QVQLQSATEVKKPKASMKVSCASGYPFTSYDISWVQAPQGGLMMGMISITSGNTDY 60  
 DB 1 QVQLVSGAEVMPKASVSKASGYFTSTGTSWVQAPQGGLMMGMISITSGNTDY 60  
 QY 61 AOKFGQRYMTTDTSRRTAYMELRLSRSDPTAVYYCAR-----DGGGAYEDVMSGEPR 114  
 DB 61 AOKLQGRVTMTTDTSTRTAYMELRLSRSDPTAVYYCARVTSLSYSSSGGY----- 111  
 QY 115 EYYAMDVWGQGITVTIVSS 132  
 DB 112 -YYGMDVWGRGTTVTIVSS 128  
 RESULT 6  
 ABP44962  
 ID ABP44962 standard; Protein; 259 AA.  
 XX  
 AC ABP44962;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human Blys binding scFv SEQ ID 973.  
 XX  
 KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200202641-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 15-JUN-2001; 2001MO-US19110.  
 XX  
 PR 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR

PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX  
 DR WPI: 2002-114799/15.  
 XX  
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 PS  
 XX  
 PS Claim 1, Page 1562-1563; 3148pp; English.  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX  
 SQ Sequence 259 AA:  
 Query Match 73.3%; Score 521.5; DB 23; Length 259;  
 Best Local Similarity 74.5%; Pred. No. 1.3e-40;  
 Matches 102; Conservative 8; Mismatches 18; Indels 9; Gaps 2;  
 QY 1 QVQLQSATEVKKPKASMKVSCASGYPFTSYDISWVQAPQGGLMMGMISITSGNTDY 60  
 DB 1 QVQLVSGAEVMPKASVSKASGYFTSTGTSWVQAPQGGLMMGMISITSGNTDY 60  
 QY 61 AOKFGQRYMTTDTSRRTAYMELRLSRSDPTAVYYCARDDGGGAYEDVMSGEPRYY-- 117  
 DB 61 AOKLQGRVTMTTDTSTRTAYMELRLSRSDPTAVYYCARGPRGPRYYDLTGT-----YIYSL 116  
 QY 118 --AMDVWGQGITVTIVSS 132  
 DB 117 SDAFDIWGQGITVTIVSS 133  
 RESULT 7  
 ABP45766  
 ID ABP45766 standard; Protein; 253 AA.  
 XX  
 AC ABP45766;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human Blys binding scFv SEQ ID 1777.  
 XX  
 KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200202641-A1.  
 PN

CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.

CC Sequence 255 AA;

Query Match 73.9%; Score 525.5; DB 23; Length 255;  
 Best Local Similarity 78.0%; Pred. No. 5.5e-41;  
 Matches 103; Conservative 8; Mismatches 18; Indels 3; Gaps 2;

QY 1 QVOLLQSGATEVKKPKGASMKVSCMASGYPTSTYDISWVROAPGGLGEMGMSISGNTDY 60  
 Db 1 QVOLLQSGATEVKKPKGASMKVSCMASGYPTSTYDISWVROAPGGLGEMGMSISGNTDY 60  
 QY 61 AOKFGGRVTMTTDTTSRRTAYMELRSLSRSDTAIVYCCARDGGGAYEDVWSGEPEYYAMD 120  
 Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDTAIVYCCARD--PSPYYDILTGTFLEPY-MD 117  
 QY 121 VMGQGTITVYSS 132  
 Db 118 VMGKGLTVYSS 129

RESULT 4  
 ABP45663  
 ID ABP45663 standard; Protein; 252 AA.  
 AC ABP45663;  
 XX  
 DT 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 1674.  
 DE  
 XX

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

OS WO200202641-A1.

XX 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX WPI; 2002-114799/15.

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for  
 XX the diagnosis and treatment of cancers and immune disorders -

PS Claim 1; Page 2400-2401; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.

XX Sequence 252 AA;

Query Match 73.7%; Score 524; DB 23; Length 252;  
 Best Local Similarity 78.0%; Pred. No. 7.5e-41;  
 Matches 103; Conservative 7; Mismatches 16; Indels 6; Gaps 2;

QY 1 QVOLLQSGATEVKKPKGASMKVSCMASGYPTSTYDISWVROAPGGLGEMGMSISGNTDY 60  
 Db 1 QVOLLQSGATEVKKPKGASMKVSCMASGYPTSTYDISWVROAPGGLGEMGMSISGNTDY 60  
 QY 61 AOKFGGRVTMTTDTTSRRTAYMELRSLSRSDTAIVYCCARDGGGAYEDVWSGEPEYYAMD 120  
 Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDTAIVYCCAR----GAYDILTGTF--YGMD 114  
 QY 121 VMGQGTITVYSS 132  
 Db 115 VMGQGLTVYSS 126

RESULT 5  
 ABP45910  
 ID ABP45910 standard; Protein; 251 AA.  
 AC ABP45910;  
 XX  
 DT 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 1921.  
 DE  
 XX

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

OS WO200202641-A1.

XX 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.





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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 42.463 Seconds

(Without alignments)  
493.415 Million cell updates/sec

Title: US-09-674-752-25

Perfect score: 1 QVQLQSLATPEVKKPGASMKV.....YPERYAMDVGQTTVTASS 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
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Database :

- A\_Geneseq\_190jun03.\*
- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
  - 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
  - 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
  - 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
  - 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
  - 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*
  - 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*
  - 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
  - 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
  - 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
  - 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
  - 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*
  - 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*
  - 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*
  - 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*
  - 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*
  - 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*
  - 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*
  - 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
  - 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
  - 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
  - 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
  - 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
  - 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	711	100.0	132	21	AAV50953
2	702	98.7	132	21	AAV50950
3	525.5	73.9	255	23	ABP45179
4	524	73.7	252	23	ABP45663
5	523	73.6	251	23	ABP45910
6	521.5	73.3	259	23	ABP44962
7	520	73.1	253	23	ABP45766
8	514.5	72.4	248	23	ABP45767
9	514.5	72.4	257	23	ABP45599

10	513	72.2	249	23	ABP45414	Human Blys binding
11	512.5	72.1	257	23	ABP45565	Human Blys binding
12	510.5	71.8	251	23	ABP45551	Human Blys binding
13	510.5	71.8	259	23	ABP45441	Human Blys binding
14	508.5	71.5	257	23	ABP45343	Human Blys binding
15	508	71.4	254	23	ABP45394	Human Blys binding
16	507.5	71.4	121	22	AAU02549	Anti-adipocyte mon
17	507	71.3	250	23	ABP45584	Human Blys binding
18	506.5	71.2	257	23	ABP45568	Human Blys binding
19	505	71.0	247	23	ABP4562	Human Blys binding
20	504.5	71.0	248	23	ABP45461	Human Blys binding
21	504	70.9	247	23	ABP45105	Human Blys binding
22	504	70.9	250	23	ABP45549	Human Blys binding
23	503.5	70.8	248	23	ABP45435	Human Blys binding
24	500.5	70.4	251	23	ABP45575	Human Blys binding
25	500.5	70.4	251	23	ABP45861	Human Blys binding
26	499.5	70.3	253	23	ABP45625	Human Blys binding
27	498.5	70.1	259	23	ABP45345	Human Blys binding
28	498	70.0	251	23	ABP45304	Human Blys binding
29	497.5	70.0	251	23	ABP45867	Human Blys binding
30	496.5	69.8	248	23	ABP45860	Human Blys binding
31	496.5	69.8	251	23	ABP45859	Human Blys binding
32	495.5	69.7	251	23	ABP45859	Human Blys binding
33	494.5	69.5	251	23	ABP45725	Human Blys binding
34	494.5	69.5	251	23	ABP45858	Human Blys binding
35	494	69.5	250	23	ABP45550	Human Blys binding
36	494	69.5	250	23	ABP45582	Human Blys binding
37	492.5	69.3	248	23	ABP45866	Human Blys binding
38	492.5	69.3	251	23	ABP45727	Human Blys binding
39	492.5	69.3	252	23	ABP45484	Human Blys binding
40	492	69.2	254	23	ABP45769	Human Blys binding
41	490.5	69.0	253	23	ABP45164	Human Blys binding
42	489.5	68.8	251	23	ABP44919	Human Blys binding
43	489.5	68.8	253	23	ABP45600	Human Blys binding
44	489.5	68.8	253	23	ABP45953	Human Blys binding
45	489	68.8	98	21	AAV50954	Human anti-factor

ALIGNMENTS

RESULT 1  
AAV50953  
ID AAV50953 strand; Protein; 132 AA.  
XX  
AC AAV50953;  
XX  
DT 23-MAR-2000 (first entry)  
XX  
DE Human anti-factor VIII antibody VH protein VH IT-2.  
XX  
KW Human; heavy chain; antibody; factor VIII; hemostatic;  
KW hemophilia A; VH protein.  
XX  
OS Homo sapiens.  
XX  
PN WO958680-A2.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-NI00285.  
XX  
PR 08-MAY-1998; 98EP-0201543.  
XX  
PA (SANO-) STICHTING SANGUIN BLOEDVOORZIENING.  
XX Voorberg JJ, Van Den Brink EN, Turenhout EM;  
XX WPI; 2000-053102/04.  
XX New polynucleotide, polypeptide and antibody useful for diagnosing the  
PT presence of neutralizing antibodies against factor VIII and for  
PT treatment of hemophilia A patients with these antibodies -

QY 1 QVOLLQATTEVKKPGASMKVSCMASGYPTSYDISWVROAPGQGLEWGMWISISGNTDY 60  
 DB 3 QVLLQOOSPEVVRPVSYSKSGSYFTFDYSMMHMLMNAQSLWIGIISTYDGNIN 62  
 QY 61 AOKFQGRVTMTTDSRRTAYWELRLSRDPTAVYYCARDGGGAYEDVWSGEYREYAMD 120  
 DB 63 NQKFKGKATLTVDKSSSTAYWELRLSRDPTAVYYCARDGGGAYEDVWSGEYREYAMD 111  
 QY 121 VMGQGTIVTVSS 132  
 DB 112 YWGQGTIVTVSS 123

## RESULT 14

Q9QXE9 PRELIMINARY; PRT; 117 AA.  
 AC Q9QXE9  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Immunoglobulin heavy chain V-D-J region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Clemens A., Rademaekers A., Specht C., Koelsch E.;  
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ225174; CAB65237.1; -  
 DR HSSP; P01810; 2PBJ.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 117  
 SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D49734 CRC64;

Query Match 53.0%; Score 376.5; DB 11; Length 117;  
 Best Local Similarity 55.3%; Pred. No. 8.2e-31;  
 Matches 73; Conservative 18; Mismatches 26; Indels 15; Gaps 1;

QY 1 QVOLLQATTEVKKPGASMKVSCMASGYPTSYDISWVROAPGQGLEWGMWISISGNTDY 60  
 DB 1 EVOLQOOSPELVKPGASVKSCKASGYFTFDYMKWKVQSHGKSLWIGIDINPNNGTIS 60  
 QY 61 AOKFQGRVTMTTDSRRTAYWELRLSRDPTAVYYCARDGGGAYEDVWSGEYREYAMD 120  
 DB 61 NQKFKGKATLTVDKSSSTAYWELRLSRDPTAVYYCARDGGGAYEDVWSGEYREYAMD 105  
 QY 121 VMGQGTIVTVSS 132  
 DB 106 YWGQGTIVTVSS 117

## RESULT 15

Q92401 PRELIMINARY; PRT; 142 AA.  
 AC Q92401  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE V23-D-J-C mu protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6.  
 RA Kozono Y., Kozono H., Azuma T.;  
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB069913; BAB63929.1; -  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 142  
 SQ SEQUENCE 142 AA; 15622 MW; 24A265CEAE4A318B CRC64;

Query Match 52.8%; Score 375.5; DB 11; Length 142;  
 Best Local Similarity 56.8%; Pred. No. 1.3e-30;  
 Matches 75; Conservative 17; Mismatches 25; Indels 15; Gaps 2;

QY 1 QVOLLQATTEVKKPGASMKVSCMASGYPTSYDISWVROAPGQGLEWGMWISISGNTDY 60  
 DB 1 QVLLQOOSPELVKPGASVKSCKASGYFTFDYSMMHMLMNAQSLWIGIISTYDGNIN 60  
 QY 61 AOKFQGRVTMTTDSRRTAYWELRLSRDPTAVYYCARDGGGAYEDVWSGEYREYAMD 120  
 DB 61 NEKFKGKATLTVDKSSSTAYWELRLSRDPTAVYYCARDGGGAYEDVWSGEYREYAMD 105  
 QY 121 VMGQGTIVTVSS 132  
 DB 106 YWGQGTIVTVSS 117

Search completed: December 30, 2003, 11:01:02  
 Job time : 32.169 secs

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QY 61 AOKFQGRVTMTTDSRRATAYMELSLRSDPTAVYYCARDGGGAYEDVWGSGEYREYAMD 120
DB 63 NEKFKGATLISVDSSSTAYMELTRLTSEDSAYVFCAR-----GDYYRRY-FD 109

QY 121 VMGCGTTVTYSS 132
DB 110 VMGCGTTVTYSS 121

RESULT 11
Q91WT1 PRELIMINARY; PRT; 481 AA.
AC Q91WT1;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical 52.1 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Colon;
RA Strausberg R.;
RL Submitted (Sep-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IGv_1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KM Hypothetical protein.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 54.9%; Score 390.5; DB 11; Length 481;
Best Local Similarity 57.6%; Pred. No. 1.7e-31;
Matches 76; Conservative 14; Mismatches 27; Indels 15; Gaps 1;

QY 1 OVOLLGATGVKKRPGASMKVSCMASGYPTFSYDISWVRQAPGCGLEMMGISTISGNTDY 60
DB 20 OVOLLGSGPELVKPGASVKISCKASGYTFSYIHWKQKRGQGLVWIGWYPGDGNTRY 79
61 AOKFQGRVTMTTDSRRATAYMELSLRSDPTAVYYCARDGGGAYEDVWGSGEYREYAMD 120
DB 80 NEKFKGATLISVDSSSTAYMELTRLTSEDSAYVFCAR-----WAFD 124

QY 121 VMGCGTTVTYSS 132
DB 125 VMGCGTTVTYSS 136

RESULT 12
Q9Y298 PRELIMINARY; PRT; 150 AA.
AC Q9Y298;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE 16g VH protein precursor (Fragment).
GN 16g VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98322155; PubMed=9657749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT 1964 monoclonal antibody derived from a hemophilia A patient with
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RT inhibitor.";
RL Blood 92:496-506 (1998).
DR EMBL; AJ224083; CAH1629.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv_1.
DR PROSITE; PS50835; IG-LIKE; 1.
KM Signal.
FT SIGNAL.
FT NON_TER. 1 19 POTENTIAL.
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match 53.8%; Score 382.5; DB 4; Length 150;
Best Local Similarity 59.1%; Pred. No. 2.7e-31;
Matches 78; Conservative 10; Mismatches 29; Indels 15; Gaps 1;

QY 1 OVOLLGATGVKKRPGASMKVSCMASGYPTFSYDISWVRQAPGCGLEMMGISTISGNTDY 60
DB 20 OVOLLGSGAEVKKRPGASVKISCKVSGYTLTELPHVHWGQAPKGLIEWVGSFDPESGESIY 79
61 AOKFQGRVTMTTDSRRATAYMELSLRSDPTAVYYCARDGGGAYEDVWGSGEYREYAMD 120
DB 80 AREFGSVTMTADTSTDIAYMELSLRSDPTAVYYCA-----VDPDAFD 124

QY 121 VMGCGTTVTYSS 132
DB 125 VMGCGTTVTYSS 136

RESULT 13
Q925S2 PRELIMINARY; PRT; 170 AA.
AC Q925S2;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE MPP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80 (2001).
DR EMBL; AF240167; AAK43732.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv_1.
DR PROSITE; PS50835; IG-LIKE; 1.
SQ SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;

Query Match 53.1%; Score 377.5; DB 11; Length 170;
Best Local Similarity 56.1%; Pred. No. 1e-30;
Matches 74; Conservative 14; Mismatches 33; Indels 11; Gaps 2;
```

OY 121 VMGCGTTVSS 132  
 DB 108 YWGCGTTVSS 119

## RESULT 8

OBWY24 PRELIMINARY; PRT: 497 AA.

DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE SNC66 protein.  
 OS Homo sapiens (Human).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxId=9606;

RP SEQUENCE FROM N.A.

RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.  
 RT "Identification and characterization of SNC66, a Ig-like gene which is  
 RT down-regulated in colorectal cancer."  
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF283666; AAL36987.1; -  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig\_4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 4.  
 DR PROSITE; PSS0290; IG\_MHC; 1.  
 SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A63E5 CRC64;

Query Match 56.8%; Score 403.5; DB 4; Length 497;  
 Best Local Similarity 59.0%; Pred. No. 8, 6e-33;  
 Matches 79; Conservative 16; Mismatches 28; Indels 11; Gaps 2;

OY 1 OVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVROAPGQGLMMGMISYSGNTDY 60  
 DB 20 QOLESSEGEVTKFGASVSKSCASGYTITAIIDINWROAPGQGLMMGMNPOTGNTDF 79  
 OY 61 AQKFGQRTMTDTSTRRTAYMELRSLSDDTAIVYCCARDG--GGGAYEDVWSGEYPEYVA 118  
 DB 80 AQKFGQRLTFSDRTSINTAYMTLSLSTEDSAITFCARGLRGGRFGVNW----- 130  
 OY 119 MDVWGCGTTVSS 132  
 DB 131 FDPWGHGLTVSS 144

## RESULT 9

OBWY24 PRELIMINARY; PRT: 116 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxId=9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus."  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035025; AAD56261.1; -  
 DR HSSP; P01810; 2FBU.

DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT NON\_TER 1 1  
 FT TER 116 116

SQ SEQUENCE 116 AA; 12605 MW; C6F9131DE13EA898 CRC64;

Query Match 55.3%; Score 393; DB 4; Length 116;  
 Best Local Similarity 62.5%; Pred. No. 1, 7e-32;  
 Matches 80; Conservative 11; Mismatches 25; Indels 12; Gaps 1;

OY 5 LOSATEVKKPGASMKVSCMASGYPTSYDISWVROAPGQGLMMGMISYSGNTDYAQKF 64  
 DB 1 VQSGAEVKKPSSSVSKVSCKASGTFSSYALISWVROAPGQGLMMGRITPILGIANYAQKF 60  
 OY 65 QGRVTMTDTSTRRTAYMELRSLSDDTAIVYCCARDGGGAYEDVWSGEYPEYVANDWQ 124  
 DB 61 QGRVTITADKSTAYVELSLRSEDPAIVYCA-----SSNMGPYWFIDLWGR 108

OY 125 GTTVTVSS 132  
 DB 109 GLTVTVSS 116

## RESULT 10

OBWY24 PRELIMINARY; PRT: 147 AA.

DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE MRP3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;

RP SEQUENCE FROM N.A.  
 RC STRAIN=BAUB/c;  
 RX PubMed=11819679;  
 RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,  
 RA Su C.;  
 RT "Mechanism of exogenous nucleic acids and their precursors improving  
 RT the repair of intestinal epithelium after irradiation in mice."  
 RL World J. Gastroenterol. 6:709-717(2000).  
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BAUB/c;  
 RA Cui D., Zeng G., Yan X., Li X., Su C.;  
 RT "Cloning of mouse genes related to repairing of intestinal epithelium  
 RT of the irradiated mice by treatment with the intestinal RNA of mice of  
 RT the same strain."  
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
 DR EMBL; AF240165; AAK33731.1; -  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

Query Match 55.1%; Score 391.5; DB 11; Length 147;  
 Best Local Similarity 59.1%; Pred. No. 3, 2e-32;  
 Matches 78; Conservative 15; Mismatches 26; Indels 13; Gaps 2;

OY 1 OVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVROAPGQGLMMGMISYSGNTDY 60  
 DB 3 OVXLHSGPEVVKPGASVSKSCASGYITSTIDWVROTPGQGLMMIGMIFPGEGSTIEY 62

OY 118 AMDVWGQTTVTSS 132  
 |||||  
 DB 135 GMDVWGQTTVTSS 149

## RESULT 5

OY 096GAG PRELIMINARY; PRT; 614 AA.  
 AC 096GAG; PRELIMINARY; PRT; 614 AA.  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)  
 DE Hypochemical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=B-cell;  
 RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC009851; AA09851.1; -  
 DR InterPro; IPR000005; HTHATAC.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_MHC.  
 DR Pfam; PF00047; Ig\_5.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00041; HTH\_ARAC\_FAMILY\_1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KW Hypochemical protein.  
 SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 59.6%; Score 423.5; DB 4; Length 614;  
 Best Local Similarity 62.9%; Pred. No. 1e-34;  
 Matches 83; Conservative 13; Mismatches 25; Indels 11; Gaps 2;

OY 1 QVOLLQSTAEVKKPGASMKVSCMASGYPTSDYSWVRQAPGQGLEMMGMSISYSGNTDY 60  
 |||||  
 DB 20 QMOLVSGAEVRKKGASVSKSCASGYTFYRYLHWVRQAPGQGLEMMGMSITPFGNTNY 79  
 |||||  
 OY 61 AOKFOGRVMTTDSRRTAYMELSLRSDDTAVYYCARDDGGAGYEDVWSGEYPEVYAMD 120  
 |||||  
 DB 80 AOKFOGRVMTTDSRRTAYMELSLRSDDTAVYYCARDDGGAGYEDVWSGEYPEVYAMD 120  
 |||||  
 OY 121 VMGQGTTLVTSS 132  
 |||||  
 DB 129 VMGQGTTLVTSS 140  
 |||||

## RESULT 6

OY 09UL92 PRELIMINARY; PRT; 124 AA.  
 AC 09UL92; PRELIMINARY; PRT; 124 AA.  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region  
 DE (fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus."  
 CLin. Immunol. Immunopathol. 87:184-192 (1998).

DR EMBL; AF035022; AA056258.1; -  
 DR HSSP; P01772; 2FB4.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 59.5%; Score 423; DB 4; Length 124;  
 Best Local Similarity 65.9%; Pred. No. 1.6e-35;  
 Matches 87; Conservative 11; Mismatches 26; Indels 8; Gaps 2;

OY 1 QVOLLQSTAEVKKPGASMKVSCMASGYPTSDYSWVRQAPGQGLEMMGMSISYSGNTDY 60  
 |||||  
 DB 1 EVOLVSGAEVRKKGASVSKSCASGYTSSYVMHWVRQAPGQGLEMMGMSISYSGNTDY 60  
 |||||  
 OY 61 AOKFOGRVMTTDSRRTAYMELSLRSDDTAVYYCARDDGGAGYEDVWSGEYPEVYAMD 120  
 |||||  
 DB 61 AOKFOGRVMTTDSRRTAYMELSLRSDDTAVYYCARDDGGAGYEDVWSGEYPEVYAMD 120  
 |||||  
 OY 121 VMGQGTTLVTSS 132  
 |||||  
 DB 113 VMGQGTTLVTSS 124  
 |||||

## RESULT 7

OY 09GY22 PRELIMINARY; PRT; 119 AA.  
 AC 09GY22; PRELIMINARY; PRT; 119 AA.  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region  
 DE (fragment).  
 OS Schistosoma japonicum (Blood fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;  
 OC Schistosomatidae; Schistosomatidae; Schistosoma.  
 NCBI\_TaxID=6182;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RA Song X.T., Feng Z.Q., Guan X.H.;  
 RT "Amplification, cloning and sequence analysis of the heavy chain  
 RT variable region gene of monoclonal anti-idiotypic antibody NP30 of  
 RT Schistosoma japonicum."  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF282622; AAG01452.1; -  
 DR HSSP; P01772; 2FB4.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 119 AA; 13567 MW; BA893873PDSFA6AB CRC64;

Query Match 58.7%; Score 417.5; DB 5; Length 119;  
 Best Local Similarity 61.4%; Pred. No. 5.5e-35;  
 Matches 81; Conservative 17; Mismatches 21; Indels 13; Gaps 1;

OY 1 QVOLLQSTAEVKKPGASMKVSCMASGYPTSDYSWVRQAPGQGLEMMGMSISYSGNTDY 60  
 |||||  
 DB 1 QVOLLQSTAEVKKPGASMKVSCMASGYPTSDYSWVRQAPGQGLEMMGMSISYSGNTDY 60  
 |||||  
 OY 61 AOKFOGRVMTTDSRRTAYMELSLRSDDTAVYYCARDDGGAGYEDVWSGEYPEVYAMD 120  
 |||||  
 DB 61 AOKFOGRVMTTDSRRTAYMELSLRSDDTAVYYCARDDGGAGYEDVWSGEYPEVYAMD 120  
 |||||

Db 1 EVOLVESGAEVKKPGASVSKASGYFTGYMHWROAPQGLEWGMWNPNSGNTY 60  
 QY 61 AOKFQGRVMTTDTSRRTAYMELRSLSDDTAIVYCCARDGGGAVEDVMSGEYFEYAMD 120  
 Db 61 AOKVGRVMTTDTSTSTVYMEELRSLSDDTAIVYCCARDGGGAVEDVMSGEYFEYAMD 113  
 QY 121 VMGQGTIVTVSS 132  
 Db 114 VMGQGTIVTVSS 125

## RESULT 2

Q9BRV0 PRELIMINARY; PRT; 500 AA.  
 AC Q9BRV0; 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RA Strauberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC005951; AAH05951.1; -.  
 DR HSSP; P01789; IMCP.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00406; Ig; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 4.  
 DR PROSITE; PSS0290; IG\_MHC; 1.  
 KM Hypothetical protein  
 SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 62.8%; Score 447; DB 4; Length 500;  
 Best Local Similarity 68.2%; Pred. No. 3, 1e-37;  
 Matches 90; Conservative 10; Mismatches 28; Indels 4; Gaps 2;

QY 1 QVQLQSATEVKKPGASVSKASGYFTGYMHWROAPQGLEWGMWNPNSGNTY 60  
 Db 20 QVHLVSGAEVMSFGASVSKASGYFTGYMHWROAPQGLEWGMWNPNSGNTY 79  
 QY 61 AOKFQGRVMTTDTSRRTAYMELRSLSDDTAIVYCCARDGGGAVEDVMSGEYFEYAMD 120  
 Db 80 AKKFGGRVMTTDTSTSTVYMEELRSLSDDTAIVYCCARDGGGAVEDVMSGEYFEYAMD 135  
 QY 121 VMGQGTIVTVSS 132  
 Db 136 VMGQGTIVTVSS 147

## RESULT 3

Q9UL94 PRELIMINARY; PRT; 119 AA.  
 AC Q9UL94; 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035020; AAD56256.1; -.  
 DR HSSP; P01810; 2FBJ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; Ig; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT NON\_TER 1 119  
 FT NON\_TER 1 119  
 SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345FA16E CRC64;

Query Match 62.8%; Score 446.5; DB 4; Length 119;  
 Best Local Similarity 67.4%; Pred. No. 6e-38;  
 Matches 89; Conservative 9; Mismatches 21; Indels 13; Gaps 2;

QY 1 QVQLQSATEVKKPGASVSKASGYFTGYMHWROAPQGLEWGMWNPNSGNTY 60  
 Db 1 EVOLVESGAEVKKPGASVSKASGYFTGYMHWROAPQGLEWGMWNPNSGNTY 60  
 QY 61 AOKFQGRVMTTDTSRRTAYMELRSLSDDTAIVYCCARDGGGAVEDVMSGEYFEYAMD 120  
 Db 61 AOKFQGRVMTTDTSTSTVYMEELRSLSDDTAIVYCCARDGGGAVEDVMSGEYFEYAMD 107  
 QY 121 VMGQGTIVTVSS 132  
 Db 108 VMGQGTIVTVSS 119

## RESULT 4

Q96QSO PRELIMINARY; PRT; 159 AA.  
 AC Q96QSO; 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Putative matrix cell adhesion molecule-3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Tilson M.D.;  
 RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3  
 RT mRNA (Matrix Cell Adhesion Molecule-3, Mac-CAM 3).";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY039025; AAK82649.1; -.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; Ig; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 62.0%; Score 441; DB 4; Length 159;  
 Best Local Similarity 67.4%; Pred. No. 3, 1e-37;  
 Matches 91; Conservative 13; Mismatches 23; Indels 8; Gaps 3;

QY 1 QVQLQSATEVKKPGASVSKASGYFTGYMHWROAPQGLEWGMWNPNSGNTY 60  
 Db 20 QVHLVSGAEVKKPGASVSKASGYFTGYMHWROAPQGLEWGMWNPNSGNTY 79  
 QY 61 AOKFQGRVMTTDTSRRTAYMELRSLSDDTAIVYCCARDGGGAVEDVMSGEYFEYAMD 117  
 Db 80 AOKFQGRVMTTDTSTSTVYMEELRSLSDDTAIVYCCARDGGGAVEDVMSGEYFEYAMD 134





Tue Dec 30 11:48:58 2003

us-09-674-752-25.rsp

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Job time : 7.07717 secs

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ID	NAME	STANDARD	PRT	136 AA
AD	HV16 MOUSE			
AC	P01783			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	15-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DS	Ig heavy chain V region MOPC 21 precursor (Fragment).			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RA	MEDLINE=81234548; PubMed=6788376;			
RA	Bochwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,			
RA	Baltimore D.,			
RT	"heavy chain variable region contribution to the NpB family of			
RT	antibodies: somatic mutation evident in a gamma 2a variable region.",			
RL	Cell 24:625-637(1981).			
RP	[2]			
RP	SEQUENCE OF 17-136.			
RX	MEDLINE=77100368; PubMed=401950;			
RA	Adetugbo K., Milstein C., Secher D.S.;			
RL	"Molecular analysis of spontaneous somatic mutants.",			
RL	Nature 265:299-304(1977).			
CC				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC				
DR	EMBL; J00522; AA015290.1; -			
DR	PIR; J00809; GIM521.			
DR	PDB; 1IGC; 03-JUN-95.			
DR	InterPro; IPR007110; Ig_1like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00406; IGV_1.			
DR	PROSITE; PSS0835; IG_LIKE; 1.			
KW	Immunoglobulin V region; Signal; 3D-structure.			
FT	NON_TER 1			
FT	SIGNAL 1			
FT	CHAIN 17 136			
FT	DOMAIN 115 119			
FT	DOMAIN 120 136			
FT	DISULFID 38 112			
FT	CONFLICT 75 78			
FT	CONFLICT 89 90			
FT	CONFLICT 115 115			
FT	CONFLICT 120 120			
FT	NON_TER 136 136			
SO	SEQUENCE 136 AA; 15071 MW; 2276A98DBDEF7016 CRC64;			
Query Match	47.5%; Score 338; DB 1; Length 136;			
Best Local Similarity	50.4%; Pred. No. 1.5e-28;			
Matches	66; Conservative 23; Mismatches 30; Indels 12; Gaps 3;			
OY	2 VOLLOSATEVKKPASKNKVSGMASGYPFTYSIDISWVROAFQGLEWNGWISYSGNTDYA 61			
Db	18 VOLVESGGGLVOPQGSRRKSLSCMASGFTFSSFGKHWVQAPEKGLEWVAVYISSSSSTLHYA 77			
OY	62 QKFGARVMTTDSRTATYAMELRSLRDDPTAVVYCAPDGGGCAVEDVWSEGEYFETAMDV 121			
Db	78 DTVAGRFTISRDNPKNITLFLQMTSLRSRSDYATYICAR-----W-GNYP-YAMKV 125			
OY	122 WGGQTTVTYSS 132			
Db	126 WGGQSTVTYSS 136			

```

RESULT 15
HVL1_MOUSE
ID HVL1_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse)
OC Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Parkin M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-631(1981).
CC -1 MISCELLANEOUS; THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
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CC -----
DR EMBL; J00539; AAA38172.1; -.
DR PIR; A02038; G2MS43.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR KMW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 1 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 20 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 137
SO SEQUENCE 137 AA; 15200 MW; ADD5881BF448BEC9 CRC64;

Query Match 47.4%; Score 337; DB 1; Length 137;
Best Local Similarity 53.8%; Pred. No. 1,9e-28;
Matches 71; Conservative 13; Mismatches 34; Indels 14; Gaps 3;

QY 1 QVOLLQATVEVKKRGASMKYSCASGYPTFTSDISVNRQAPQGLLEWGMISYSGNTDY 60
DB 20 QVOLLQPGAEFVPGVGSVYLSCASGYTFTSYLMHWNPQPGGLGWIGRIDPNSGITY 79
QY 61 AQRQGRVMTTDTSTRTAYMELRSRSDTAVYVYCARQGGGAGVADWVGSEYPEYVAMD 120
DB 80 NEHFREKATLTIDKPESTAYVMDLSLTSBDSAVYICAR-----YR--LGRY----PD 125
QY 121 VNGQGTIVYSS 132
DB 126 YWGGGTTLTVSS 137

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FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DOMAIN 118 124 D SEGMENT.  
 FT DOMAIN 125 139 JH2 SEGMENT.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON TER 139 139  
 SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC09465 CRC64;

Query Match 49.8%; Score 354; DB 1; Length 139;  
 Best Local Similarity 54.1%; Pred. No. 3.3e-30;  
 Matches 72; Conservative 16; Mismatches 31; Indels 14; Gaps 2;

QY 1 QVQLQSGATEVKKPGASMKVSCMASGYPTFTSYDISWVROAPGQGLMMGMWISYSGNTDY 60  
 DB 20 QVQLQSGAPALVKKPKASVYKLSCKSGSYFTFTSYMMHWVKKRGRGLEWIGRIDPNSGGTKY 79  
 QY 61 AOKFGGRVTMTTDSRRRAYMELRLSRSDDTAVYYCAR-DGGGGAVEDVMSGEYPERYYAM 119  
 DB 80 NEKFKSKATLTIVDKPSSTAYWQSLTSEDSANVYCARVDYSSY-----F 126  
 QY 120 DVMGGTTVTYSS 132  
 DB 127 DVMGGTTLTVSS 139

RESULT 12  
 HV00\_MOUSE STANDARD; PRT; 114 AA.  
 AC P01741;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region (Anti-arsonate antibody).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE.  
 RA STRAIN=A/J;  
 RX MEDLINE=79195438; PubMed=109536;  
 RT Capra J.D., Nisenoft A.;  
 RT "Structural studies on induced antibodies with defined idiotypic  
 RT specificities. VII. The complete amino acid sequence of the heavy  
 RT chain variable region of anti-p-azophenylarsenate antibodies from A/J  
 RT mice bearing a cross-reactive idioype.";  
 RL J. Immunol. 123:279-284 (1979).  
 CC -I- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF  
 CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V  
 CC REGION SEQUENCE.  
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02022; GMSAA.  
 DR HSSP; P01772; 2FB4.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 106 IG-LIKE.  
 FT NON TER 114 114  
 SQ SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A9FA8E CRC64;

Query Match 48.0%; Score 341; DB 1; Length 114;  
 Best Local Similarity 55.5%; Pred. No. 6e-29;  
 Matches 71; Conservative 16; Mismatches 27; Indels 14; Gaps 2;

QY 1 QVQLQSGATEVKKPGASMKVSCMASGYPTFTSYDISWVROAPGQGLMMGMWISYSGNTDY 60  
 DB 1 EVQLQSGALVKKASGVSKATGYTFSSYELVWVROAPGQGLDGLYSSSAVYNY 60  
 QY 61 AOKFGGRVTMTTDSRRRAYMELRLSRSDDTAVYYCAR-DGGGGAVEDVMSGEYPERYYAM 120  
 DB 127 DVMGGTTLTVSS 139

DB 61 AOKFGGRVTMTTDESTNTAYMELSLRSDDTAVYFCA-----VRVISRYF--D 106  
 QY 121 VMCGGTTV 128  
 DB 107 GVMGGTTLV 114

RESULT 13  
 HV15\_MOUSE STANDARD; PRT; 136 AA.  
 AC P01759;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region BCL1 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RX MEDLINE=82222262; PubMed=6806821;  
 RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,  
 RA Blatner F.R.;  
 RT "Simultaneous expression of immunoglobulin mu and delta heavy chains  
 RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared  
 RT by two adjacent CH genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000 (1982).  
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
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CC EMBL; J00494; AAA8130.1; -.  
 DR PIR; A02042; HMM8B1.  
 DR HSSP; P01772; 2FB4.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT CHAIN 1 19  
 FT DOMAIN 20 136 IG HEAVY CHAIN V REGION BCL1.  
 FT NON TER 136 136 IG-LIKE.  
 SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 47.7%; Score 339.5; DB 1; Length 136;  
 Best Local Similarity 51.5%; Pred. No. 1.1e-28;  
 Matches 68; Conservative 16; Mismatches 33; Indels 15; Gaps 2;

QY 1 QVQLQSGATEVKKPGASMKVSCMASGYPTFTSYDISWVROAPGQGLMMGMWISYSGNTDY 60  
 DB 20 QVQLQSGEPVAPRGVSKVSKSGSYFTFTSYMMHWVKKSHASLEWIGISTVYNNTSY 79  
 QY 61 AOKFGGRVTMTTDSRRRAYMELRLSRSDDTAVYYCAR-DGGGGAVEDVMSGEYPERYYAM 120  
 DB 80 NOKFKGATMTVDKSSSTVMEIARLTSEDSANLVYCAR-----YGNV-----FD 124  
 QY 121 VMCGGTTVTYSS 132  
 DB 125 YMCGGTTLTVSS 136

RESULT 14  
 HV16\_MOUSE

RP DISULFIDE BOND.  
RX MEDLINE=71064027; PubMed=4923144;  
RA Gali W.B.; Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.  
RL Biochemistry 9:3168-3196(1970).  
CC MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS  
CC MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A90563; GIHUEU.  
DR HSSP; P01772; 2FB4.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IG\_1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
DR Immunoglobulin V region; Pyroliidone carboxylic acid.  
KW DOMAIN 1 112  
FT MOD\_RES 1 112  
FT DISULFID 1 112  
FT NON\_TER 117 96  
FT SEQUENCE 117 AA; 12472 MW; 99D60ADAEBD52818 CRC64;  
SQ  
Query Match 50.4%; Score 358.5; DB 1; Length 117;  
Best Local Similarity 60.6%; Pred. No. 9e-31;  
Matches 80; Conservative 8; Mismatches 29; Indels 15; Gaps 3;  
QY 1 QVOLLQSGAEVKKKSGASMKVSCMASGYPFTSYDTSWROAPGQGLWMGMISISGNTDY 60  
DB 1 QVOLLQSGAEVKKKSGASMKVSCMASGYPFTSYDTSWROAPGQGLWMGMISISGNTDY 60  
QY 61 AOKFQGRVMTTDTSRRTAYMELRSDDPAVYCCARPGGAGYEDWVGSEYPEYAMD 120  
DB 61 AOKFQGRVMTTDTSRRTAYMELRSDDPAVYCCARPGGAGYEDWVGSEYPEYAMD 120  
QY 61 AOKFQGRVMTTDTSRRTAYMELRSDDPAVYCCARPGGAGYEDWVGSEYPEYAMD 120  
DB 61 AOKFQGRVMTTDTSRRTAYMELRSDDPAVYCCARPGGAGYEDWVGSEYPEYAMD 120  
QY 121 VMGCGTTVTVSS 132  
DB 109 ---NGGLTVTVSS 117  
Db 109 ---NGGLTVTVSS 117  
RESULT 10  
HV51 MOUSE STANDARD; PRT; 118 AA.  
ID HV51 MOUSE  
AC P06330;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region AC38 205.12.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=84182519; PubMed=6201362;  
RA Dildrop R.; Boyens J.; Stekevitz M.; Beyreuther K.; Rajewsky K.;  
RT "A V region determinant (idiotope) expressed at high frequency in B  
RT lymphocytes is encoded by a large set of antibody structural genes.";  
RL J. Immunol. 153:517-523(1994).  
DR PIR; A02040; MMS38.  
DR HSSP; P01789; 1MCP.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IG\_1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 98  
FT SEQUENCE V SEGMENT.

FT DOMAIN 99 104 D SEGMENT.  
FT DOMAIN 105 118 J SEGMENT.  
FT DISULFID 22 96 BY SIMILARITY.  
FT NON\_TER 118 118  
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;  
Query Match 50.4%; Score 358; DB 1; Length 118;  
Best Local Similarity 53.8%; Pred. No. 1e-30;  
Matches 71; Conservative 17; Mismatches 30; Indels 14; Gaps 1;  
QY 1 QVOLLQSGAEVKKKSGASMKVSCMASGYPFTSYDTSWROAPGQGLWMGMISISGNTDY 60  
DB 1 EVOLLQSGAEVKKKSGASMKVSCMASGYPFTSYDTSWROAPGQGLWMGMISISGNTDY 60  
QY 61 AOKFQGRVMTTDTSRRTAYMELRSDDPAVYCCARPGGAGYEDWVGSEYPEYAMD 120  
DB 61 AOKFQGRVMTTDTSRRTAYMELRSDDPAVYCCARPGGAGYEDWVGSEYPEYAMD 120  
QY 121 VMGCGTTVTVSS 132  
DB 107 VMGCGTTVTVSS 118  
Db 107 VMGCGTTVTVSS 118  
RESULT 11  
HV07 MOUSE STANDARD; PRT; 139 AA.  
ID HV07 MOUSE  
AC P01751; P01752;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region B1-8/186-2 precursor.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=81234548; PubMed=6788376;  
RA Bothwell A.L.M.; Paekind M.; Reith M.; Imanishi-Kari T.; Rajewsky K.;  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NpB family of  
RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN mRNA WAS CLONED FROM A HYBRIDOMA  
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
CC (NPB ANTIBODIES).  
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CC -----  
CC EMBL; J00529; AAA38170.1; --  
DR PIR; A90809; MMS18.  
DR PDB; 1A6W; 15-JUL-98.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IG\_1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal; 3D-structure.  
FT SIGNAL 1 19  
FT CHAIN 20 139  
FT DOMAIN 20 49  
FT DOMAIN 50 54  
FT DOMAIN 55 68  
FT DOMAIN 69 85  
FT SEQUENCE IG HEAVY CHAIN V REGION B1-8/186-2.  
FT SEQUENCE FRAMEWORK-1.  
FT SEQUENCE COMPLEMENTARITY-DETERMINING-1.  
FT SEQUENCE FRAMEWORK-2.  
FT SEQUENCE COMPLEMENTARITY-DETERMINING-2.

```

OY      121 VMGGGTTVTSS 132
DB      109 VMGGTITVTSS 120

RESULT 7
HV02_MOUSE STANDARD; PRT; 140 AA.
ID HV02_MOUSE
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 9367 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sins J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL: J00493; AAA8128.1; -
CC PIR: A94264; HVMSG7.
CC HSSP: P01810; 2FBJ.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam: PF00047; Ig_1.
CC SMART: SM00406; IGV; 1.
CC PROSITE: PS50835; IG LIKE; 1.
CC Immunoglobulin V region; Hydridoma; Signal.
CC SIGNAL 1 19
CC CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.
CC DOMAIN 20 139 IG-LIKE.
CC NON TER 140 140
CC SEQUENCE 140 AA; 15514 MW; 25A4CBEB31DASC68 CRC64;

Query Match 50.7%; Score 360.5; DB 1; Length 140;
Best Local Similarity 53.0%; Pred. No. 6,8e-31;
Matches 70; Conservative 22; Mismatches 29; Indels 11; Gaps 1;

OY      1 OVQLQSLATEVKKPKASGMKVSCKASGYPTSYDISWVRQAPGQGLEWMGMSISVSGNTDY 60
DB      20 EVQLQDSGAEELVRASSVSKASGYFTSYGINWVKRPPQGLSLEWIGINPGMGYNY 79
OY      61 AOKFQGRVMTTDTSRRTAYMELRSILRSDDTAVYYCARDGGGAGAYEDVWSGEYPEYVAMD 120
DB      80 NKKFPGKTLTLVDKSSSTAYVQMLRSLTSDSAVYFCAR-----SHYGGSGSYDFD 128
OY      121 VMGGGTTVTSS 132
DB      129 VMGGGTTVTSS 140

RESULT 8
HV12_MOUSE STANDARD; PRT; 117 AA.
ID HV12_MOUSE
AC P01756;

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DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kenty W.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR: A02039; MHMS4E.
CC HSSP: P01789; 1MCP.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam: PF00047; Ig_1.
CC SMART: SM00406; IGV; 1.
CC PROSITE: PS50835; IG LIKE; 1.
CC Immunoglobulin V region; Glycoprotein.
CC DOMAIN 1 116
CC DISULFID 22 96 BY SIMILARITY.
CC CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
CC NON TER 117 117
CC SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447841 CRC64;

Query Match 50.6%; Score 359.5; DB 1; Length 117;
Best Local Similarity 54.5%; Pred. No. 7.1e-31;
Matches 72; Conservative 18; Mismatches 27; Indels 15; Gaps 2;

OY      1 OVQLQSLATEVKKPKASGMKVSCKASGYPTSYDISWVRQAPGQGLEWMGMSISVSGNTDY 60
DB      1 EVQLQSGPELVKPGASVSKASGYFTFDYIMKVKVKGSLSEWIGINRNGTSTY 60
OY      61 AOKFQGRVMTTDTSRRTAYMELRSILRSDDTAVYYCARDGGGAGAYEDVWSGEYPEYVAMD 120
DB      61 NKKFPGKTLTLVDKSSSTAYVQMLRSLTSDSAVYFCAR-----YDWYF--D 105
OY      121 VMGGGTTVTSS 132
DB      106 VMGGGTTVTSS 117

RESULT 9
HV1A_HUMAN STANDARD; PRT; 117 AA.
ID HV1A_HUMAN
AC P01742;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-1 region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064024; PubMed=5489771;
RX Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RX Maxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [2]

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8131846; PubMed=6186498;  
 RA Stekevitz M., Gefter M.L., Brodeur P., Riblet R.,  
 RA Marshak-Rothstein A.;  
 RT "The genetic basis of antibody production: the dominant anti-arsenate  
 idotype response of the strain A mouse.";  
 RL Eur. J. Immunol. 12:1023-1032(1982).  
 CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER  
 CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS  
 CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J  
 CC SEGMENT. JH2.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR HSSP: P01789; IMCP.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Hybridoma.  
 KM DOMAIN 1 111  
 FT NON\_TER 120 120  
 FT IG-LIKE.  
 SQ SEQUENCE 120 AA; 13307 MW; F04E4A167B654AF CRC64;

Query Match 51.7%; Score 367.5; DB 1; Length 120;  
 Best Local Similarity 55.0%; Pred. No. 1.1e-31;  
 Matches 72; Conservative 20; Mismatches 28; Indels 11; Gaps 1;

OY 2 VOLLOSGATEVKKPGASMKVSCMASGYPTSTYDISWVRAPGQGLEMGWISYSGNTDY 61  
 DB 1 VOLLOSGAELVIRAGSVSMSCASGYTTFTSYGNVKKRPGQGLEMGWISYSGNTDY 60  
 OY 62 OKFQGRVMTTDTTSRTAYMELRLSDDTAVYYCARDCGGAGVEDVWSGEYPEYAMDV 121  
 DB 61 EKFKKATLTVDKSSSTAYMQLRSLTSDSAVYCAR-----SVYGGSTYFPDY 109  
 OY 122 WGGGTTTVSS 132  
 DB 110 WGGGTTTVSS 120

## RESULT 5

HV13\_MOUSE STANDARD; PRT; 117 AA.  
 AC P01757;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region J558.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=80078170; PubMed=6765983;  
 RA Schilling J., Clevinger B., Davie J.M., Hood L.;  
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA  
 RT rearrangements in heavy chain V-region gene segments.";  
 RL Nature 283:35-40(1980).  
 CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO  
 CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF  
 CC WHICH OCCUR IN THE D AND J SEGMENTS.  
 CC -1- SIMILARITY: THIS PROTEIN BINDS DEXTRAN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR HSSP: P01789; IMCP.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.

DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 116  
 FT DISULFID 22 96  
 FT NON\_TER 117 117  
 FT BY SIMILARITY.  
 SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 51.1%; Score 363.5; DB 1; Length 117;  
 Best Local Similarity 53.8%; Pred. No. 2.7e-31;  
 Matches 71; Conservative 18; Mismatches 28; Indels 15; Gaps 1;

OY 1 OVOLLOSGATEVKKPGASMKVSCMASGYPTSTYDISWVRAPGQGLEMGWISYSGNTDY 60  
 DB 1 EVOLLOSGPELVKPGASVSMSCASGYTFDYVMKWVKQSHGKSLKLEMGWISYSGNTDY 60  
 OY 61 AOKFQGRVMTTDTTSRTAYMELRLSDDTAVYYCARDCGGAGVEDVWSGEYPEYAMD 120  
 DB 61 NOKFKGATLTVDKSSSTAYMQLRSLTSDSAVYCAR-----RYWYFD 105  
 OY 121 WGGGTTTVSS 132  
 DB 106 WGGGTTTVSS 117

## RESULT 6

HV50\_MOUSE STANDARD; PRT; 120 AA.  
 ID HV50\_MOUSE  
 AC P06329;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUN-1998 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region AC38 15.3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=84182519; PubMed=6201362;  
 RA Dildrop R., Bovens L., Stekevitz M., Beyreuther K., Rajewsky K.;  
 RT "A V region determinant (idiotope) expressed at high frequency in B  
 RT lymphocytes is encoded by a large set of antibody structural genes.";  
 RL EMBO J. 3:517-523(1984).  
 DR PIR: A02037; MEMS15.  
 DR HSSP: P01810; 2PRJ.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region.  
 FT DOMAIN 1 98  
 FT DOMAIN 99 105  
 FT DOMAIN 106 120  
 FT DISULFID 22 96  
 FT NON\_TER 120 120  
 FT BY SIMILARITY.  
 SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09814 CRC64;

Query Match 50.8%; Score 361; DB 1; Length 120;  
 Best Local Similarity 53.8%; Pred. No. 5.1e-31;  
 Matches 71; Conservative 18; Mismatches 31; Indels 12; Gaps 2;

OY 1 OVOLLOSGATEVKKPGASMKVSCMASGYPTSTYDISWVRAPGQGLEMGWISYSGNTDY 60  
 DB 1 OVOLLOSGTELVKPGASVSMSCASGYTTFTSYGNVKKRPGQGLEMGWISYSGNTDY 60  
 OY 61 AOKFQGRVMTTDTTSRTAYMELRLSDDTAVYYCARDCGGAGVEDVWSGEYPEYAMD 120  
 DB 61 NEKFKGATLTVDKSSSTAYMQLRSLTSDSAVYCAR-----WDYEDRIF--D 108

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QY 1 QVOLLQSAITEVKKPGASMKVSCMASGYPTSYDISWROAPGQGLEMMGWISYSGNDY 60
DB 20 QVOLLQVQSGAEVKKPGASVRSCKASGYTFIDSYIMIMQAQGHGLEWGMINPNSGGINY 79
QY 61 AOKFGQGVMTTDTSTRTAYMELRLSRDSDTAIVYCARDDGGGAYEDVWGEYEP-EY-YA 118
DB 80 AFRFGQGVMTTRDASFTAYMDRLRLSRDSDSAVFYCAKAS-----DPFWSDYTFYFDYSYT 133
QY 119 MDVWQGGTTVTVSS 132
DB 134 LDVWQGGTTVTVSS 147

```

## RESULT 2

HVLB\_HUMAN

ID HVLB\_HUMAN STANDARD; PRT; 117 AA.

AC P01743;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V-I region H3 precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83144028; PubMed=6298778;

RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;

RT "Evolutionary aspects of immunoglobulin heavy chain variable region

Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

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CC -----

CC EMBL; J00240; AAA52988.1; -.

DR PIR; A02024; HVHUG.

DR HSSP; P01772; 2P84.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003006; IG-MHC.

DR Pfam; PF00047; Ig\_V.

DR SMART; SM00406; IGV\_1.

DR PROSITE; PS00835; IG-LIKE; 1.

KM Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION H3.

FT DOMAIN 20 &gt;117 IG-LIKE.

FT NON TER 117 117

SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 54.3%; Score 386; DB 1; Length 117;

Best Local Similarity 76.5%; Pred. No. 1.2e-33;

Matches 75; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

```

QY 1 QVOLLQSAITEVKKPGASMKVSCMASGYPTSYDISWROAPGQGLEMMGWISYSGNDY 60
DB 20 QVOLLQVQSGAEVKKPGASVRSCKASGYTFIDSYIMIMQAQGHGLEWGMINPNSGGINY 79
QY 61 AOKFGQGVMTTDTSTRTAYMELRLSRDSDTAIVYCAR 98
DB 80 AOKFGQGVMTTRDTSTSTVYMWELSLRSDTAIVYCAR 117

```

```

RESULT 3
HVLB_HUMAN
ID HVLB_HUMAN STANDARD; PRT; 117 AA.
AC P3083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus."
RL EMBO J. 7:1047-1051(1988).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

```

CC -----
DR EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR PIR; S00476; HVHJ35.
DR HSSP; P01772; 2P84.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS00835; IG-LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
FT DOMAIN 20 >117 IG-LIKE.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13009 MW; BE6ICE63F8CE97BD CRC64;

```

Query Match 53.7%; Score 382; DB 1; Length 117;  
 Best Local Similarity 76.5%; Pred. No. 3.1e-33;  
 Matches 75; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

```

QY 1 QVOLLQSAITEVKKPGASMKVSCMASGYPTSYDISWROAPGQGLEMMGWISYSGNDY 60
DB 20 QVOLLQVQSGAEVKKPGASVRSCKASGYTFIDSYIMIMQAQGHGLEWGMINPNSGGINY 79
QY 61 AOKFGQGVMTTDTSTRTAYMELRLSRDSDTAIVYCAR 98
DB 80 AOKFGQGVMTTRDTSTSTVYMWELSLRSDTAIVYCAR 117

```

RESULT 4

HV03\_MOUSE

ID HV03\_MOUSE STANDARD; PRT; 120 AA.

AC P01747;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region 36-65.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 7.07717 Seconds

(Without alignments)  
877.119 Million cell updates/sec

Title: US-09-674-752-25

Perfect score: 711  
Sequence: 1 QVQLLOSATEVKKPGASMKV.....YPEYVNDVWGQGTIVTSS 132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	427	60.1	147	1	HV1C_HUMAN
2	386	54.3	117	1	HV1B_HUMAN
3	382	53.7	117	1	HV1G_HUMAN
4	367.5	51.7	120	1	HV03_MOUSE
5	363.5	51.1	117	1	HV13_MOUSE
6	361	50.8	120	1	HV05_MOUSE
7	360.5	50.7	140	1	HV02_MOUSE
8	359.5	50.6	117	1	HV12_MOUSE
9	358.5	50.4	117	1	HV1A_HUMAN
10	358	50.4	118	1	HV51_MOUSE
11	354	49.8	139	1	HV07_MOUSE
12	341	48.0	114	1	HV00_MOUSE
13	339.5	47.7	136	1	HV15_MOUSE
14	338	47.5	136	1	HV16_MOUSE
15	337	47.4	137	1	HV11_MOUSE
16	335	47.1	117	1	HV52_MOUSE
17	335	47.1	120	1	HV1H_HUMAN
18	325.5	45.8	121	1	HV33_HUMAN
19	323.5	45.5	121	1	HV01_MOUSE
20	323.5	45.5	125	1	HV1F_HUMAN
21	323.5	45.5	138	1	HV48_MOUSE
22	319	44.9	122	1	HV3G_HUMAN
23	318	44.7	117	1	HV09_MOUSE
24	318	44.7	117	1	HV14_MOUSE
25	316	44.4	117	1	HV04_MOUSE
26	313	44.0	126	1	HV3K_HUMAN
27	309	43.5	117	1	HV06_MOUSE
28	306	43.0	122	1	HV3H_HUMAN
29	306	43.0	146	1	HV21_HUMAN
30	303	42.6	119	1	HV38_MOUSE
31	302.5	42.5	115	1	HV3D_HUMAN
32	301	42.3	124	1	HV1E_HUMAN
33	300	42.2	116	1	HV3T_HUMAN

34	299	42.1	117	1	HV05_MOUSE	P01749 mus musculu
35	299	42.1	124	1	HV1D_HUMAN	P01760 homo sapien
36	298.5	42.0	119	1	HV31_HUMAN	P01770 homo sapien
37	297.5	41.8	117	1	HV02_CANFA	P01785 canis fam1
38	297.5	41.8	144	1	HV43_MOUSE	P01819 mus musculu
39	296.5	41.7	117	1	HV42_MOUSE	P01812 mus musculu
40	296	41.6	117	1	HV10_MOUSE	P01784 mus musculu
41	296	41.6	117	1	HV49_MOUSE	P06328 mus musculu
42	295	41.5	122	1	HV3A_HUMAN	P01762 homo sapien
43	292	41.1	120	1	HV3J_HUMAN	P01782 homo sapien
44	290.5	40.9	123	1	HV24_MOUSE	P01793 mus musculu
45	290	40.8	114	1	HV01_CANFA	P01784 canis fam1

## ALIGNMENTS

RESULT 1  
HV1C\_HUMAN STANDARD; PRT; 147 AA.

AC P01744;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE IG heavy chain V-I region ND precursor (Fragments).  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83065234; PubMed=6815656;  
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,  
RA Bell L.O., Gould H.J.;  
RT "Cloning and sequence determination of the gene for the human  
RT immunoglobulin epsilon chain expressed in a myeloma cell line."  
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).

RP SEQUENCE OF 20-147.  
RA Bemmich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;  
RL (In) Bach M.K. (eds.);  
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,  
RL Marcel Dekker, New York (1978).  
CC -I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA  
CC PROTEIN.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSP: P01789; 1MCP.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003623; F:antigen binding activity; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_v.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; Ig; 1.  
DR POSITIVE: PSS0835; IG LIKE; 1.  
DR Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.

KM Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.  
FT CHAIN 1 19 IG HEAVY CHAIN V-I REGION ND.  
FT DOMAIN 20 131 IG-LIKE.  
FT MOD\_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 41 115  
FT CONFLICT 21 21 T -> V (IN REF. 2).  
FT CONFLICT 53 54 IH -> HI (IN REF. 2).  
FT CONFLICT 67 68 VG -> GV (IN REF. 2).  
FT CONFLICT 125 125 MISSING (IN REF. 2).  
FT NON\_TER 147 147  
SQ SEQUENCE 147 AA; 16491 MW; 948PF72A536C20 CRC64;

Query Match 60.1%; Score 427; DB 1; Length 147;  
Best Local Similarity 62.7%; Pred. No. 7,76-18;  
Matches 84; Conservative 16; Mismatches 26; Indels 8; Gaps 3;







C:Accession: S26792  
 R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.  
 Eur. J. Immunol. 22, 241-245, 1992  
 A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family  
 A:Reference number: S26786; MUID:9211632; PMID:1730251  
 A:Accession: S26792  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-131 <MAR>  
 A:Cross-references: EMBL:X61012; NID:932804; PIDN:CAA43346.1; PID:91335131  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterodimer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match  
 Best Local Similarity 66.7%; Score 474.5; DB 2; Length 131;  
 Matches 89; Conservative 17; Mismatches 25; Indels 1; Gaps 1;  
 QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYFTSYDTSWVROAPGCGLEWGMISTISGNTDY 60  
 Db 1 QVOLLQSAATEVKKPGASMKVSCMASGYFTSYDTSWVROAPGCGLEWGMISTISGNTDY 60  
 QY 61 AOKFGRTVMTTDSRRTAYWELSLRSDDTAVYYCARDGGGAYEDVWSGEYPEYAMD 120  
 Db 61 AOKFGRTVMTTDSRRTAYWELSLRSDDTAVYYCARDGGGAYEDVWSGEYPEYAMD 120  
 QY 121 VMGCGTTVTYVSS 132  
 Db 120 VMGCGTTVTYVSS 131

## RESULT 7

PH0954  
 Ig heavy chain V region (G6+ CUL-HEN) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
 C:Accession: PH0954  
 R:Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.  
 J. Exp. Med. 175, 983-991, 1992  
 A:Title: Evidence for somatic selection of natural autoantibodies.  
 A:Reference number: PH0952; MUID:92202880; PMID:1552291  
 A:Accession: PH0954  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-132 <MAR>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterodimer; immunoglobulin  
 F:1-30/Region: framework 1  
 F:15-98/Domain: immunoglobulin homology <IMM>  
 F:31-35/Region: complementarity-determining 1  
 F:36-50/Region: framework 2  
 F:51-67/Region: complementarity-determining 2  
 F:68-98/Region: framework 3  
 F:99-120/Region: complementarity-determining 3

Query Match  
 Best Local Similarity 66.5%; Score 473; DB 2; Length 132;  
 Matches 95; Conservative 9; Mismatches 26; Indels 4; Gaps 2;  
 QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYFTSYDTSWVROAPGCGLEWGMISTISGNTDY 60  
 Db 1 QVOLLQSAATEVKKPGASMKVSCMASGYFTSYDTSWVROAPGCGLEWGMISTISGNTDY 60  
 QY 61 AOKFGRTVMTTDSRRTAYWELSLRSDDTAVYYCARDGGGAYEDVWSGEYPEYAMD 118  
 Db 61 AOKFGRTVMTTDSRRTAYWELSLRSDDTAVYYCARDGGGAYEDVWSGEYPEYAMD 118  
 QY 119 MDVWGCGTTVTYVSS 132  
 Db 119 MDVWGCGTTVTYVSS 132

## RESULT 8

S34014  
 Ig heavy chain V region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
 C:Accession: S34014; S30535  
 R:Marlette, X.; Teaple, A.; Brouet, J.C.  
 Eur. J. Immunol. 23, 846-851, 1993  
 A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal  
 A:Reference number: S34001; MUID:93209281; PMID:7681398  
 A:Accession: S34014  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-127 <MAR>  
 A:Cross-references: EMBL:Z18321  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterodimer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match  
 Best Local Similarity 65.2%; Score 463.5; DB 2; Length 127;  
 Matches 94; Conservative 12; Mismatches 21; Indels 5; Gaps 2;  
 QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYFTSYDTSWVROAPGCGLEWGMISTISGNTDY 60  
 Db 1 QVOLLQSAATEVKKPGASMKVSCMASGYFTSYDTSWVROAPGCGLEWGMISTISGNTDY 60  
 QY 61 AOKFGRTVMTTDSRRTAYWELSLRSDDTAVYYCARDGGGAYEDVWSGEYPEYAMD 120  
 Db 61 AOKFGRTVMTTDSRRTAYWELSLRSDDTAVYYCARDGGGAYEDVWSGEYPEYAMD 120  
 QY 121 VMGCGTTVTYVSS 132  
 Db 116 VMGCGTTVTYVSS 127

## RESULT 9

C33548  
 Ig heavy chain V-1 region (783) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996  
 C:Accession: C33548  
 R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffly, S.; Chen, P.P.; Carson, D.A.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989  
 A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene  
 A:Reference number: A33548; MUID:89345575; PMID:2503826  
 A:Accession: C33548  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: DNA  
 A:Residues: 1-133 <KIP>  
 A:Experimental source: the sequence was determined from the differentiated gene  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterodimer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match  
 Best Local Similarity 65.0%; Score 462.5; DB 2; Length 133;  
 Matches 94; Conservative 8; Mismatches 27; Indels 7; Gaps 2;  
 QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYFTSYDTSWVROAPGCGLEWGMISTISGNTDY 60  
 Db 1 QVOLLQSAATEVKKPGASMKVSCMASGYFTSYDTSWVROAPGCGLEWGMISTISGNTDY 60  
 QY 61 AOKFGRTVMTTDSRRTAYWELSLRSDDTAVYYCARDGGGAYEDVWSGEYPEYAMD 116  
 Db 61 AOKFGRTVMTTDSRRTAYWELSLRSDDTAVYYCARDGGGAYEDVWSGEYPEYAMD 116  
 QY 117 YAMDVWGCGTTVTYVSS 132  
 Db 118 YAMDVWGCGTTVTYVSS 133

## RESULT 10

S14683



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 ; Search time 12.6531 Seconds  
(without alignments)  
1003.251 Million cell updates/sec

Title: US-09-674-752-25

Perfect score: 711

Sequence: 1 QVQLQSGATVEKVKPKGASMKV.....YPEYVMDVWGCGTTVTSS 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	520.5	73.2	129	2 S36260	Ig heavy chain V r
2	507.5	71.4	122	2 S36271	Ig heavy chain V r
3	486	68.4	124	2 S19665	Ig heavy chain V r
4	481.5	67.7	160	2 PL0105	anti-PR2 erythrocy
5	478.5	66.7	129	2 S46393	Ig heavy chain V r
6	474.5	66.7	131	2 S26792	Ig heavy chain V r
7	473	66.5	132	2 PH0954	Ig heavy chain V r
8	463.5	65.2	127	2 S34014	Ig heavy chain V r
9	462.5	65.0	133	2 C33548	Ig heavy chain V-1
10	462.5	65.0	627	2 S14683	Ig mu chain precur
11	460	64.7	136	2 S31600	Ig heavy chain V r
12	454	63.9	114	2 PH1667	Ig heavy chain V r
13	453	63.7	118	2 PH1666	Ig heavy chain V r
14	452.5	63.4	125	2 S68170	Ig heavy chain V r
15	451	63.4	118	2 S36265	Ig heavy chain V r
16	450	63.3	98	2 S26919	Ig heavy chain V r
17	450	63.3	128	2 PH0952	Ig heavy chain V r
18	449.5	63.2	123	2 D33548	Ig heavy chain V-1
19	446	62.7	110	2 PH1670	Ig heavy chain V r
20	445	62.6	131	2 S21924	Ig heavy chain V r
21	443	62.3	135	2 S49530	Ig heavy chain V r
22	443	62.3	136	2 PH0961	anti-Sm antibody V
23	442.5	62.2	119	2 PH0960	Ig heavy chain V r
24	438.5	61.7	127	2 PH0955	Ig heavy chain V r
25	434	61.0	135	2 B32274	Ig heavy chain pre
26	433	60.9	126	2 B33548	Ig heavy chain V-1
27	433	60.7	121	2 S23623	Ig heavy chain V r
28	431.5	60.7	125	2 PH0957	Ig heavy chain V r
29	429.5	60.4	129	2 A33548	Ig heavy chain V-1

#### ALIGNMENTS

##### RESULT 1

Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
C:Accession: S36260  
R:Giffiths, A.D.; Malngviat, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J  
EMBO J. 12, 725-734, 1993  
A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
A:Reference number: S36256; WUID:93178448; PMID:7679990  
A:Accession: S36260  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-129 <GR1>  
A:Cross-references: EMBL:Z18851; NID:G33124; PID:CAA79303.1; PID:G939903  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMV>

Query Match 73.2%; Score 520.5; DB 2; Length 129;  
Best Local Similarity 79.5%; Pred. No. 5.6e-41;  
Matches 105; Conservative 4; Mismatches 20; Indels 3; Gaps 2;

QY 1 QVQLQSGATVEKVKPKGASMKVCSWASGYPTFSYDLSWROAPGGGLEMGWISYSGNTDY 60  
DB 1 QVQLQSGATVEKVKPKGASVKSCASGTTFTSYGISWROAPGGGLEMGWISYNGNTNY 60  
QY 61 AGRFQGRVTMTTDTSRRTAVMELRSLSRSDTAVYCCARDGGGAYEDVMSGEYPEYVAMD 120  
DB 61 AQLQGRVTMTTDTSTSTAVMELRSLSRSDTAVYCCARDGFG--YCSSTSCPY-YYYVMD 117  
QY 121 VMGCGTTVTSS 132  
DB 118 VMGKGTTVTSS 129

##### RESULT 2

Ig heavy chain V region (clone alpha-THY-29) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
C:Accession: S36271  
R:Giffiths, A.D.; Malngviat, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J  
EMBO J. 12, 725-734, 1993  
A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
A:Reference number: S36256; WUID:93178448; PMID:7679990  
A:Accession: S36271  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-122 <GR1>  
A:Cross-references: EMBL:Z18832; NID:G33115; PID:CAA79284.1; PID:G939895  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2422
; TELEFAX: 415-326-2400
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION: /label= HUMAN_1
US-08-964-690-22

```

Query Match 68.5%; Score 471; DB 3; Length 128;  
 Best Local Similarity 72.6%; Pred. No. 2e-41;

Matches 98; Conservative 6; Mismatches 19; Indels 12; Gaps 3;

```

QY 1 QVQLVSGAEAKKPKGSSVKVSCKASGDTFNSPISWRQAPGQGLEWMGCIIPF-FGSTK 59
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 QVQLVSGAEVKKPKGSSVKVSCKASGYTFSTAIISWRQAPGQGLEMMGWINPYGNGDTN 60
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 60 YAKFGGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQ-----ONGGWYEGPLEPRPD 115
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 YAKFGGRVTITADTSTAYMELSLRSEDTAVYYCARAPGYSGGCGYRG-----D 113
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 116 ALDIMQGTMVTYSS 130
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 114 YFDYWGQTLVTYSS 128
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

RESULT 15

US-08-217-918-4  
 ; Sequence 4, Application US/08217918  
 ; Patent No. 5506132

; GENERAL INFORMATION:

; APPLICANT: LAKE, PHILIP  
 ; APPLICANT: OSTBERG, LARS  
 ; TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST  
 ; TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew  
 ; STREET: 379 Lytton Avenue  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/217,918

; FILING DATE: 24-MAR-1994

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M

; REGISTRATION NUMBER: 30,223

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2422

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 147 amino acids

; TYPE: amino acid

; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-217-918-4

Query Match 68.5%; Score 471; DB 1; Length 147;  
 Best Local Similarity 70.7%; Pred. No. 2.4e-41;

Matches 94; Conservative 13; Mismatches 18; Indels 8; Gaps 2;

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QY 1 QVQLVSGAEAKKPKGSSVKVSCKASGDTFNSPISWRQAPGQGLEWMGCIIPFSTKY 60
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 20 QVQLVSGAEVKKPKGSSVKVSCKASGDTFNSPISWRQAPGQGLEMMGRIMPLFVTSTY 79
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 61 AOKFGGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGGWYEGPLEPRPD---DAL 117
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 80 AOKFGGRVTISADASTSTAYMELSLRSDPTAVYYCARD-----ITAPGAAPTPLNFGM 134
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 118 DIMQGTMVTYSS 130
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 135 DVWGQGTITVYSS 147
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Search completed: December 30, 2003, 11:05:31  
 Job time : 14.284 secs

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9525004.9  
FILING DATE: 07-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02240  
FILING DATE: 02-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/244,597  
FILING DATE: 01-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33308  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-652-816A-9

Query Match 68.5%; Score 471.5; DB 2; Length 123;  
Best Local Similarity 71.5%; Pred. No. 1,7e-41;  
Matches 93; Conservative 13; Mismatches 17; Indels 7; Gaps 1;

QY 1 QVQLVDSGAEAKKPGSSVYKSCASGDTFNSFPISWVRQAPGQGLEWMGIIPIFGSTY 60  
DB 1 QVQLVDSGAEVKKPGSSVKVKSCASGDTFNSDPIDMVRQAPGQGLEWMGSIIPSTRTANY 60  
QY 61 AQKFGKRVITADGSTAYAMELNSLRSEPTATYYCARQONGWYEGPLLEPRPDLDI 120  
DB 61 AQKFGKRLITADGSTAYAMELNSLRSEDTAVYYCARGSH-----TYELYYMYMDW 113  
QY 121 GGGTMTVSS 130  
DB 114 GGGTMTVSS 123

RESULT 13  
US-08-202-047-22  
Sequence 22, Application US/08202047  
Patent No. 5800815  
GENERAL INFORMATION:  
APPLICANT: CHESNUT, Robert W.  
APPLICANT: POLLEY, Margaret J.  
APPLICANT: PAULSON, James C.  
APPLICANT: JONES, S. Tarran  
APPLICANT: SALDANHA, Jose W.  
APPLICANT: BENDIG, Mary M.  
TITLE OF INVENTION: Antibodies to P-selectin and Their Uses  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,047  
FILING DATE: 25-FEB-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14137-77  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..128  
OTHER INFORMATION: /label= HUMAN\_1  
US-08-202-047-22

Query Match 68.5%; Score 471; DB 1; Length 128;  
Best Local Similarity 72.6%; Pred. No. 2e-41;  
Matches 98; Conservative 6; Mismatches 19; Indels 12; Gaps 3;

QY 1 QVQLVDSGAEAKKPGSSVYKSCASGDTFNSFPISWVRQAPGQGLEWMGIIPI-FASTK 59  
DB 1 QVQLVDSGAEVKKPGSSVKVKSCASGDTFTSYAISWVRQAPGQGLEWMGWIPIFGNDITN 60  
QY 60 YAKFGKRVITADGSTAYAMELNSLRSEPTATYYCARQ-----QNGWYEGPLLEPRPD 115  
DB 61 YAKFGKRVITADGSTAYAMELNSLRSEDTAVYYCARAPGVSGCGCYRG-----D 113  
QY 116 ALDIWGCGTMTVSS 130  
DB 114 YFDYWGCGTMTVSS 128

RESULT 14  
US-08-964-690-22  
Sequence 22, Application US/08964690  
Patent No. 6033667  
GENERAL INFORMATION:  
APPLICANT: CHESNUT, Robert W.  
APPLICANT: POLLEY, Margaret J.  
APPLICANT: PAULSON, James C.  
APPLICANT: JONES, S. Tarran  
APPLICANT: SALDANHA, Jose W.  
APPLICANT: BENDIG, Mary M.  
TITLE OF INVENTION: Antibodies to P-selectin and Their Uses  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/964,690  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,047  
FILING DATE: 25-FEB-1994

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/33308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-652-816A-8

```

```

Query Match      69.7%; Score 479.5; DB 2; Length 123;
Best Local Similarity 70.1%; Pred. No. 2,6e-42;
Matches 94; Conservative 13; Mismatches 12; Indels 15; Gaps 2;

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QY 1 QVQLVSGAEAKKPGSSVYVSCSKASGDTFNSPISWVRQAPQGLEWMGSIIPFGSTKY 60
DB 1 QVQLVSGAEVKKPGSSVYVSCSKASGDTFNSPISWVRQAPQGLEWMGSIIPFGSTKY 60
QY 61 AOKFGRLTITADGSTAYMELSLRSEDTAIYYCA-RQNGCWYEGGLEPRDADI 116
DB 61 AOKFGRLTITADGSTAYMELSLRSEDTAIYYCA-RQNGCWYEGGLEPRDADI 116
QY 117 LDIMGGTMTVSS 130
DB 110 MDVMGGTMTVSS 123

```

```

RESULT 11
US-08-652-816A-1
; Sequence 1, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Oxbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (ERO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.8
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525004.9
; FILING DATE: 07-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9610824.6
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/33308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-652-816A-1

```

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Query Match      69.0%; Score 474.5; DB 2; Length 123;
Best Local Similarity 72.5%; Pred. No. 8,5e-42;
Matches 95; Conservative 11; Mismatches 16; Indels 9; Gaps 2;

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QY 1 QVQLVSGAEAKKPGSSVYVSCSKASGDTFNSPISWVRQAPQGLEWMGSIIPFGSTKY 60
DB 1 QVQLVSGAEVKKPGSSVYVSCSKASGDTFNSPISWVRQAPQGLEWMGSIIPFGSTKY 60
QY 61 AOKFGRLTITADGSTAYMELSLRSEDTAIYYCA-RQNGCWYEGGLEPRDADI 119
DB 61 AOKFGRLTITADGSTAYMELSLRSEDTAIYYCA-RQNGCWYEGGLEPRDADI 119
QY 120 WCGTMTVSS 130
DB 113 WCGTMTVSS 123

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```

RESULT 12
US-08-652-816A-9
; Sequence 9, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Oxbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25 (ERO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.8
; FILING DATE: 02-DEC-1991

```



FILING DATE: 29-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Howell, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: FD-2630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: KAS  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..120  
US-08-428-197-13

Query Match 69.8%; Score 480.5; DB 2; Length 120;  
Best Local Similarity 73.6%; Pred. No. 2e-42;  
Matches 95; Conservative 10; Mismatches 15; Indels 9; Gaps 2;

QY 2 VLVVSGAEAKKPGSSVVKVSCKASGDTFNSFPISWVROAPGQGLEWNGIIPFGSTKYA 61  
DB 1 VHLVSGAEVKKPGSSVVKVSCKASGDTFSSVAISWVROAPGQGLEWNGIIPFGQANYA 60  
QY 62 QKFGKVTMTADGSTSTAYMEINLSRSEDTAIYYCARQONGWYEGPLLEPRDALDIWG 121  
DB 61 QKFGKVTMTADGSTSTAYMEINLSRSEDTAIYYCARQONGWYEGPLLEPRDALDIWG 121  
QY 122 QGTWTVSS 130  
DB 112 QGTWTVSS 120

RESULT 9  
PCT-US93-10555-13  
Sequence 13, Application PC/TUS9310555  
GENERAL INFORMATION:  
APPLICANT: SILVERMAN, GREGG J.  
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF  
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH  
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONUGATES  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Unbas & Lubitz  
STREET: 1880 Century Park East - Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10555  
FILING DATE: 29-OCT-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Howell, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: FD-2630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: KAS  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..120  
PCT-US93-10555-13

Query Match 69.8%; Score 480.5; DB 5; Length 120;  
Best Local Similarity 73.6%; Pred. No. 2e-42;  
Matches 95; Conservative 10; Mismatches 15; Indels 9; Gaps 2;

QY 2 VLVVSGAEAKKPGSSVVKVSCKASGDTFNSFPISWVROAPGQGLEWNGIIPFGSTKYA 61  
DB 1 VHLVSGAEVKKPGSSVVKVSCKASGDTFSSVAISWVROAPGQGLEWNGIIPFGQANYA 60  
QY 62 QKFGKVTMTADGSTSTAYMEINLSRSEDTAIYYCARQONGWYEGPLLEPRDALDIWG 121  
DB 61 QKFGKVTMTADGSTSTAYMEINLSRSEDTAIYYCARQONGWYEGPLLEPRDALDIWG 121  
QY 122 QGTWTVSS 130  
DB 112 QGTWTVSS 120

RESULT 10  
US-08-652-816A-8  
Sequence 8, Application US/08652816A  
Patent No. 5872215  
GENERAL INFORMATION:  
APPLICANT: Osbourn, JK  
APPLICANT: Allen, DJ  
TITLE OF INVENTION: Specific binding members, materials and  
TITLE OF INVENTION: methods.  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,816A  
FILING DATE: 23-MAY-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.4  
FILING DATE: 02-DEC-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.8  
FILING DATE: 02-DEC-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9206316.9  
FILING DATE: 24-MAR-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9525004.9  
FILING DATE: 07-DEC-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,081B  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: SVENSSON, LEONARD R  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 20-3484  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-232-081B-41

Query Match 70.1%; Score 482.5; DB 2; Length 121;  
Best Local Similarity 73.1%; Pred. No. 1.2e-42;  
Matches 95; Conservative 11; Mismatches 15; Indels 9; Gaps 2;

OY 1 QVQVQSGAEAKKPGSSVSVSCASGDTFNSFPISWVROAPQGLMMGGIPIFGSTKY 60  
DB 1 EVHLVQSGAEVKKPGSSVSVSCASGDTFNSFPISWVROAPQGLMMGGIPIFGQANT 60  
OY 61 AOKQGRVTMTADGSTATYAMELNSRSEDTAIYYCARQONGWYEGPDLLEPRDALDIW 120  
DB 61 AOKQGRVTMTADGSTATYAMELNSRSEDTAIYYCARQONGWYEGPDLLEPRDALDIW 120  
OY 121 GQGTMTVTVSS 130  
DB 112 GQGTMTVTVSS 121

RESULT 7  
US-08-983-607-50  
Sequence 50, Application US/08983607  
Patent No. 6140470  
GENERAL INFORMATION:  
APPLICANT: XIAOHONG CAI  
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-  
TITLE OF INVENTION: Bodies  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Department of Molecular Biophysics  
and Biochemistry, Yale University  
STREET: 266 Whitney Avenue  
CITY: New Haven  
STATE: Connecticut  
COUNTRY: United States of America  
ZIP: 06520-8114  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" 1.44 Mb diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Word Processing  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/983,607  
FILING DATE: April 27, 1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/IB96/01032  
FILING DATE: June 28, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Mary M. Kinsky  
REGISTRATION NUMBER: 32423  
REFERENCE/DOCKET NUMBER: OCR-679  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 203-773-9544  
TELEFAX: 203-773-1183  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 residues  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: polypeptide  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens (melanoma patient  
immunized with autologous tumor cells)  
INDIVIDUAL ISOLATE: peripheral blood lympho-  
INDIVIDUAL ISOLATE: cytes  
IMMEDIATE SOURCE:  
LIBRARY: VH antibodies obtained from fuses  
LIBRARY: fusion phage construct  
CLONE: 2-71  
FEATURE:  
NAME/KEY: heavy chain  
US-08-983-607-50

Query Match 70.0%; Score 481.5; DB 3; Length 119;  
Best Local Similarity 77.2%; Pred. No. 1.5e-42;  
Matches 95; Conservative 7; Mismatches 10; Indels 11; Gaps 2;

OY 8 GAELKPGSSVSVSCASGDTFNSFPISWVROAPQGLMMGGIPIFGSTYAKPGGR 67  
DB 8 GLEVKKPGSSVSVSCASGDTFNSFPISWVROAPQGLMMGGIPIFGTANYAKPGGR 67  
OY 68 VMTADGSTATYAMELNSRSEDTAIYYCARQONGWYEGPDLLEPRDALDIWGGTMYT 127  
DB 68 VMTADGSTATYAMELNSRSEDTAIYYCARQONGWYEGPDLLEPRDALDIWGGTMYT 127  
OY 128 VSS 130  
DB 117 VSS 119

RESULT 8  
US-08-428-197-13  
Sequence 13, Application US/08428197  
Patent No. 5891438  
GENERAL INFORMATION:  
APPLICANT: SILVERMAN, GREGG J.  
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF  
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH  
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERNATANT AND CONJUGATES  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East - Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/428,197  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10555

APPLICANT: SILVERMAN, GREGG J.  
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF  
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH  
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East - Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/428,197  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10555  
FILING DATE: 29-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Howells, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: FD-2630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: BOR  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..120  
US-08-428-197-12

Query Match 70.4%; Score 484.5; DB 2; Length 120;  
Best Local Similarity 75.2%; Pred. No. 7.7e-43;  
Matches 97; Conservative 9; Mismatches 14; Indels 9; Gaps 2;

QY 2 VOLVSGAEAKKPGSSVYKVCCKASGDTFNSPISWVROAPGQLEMMGGIIPFGSTKYA 61  
DB 1 VOLVSGAEVKKPGSSVYKVCCKASGDTFSSAISWVROAPGQLEMMGGIIPFGTNYA 60

QY 62 OKFOGRVTMTADGSTAYMELNSLRSEDTAIYYCARQONGCWYEGPBLEPRPDALDING 121  
DB 61 OKFOGRVTITTDSTAYMEVSLRSSEDTALYYCAR-----EGRRMAINP--FDYWG 111

QY 122 OGTMVTVSS 130  
DB 112 OGTLVTVSS 120

RESULT 5  
PCT-US93-10555-12  
Sequence 12, Application PC/TUS9310555  
GENERAL INFORMATION:  
APPLICANT: SILVERMAN, GREGG J.  
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF  
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH  
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES  
NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East - Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10555  
FILING DATE: 29-OCT-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Howells, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: FD-2630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: BOR  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..120  
PCT-US93-10555-12

Query Match 70.4%; Score 484.5; DB 5; Length 120;  
Best Local Similarity 75.2%; Pred. No. 7.7e-43;  
Matches 97; Conservative 9; Mismatches 14; Indels 9; Gaps 2;

QY 2 VOLVSGAEAKKPGSSVYKVCCKASGDTFNSPISWVROAPGQLEMMGGIIPFGSTKYA 61  
DB 1 VOLVSGAEVKKPGSSVYKVCCKASGDTFSSAISWVROAPGQLEMMGGIIPFGTNYA 60

QY 62 OKFOGRVTMTADGSTAYMELNSLRSEDTAIYYCARQONGCWYEGPBLEPRPDALDING 121  
DB 61 OKFOGRVTITTDSTAYMEVSLRSSEDTALYYCAR-----EGRRMAINP--FDYWG 111

QY 122 OGTMVTVSS 130  
DB 112 OGTLVTVSS 120

RESULT 6  
US-08-232-081B-41  
Sequence 41, Application US/08232081B  
Patent No. 5886152  
GENERAL INFORMATION:  
APPLICANT: NAKATANI, TOMOYUKI  
APPLICANT: GOMI, HIDEYUKI  
APPLICANT: WIDENES, JOHN  
APPLICANT: NOGUCHI, HIROSHI  
TITLE OF INVENTION: HUMANIZED B-B10  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:

QY 1 0VOLVSGAEAKKPKSSVSVKSCASGDTFNSFPISWVROAPGQGLEWNGIIPFGSTKY 60  
DB 1 0VOLVSGAEAKKPKSSVSVKSCASGDTFNSFPISWVROAPGQGLEWNGIIPFGSTKY 60  
QY 61 AOKFQGRVITTADESTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRDALDIW 120  
DB 61 AOKFQGRVITTADESTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRDALDIW 120  
QY 121 GGGTMTVSS 130  
DB 111 GGGTMTVSS 120

## RESULT 2

US-09-025-7698-57  
Sequence 57, Application US/090257698  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,7698  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-7698-57

Query Match 74.4%; Score 512; DB 4; Length 120;  
Best Local Similarity 76.9%; Pred. No. 1,le-45;  
Matches 100; Conservative 9; Mismatches 11; Indels 10; Gaps 1;  
QY 1 0VOLVSGAEAKKPKSSVSVKSCASGDTFNSFPISWVROAPGQGLEWNGIIPFGSTKY 60  
DB 1 0VOLVSGAEAKKPKSSVSVKSCASGDTFNSFPISWVROAPGQGLEWNGIIPFGSTKY 60  
QY 61 AOKFQGRVITTADESTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRDALDIW 120  
DB 61 AOKFQGRVITTADESTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRDALDIW 120  
QY 121 GGGTMTVSS 130  
DB 121 GGGTMTVSS 130

DB 111 GGGTMTVSS 120

## RESULT 3

US-09-025-7698-21  
Sequence 21, Application US/090257698  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,7698  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-7698-21

Query Match 72.2%; Score 496.5; DB 4; Length 119;  
Best Local Similarity 76.2%; Pred. No. 4.4e-44;  
Matches 99; Conservative 8; Mismatches 12; Indels 11; Gaps 2;  
QY 1 0VOLVSGAEAKKPKSSVSVKSCASGDTFNSFPISWVROAPGQGLEWNGIIPFGSTKY 60  
DB 1 0VOLVSGAEAKKPKSSVSVKSCASGDTFNSFPISWVROAPGQGLEWNGIIPFGSTKY 60  
QY 61 AOKFQGRVITTADESTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRDALDIW 120  
DB 61 AOKFQGRVITTADESTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRDALDIW 120  
QY 121 GGGTMTVSS 130  
DB 110 GGGTMTVSS 119  
RESULT 4  
US-08-428-197-12  
Sequence 12, Application US/08428197  
Patent No. 5891438  
GENERAL INFORMATION:

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 30, 2003, 10:47:45 (Search time 13.2007 Seconds  
(without alignments)  
416.677 Million cell updates/sec

Title: US-09-674-752-23

Sequence: 1 QVQLVSGAARAKKPGSSVKY.....EPRPDALDIWGQMTVTSS 130

Scoring table: BLOSUM62

Gapop 10.0, Gapex 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:\*

1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:.\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:.\*  
3: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:.\*  
4: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:.\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:.\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	512	74.4	120	4	US-09-025-769B-35
2	512	74.4	120	4	US-09-025-769B-57
3	496.5	72.2	119	4	US-09-025-769B-21
4	484.5	70.4	120	2	US-08-428-197-12
5	484.5	70.4	120	5	PCT-US93-10555-12
6	482.5	70.1	121	2	US-08-232-081B-41
7	481.5	70.0	121	3	US-08-983-607-50
8	480.5	69.8	120	2	US-08-428-197-13
9	479.5	69.7	120	5	PCT-US93-10555-13
10	479.5	69.7	123	2	US-08-652-816A-8
11	474.5	68.0	123	2	US-08-652-816A-1
12	471.5	68.5	128	1	US-08-202-047-22
13	471	68.5	128	3	US-08-964-690-22
14	471	68.5	147	1	US-08-217-918-4
15	471	68.5	129	2	US-08-652-816A-6
16	469.5	68.2	123	2	US-08-561-521-45
17	465.5	67.7	129	4	US-08-525-539A-77
18	465.5	67.7	129	5	PCT-US95-01219-45
19	463.5	67.4	126	4	US-09-025-769B-36
20	463.5	67.4	120	4	US-09-025-769B-59
21	463	67.3	123	1	US-08-482-862-53
22	463	67.3	123	2	US-08-487-113D-53
23	462.5	67.2	123	2	US-08-473-503-53
24	462.5	67.2	123	2	US-08-483-389-53
25	462.5	67.2	123	2	US-08-483-389-53
26	462.5	67.2	123	2	US-08-483-389-53
27	462.5	67.2	123	2	US-08-483-389-53

28	462.5	67.2	123	2	US-08-720-420A-53	Sequence 53, Appl
29	462.5	67.2	123	3	US-08-714-017-53	Sequence 53, Appl
30	462.5	67.2	123	3	US-08-475-680-53	Sequence 53, Appl
31	461.5	67.1	123	2	US-08-652-816A-7	Sequence 7, Appl
32	461.5	67.1	125	3	US-09-199-149-3	Sequence 3, Appl
33	459	66.6	139	4	US-09-355-925-7	Sequence 7, Appl
34	456.5	66.6	117	4	US-09-025-769B-22	Sequence 22, Appl
35	454	66.0	139	4	US-09-355-925-8	Sequence 8, Appl
36	447.5	65.0	121	3	US-08-579-378A-8	Sequence 12, Appl
37	447.5	65.0	140	3	US-08-579-378A-12	Sequence 12, Appl
38	447.5	65.0	140	5	PCT-US93-11612-12	Sequence 12, Appl
39	446	64.8	139	1	US-08-233-877C-19	Sequence 19, Appl
40	446	64.8	139	2	US-08-452-164A-19	Sequence 19, Appl
41	446	64.8	139	3	US-08-603-024-18	Sequence 18, Appl
42	446	64.8	139	4	US-08-450-809-14	Sequence 14, Appl
43	443.5	64.5	122	5	PCT-US95-00067-2	Sequence 2, Appl
44	437.5	63.6	140	3	US-08-836-561-63	Sequence 63, Appl
45	437.5	63.6	140	4	US-09-434-122-63	Sequence 63, Appl

## ALIGNMENTS

RESULT 1  
US-09-025-769B-35  
Sequence 35, Application US/09025769B  
Patent No. 630064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckhuhn, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-35  
Query Match 74.4%, Score 512, DB 4, Length 120,  
Best Local Similarity 76.9%, Pred. No. 1,le-45;  
Matches 100, Conservative 9, Mismatches 11, Indels 10, Gaps 1,

## RESULT 13

US-09-880-748-1866  
 ; Sequence 1866, Application US/09880748  
 ; Publication No. US2003005937A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
 ; FILE REFERENCE: PF523  
 ; CURRENT APPLICATION NUMBER: US/09/880,748  
 ; CURRENT FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: 60/212,210  
 ; PRIOR FILING DATE: 2000-06-15  
 ; PRIOR APPLICATION NUMBER: 60/240,816  
 ; PRIOR FILING DATE: 2000-10-17  
 ; PRIOR APPLICATION NUMBER: 60/276,248  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/277,379  
 ; PRIOR FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/293,499  
 ; PRIOR FILING DATE: 2001-05-25  
 ; NUMBER OF SEQ ID NOS: 3239  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1866  
 ; LENGTH: 254  
 ; TYPE: PR1  
 ; ORGANISM: Homo sapiens  
 US-09-880-748-1866

Query Match 73.8%; Score 508; DB 11; Length 254;  
 Best Local Similarity 71.4%; Pred. No. 5,1e-39;

Matches 100; Conservative 10; Mismatches 8; Indels 22; Gaps 2;  
 QY 1 QVOLVSGAEVKKRSSVYKVCCKASGDTFNSPISWVRQAPGQLEWNGIIPFGSTKY 60  
 DB 1 QVOLVSGAEVKKRSSVYKVCCKASGDTFNSPISWVRQAPGQLEWNGIIPFGTANY 60  
 QY 61 AOKFOGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQO-----NGMYEGPPL 110  
 DB 61 AOKFOGRVTITADGSTSTAYMELNSLRSEDTAIYYCARQO-----NGMYEGPPL 110  
 QY 111 EPRDADIMGCGMTWTVSS 130  
 DB 116 -----DPMGKGTLYTVSS 128

## RESULT 14

US-10-269-805-35  
 ; Sequence 35, Application US/10269805  
 ; Publication No. US20030124129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OLINER, JONATHAN D.  
 ; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS  
 ; FILE REFERENCE: A-722  
 ; CURRENT APPLICATION NUMBER: US/10/269,805  
 ; CURRENT FILING DATE: 2002-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/328,604  
 ; PRIOR FILING DATE: 2001-10-11  
 ; NUMBER OF SEQ ID NOS: 76  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 35  
 ; LENGTH: 125  
 ; TYPE: PR1  
 ; ORGANISM: Homo sapiens  
 US-10-269-805-35

Query Match 73.8%; Score 507.5; DB 15; Length 125;  
 Best Local Similarity 78.5%; Pred. No. 2.7e-39;

Matches 102; Conservative 9; Mismatches 14; Indels 5; Gaps 2;  
 QY 1 QVOLVSGAEVKKRSSVYKVCCKASGDTFNSPISWVRQAPGQLEWNGIIPFGSTKY 60  
 DB 1 QVOLVSGAEVKKRSSVYKVCCKASGDTFNSPISWVRQAPGQLEWNGIIPFGSTKY 60

DB 1 QVOLVSGAEVKKRSSVYKVCCKASGDTFNSPISWVRQAPGQLEWNGIIPFGTANY 60

QY 61 AOKFOGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPPLPREPDALDIW 120  
 DB 61 AOKFOGRVTITADGSTSTAYMELNSLRSEDTAIYYCARSP---YD---ILTGDADADIW 115

QY 121 GCGTMTWTVSS 130  
 DB 116 GCGTMTWTVSS 125

## RESULT 15

US-10-269-805-9  
 ; Sequence 9, Application US/10269805  
 ; Publication No. US20030124129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OLINER, JONATHAN D.  
 ; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS  
 ; FILE REFERENCE: A-722  
 ; CURRENT APPLICATION NUMBER: US/10/269,805  
 ; CURRENT FILING DATE: 2002-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/328,604  
 ; PRIOR FILING DATE: 2001-10-11  
 ; NUMBER OF SEQ ID NOS: 76  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 9  
 ; LENGTH: 121  
 ; TYPE: PR1  
 ; ORGANISM: Homo sapiens  
 US-10-269-805-9

Query Match 73.6%; Score 506.5; DB 15; Length 121;  
 Best Local Similarity 78.5%; Pred. No. 3.2e-39;

Matches 102; Conservative 6; Mismatches 13; Indels 9; Gaps 2;  
 QY 1 QVOLVSGAEVKKRSSVYKVCCKASGDTFNSPISWVRQAPGQLEWNGIIPFGSTKY 60  
 DB 1 QVOLVSGAEVKKRSSVYKVCCKASGDTFNSPISWVRQAPGQLEWNGIIPFGTANY 60  
 QY 61 AOKFOGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPPLPREPDALDIW 120  
 DB 61 AOKFOGRVTITADGSTSTAYMELNSLRSEDTAIYYCAA-----FSPFTE--TDAPDIW 111  
 QY 121 GCGTMTWTVSS 130  
 DB 112 GCGTMTWTVSS 121

Search completed: December 30, 2003, 11:45:22  
 Job time : 28.8798 secs

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Query Match          74.4%; Score 512; DB 15; Length 120;
Best Local Similarity 76.9%; Pred. No. 9,8e-40;
Matches 100; Conservative 9; Mismatches 11; Indels 10; Gaps 1;

QY 1 QVOLVSGAEAKKPGSSVVKVSCASGDTFNSPFIISWVROAPGQGLEMMGIIPIFGSTKY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLVSGAEVKKPGSSVVKVSCASGDTFSSVAISWVROAPGQGLEMMGIIPIFGTANY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQ-----NGWYEGPL 110
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Db 61 AOKFQGRVTITADESTSTAYMELSLRSSEDTAVYYCARQGYDILTYGEGCF----- 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 111 EPPDALDINGGCTMTVSS 130
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 116 -----DPMGKGTMTVSS 128
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-09-880-748-1509
; Sequence 1509, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1509
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1509

Query Match          74.3%; Score 511; DB 11; Length 253;
Best Local Similarity 72.1%; Pred. No. 2,7e-39;
Matches 101; Conservative 9; Mismatches 8; Indels 22; Gaps 2;

QY 1 QVOLVSGAEAKKPGSSVVKVSCASGDTFNSPFIISWVROAPGQGLEMMGIIPIFGSTKY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLVSGAEVKKPGSSVVKVSCASGDTFSSVAISWVROAPGQGLEMMGIIPIFGTANY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQ-----NGWYEGPL 110
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKFQGRVTITADESTSTAYMELSLRSSEDTAVYYCARQGYDILTYGEGCF----- 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 111 EPPDALDINGGCTMTVSS 130
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 116 -----DPMGKGTMTVSS 128
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-10-047-542-47
; Sequence 47, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNODIAGNOSTICS FOR TREATING AND PREVENTING VIRAL
; FILE REFERENCE: 030905.0004.C1P1
; CURRENT APPLICATION NUMBER: US/10/047,542
```

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; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-47

Query Match          74.1%; Score 509.5; DB 14; Length 627;
Best Local Similarity 72.7%; Pred. No. 9,9e-39;
Matches 101; Conservative 10; Mismatches 13; Indels 15; Gaps 3;

QY 1 QVOLVSGAEAKKPGSSVVKVSCASGDTFNSPFIISWVROAPGQGLEMMGIIPIFGSTKY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVOLVSGAEVKKPGSSVVKVSCASGDTFSSVAISWVROAPGQGLEMMGIIPIFGTANY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCAR-----QONGWYEGPLPRPD 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AOKFQGRVTITADESTSTAYMELSLRSSEDTAVYYCAKTIIGPISSGWY-----PNSD 133
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 116 ----ALDINGGCTMTVSS 130
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 134 YYYGMDVWGCTTVTVSS 152
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-09-880-748-1880
; Sequence 1880, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1880
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1880

Query Match          73.9%; Score 508.5; DB 11; Length 253;
Best Local Similarity 74.6%; Pred. No. 4,6e-39;
Matches 100; Conservative 11; Mismatches 12; Indels 11; Gaps 2;

QY 1 QVOLVSGAEAKKPGSSVVKVSCASGDTFNSPFIISWVROAPGQGLEMMGIIPIFGSTKY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLVSGAEVKKPGSSVVKVSCASGDTFSSVAISWVROAPGQGLEMMGIIPIFGTANY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AOKFQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQ-----GWYEGPLPRPD 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKFQGRVTITADESTSTAYMELSLRSSEDTAVYYCARSHYDILTYGYSNP-----S 113
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 117 LDIWGCTMTVSS 130
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 114 FDIWGCTMTVSS 127
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Db 61 AOKFOGRVITTADESTSTAYMELSLRSEDPAVYVCAREDTSGMYH-----YV 108

QY 121 GCGTMTVSS 130

Db 109 GCGTMTVSS 118

## RESULT 6

US-09-880-748-1881

; Sequence 1881, Application US/09880748

; Publication No. US20030059937A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523

; CURRENT APPLICATION NUMBER: US/09/880,748

; CURRENT FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1881

; LENGTH: 244

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-880-748-1881

Query Match 74.8%; Score 514.5; DB 11; Length 244;  
Best Local Similarity 76.9%; Pred. No. 1.2e-39;  
Matches 100; Conservative 9; Mismatches 12; Indels 9; Gaps 1;

QY 1 QVQLVDSGAEAKKPGSSVKVSCKASGDTFNSFPISWYRQAPGQGLEWMGIIPIFGSTKY 60

Db 1 QVQLVDSGAEVKKRQSSVKVSCKASGDTFSSYALSWRQAPGQGLEWMGIIPIFGTANY 60

QY 61 AOKFOGRVITTADESTSTAYMELSLRSEDPAVYVCARQONGWYEGPLLEPRPDLDIW 120

Db 61 AOKFOGRVITTADESTSTAYMELSLRSDPAVYVCARDGSGYY-----DAFDIW 111

QY 121 GCGTMTVSS 130

Db 112 GCGTMTVSS 121

## RESULT 7

US-10-269-805-25

; Sequence 25, Application US/10269805

; Publication No. US20030124129A1

; GENERAL INFORMATION:

; APPLICANT: OLINER, JONATHAN D.

; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS

; FILE REFERENCE: A-722

; CURRENT APPLICATION NUMBER: US/10/269,805

; CURRENT FILING DATE: 2002-10-10

; PRIOR APPLICATION NUMBER: US 60/328,604

; PRIOR FILING DATE: 2001-10-11

; NUMBER OF SEQ ID NOS: 76

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 25

; LENGTH: 124

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-269-805-25

Query Match 74.6%; Score 513; DB 15; Length 124;

Best Local Similarity 79.2%; Pred. No. 8.2e-40;  
Matches 103; Conservative 9; Mismatches 12; Indels 6; Gaps 2;

QY 1 QVQLVDSGAEAKKPGSSVKVSCKASGDTFNSFPISWYRQAPGQGLEWMGIIPIFGSTKY 60

Db 1 QVQLVDSGAEVKKRQSSVKVSCKASGDTFSSYALSWRQAPGQGLEWMGIIPIFGTANY 60

QY 61 AOKFOGRVITTADESTSTAYMELSLRSEDPAVYVCARQONGWYEGPLLEPRPDLDIW 120

Db 61 AOKFOGRVITTADESTSTAYMELSLRSEDPAVYVCARGYD--FWSGYSL---DAFDIW 114

QY 121 GCGTMTVSS 130

Db 115 GCGTMTVSS 124

## RESULT 8

US-10-025-687-1

; Sequence 1, Application US/10025687

; Publication No. US20020142255A1

; GENERAL INFORMATION:

; APPLICANT: Luo, Peter

; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY

; FILE REFERENCE: 26050-705

; CURRENT APPLICATION NUMBER: US/10/025,687

; CURRENT FILING DATE: 2002-04-17

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 120

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Human consensus antibody heavy chain variable region

US-10-025-687-1

Query Match 74.4%; Score 512; DB 14; Length 120;  
Best Local Similarity 76.9%; Pred. No. 9.8e-40;  
Matches 100; Conservative 9; Mismatches 11; Indels 10; Gaps 1;

QY 1 QVQLVDSGAEAKKPGSSVKVSCKASGDTFNSFPISWYRQAPGQGLEWMGIIPIFGSTKY 60

Db 1 QVQLVDSGAEVKKRQSSVKVSCKASGDTFSSYALSWRQAPGQGLEWMGIIPIFGTANY 60

QY 61 AOKFOGRVITTADESTSTAYMELSLRSEDPAVYVCARQONGWYEGPLLEPRPDLDIW 120

Db 61 AOKFOGRVITTADESTSTAYMELSLRSEDPAVYVCARGGDSGFY-----AMDYV 110

QY 121 GCGTMTVSS 130

Db 111 GCGTMTVSS 120

## RESULT 9

US-10-125-687-1

; Sequence 1, Application US/10125687

; Publication No. US20030054407A1

; GENERAL INFORMATION:

; APPLICANT: Luo, Peter

; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY

; FILE REFERENCE: 26050-705

; CURRENT APPLICATION NUMBER: US/10/125,687

; CURRENT FILING DATE: 2002-04-17

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 120

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Human consensus antibody heavy chain variable region

US-10-125-687-1



```
US-10-300-675-14
; Sequence 14, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519
; CURRENT APPLICATION NUMBER: US/10/300,675
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 118
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant variant
US-10-300-675-14
```

```
Query Match
Best Local Similarity 75.9%; Score 522; DB 12; Length 118;
Matches 100; Conservative 8; Mismatches 10; Indels 12; Gaps 1;
```

```
OY 1 QVQLVQSGAEAKKPKSSVYKSCKASGDTFNSFPISWVROAPGQGLEWMGGIIPFGSTKY 60
DB 1 QVQLVQSGAEVKKPKSSVYKSCKASGDTFNSFPISWVROAPGQGLEWMGGIIPFGTANY 60
OY 61 AOKFGQRYMTADGSTAYVMEINLSRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 120
DB 61 AOKFGQRYMTADGSTAYVMEINLSRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 120
OY 121 GGGTMTVTVSS 130
DB 109 GGGTLTVTVSS 118
```

```
RESULT 3
US-10-300-675-6
; Sequence 6, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519
; CURRENT APPLICATION NUMBER: US/10/300,675
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 118
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-300-675-6
```

```
Query Match
Best Local Similarity 75.1%; Score 517; DB 12; Length 118;
Matches 99; Conservative 9; Mismatches 10; Indels 12; Gaps 1;
```

```
OY 1 QVQLVQSGAEAKKPKSSVYKSCKASGDTFNSFPISWVROAPGQGLEWMGGIIPFGSTKY 60
DB 1 QVQLVQSGAEVKKPKSSVYKSCKASGDTFNSFPISWVROAPGQGLEWMGGIIPFGTANY 60
OY 61 AOKFGQRYMTADGSTAYVMEINLSRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 120
DB 61 AOKFGQRYMTADGSTAYVMEINLSRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 120
OY 121 GGGTMTVTVSS 130
DB 109 GGGTLTVTVSS 118
```

```
RESULT 4
US-10-300-675-10
; Sequence 10, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519
; CURRENT APPLICATION NUMBER: US/10/300,675
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 118
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant variant
US-10-300-675-10
```

```
Query Match
Best Local Similarity 75.0%; Score 516; DB 12; Length 118;
Matches 99; Conservative 8; Mismatches 11; Indels 12; Gaps 1;
```

```
OY 1 QVQLVQSGAEAKKPKSSVYKSCKASGDTFNSFPISWVROAPGQGLEWMGGIIPFGSTKY 60
DB 1 QVQLVQSGAEVKKPKSSVYKSCKASGDTFNSFPISWVROAPGQGLEWMGGIIPFGTANY 60
OY 61 AOKFGQRYMTADGSTAYVMEINLSRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 120
DB 61 AOKFGQRYMTADGSTAYVMEINLSRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 120
OY 121 GGGTMTVTVSS 130
DB 109 GGGTLTVTVSS 118
```

```
RESULT 5
US-10-300-675-12
; Sequence 12, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519
; CURRENT APPLICATION NUMBER: US/10/300,675
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 118
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant variant
US-10-300-675-12
```

```
Query Match
Best Local Similarity 75.0%; Score 516; DB 12; Length 118;
Matches 99; Conservative 8; Mismatches 11; Indels 12; Gaps 1;
```

```
OY 1 QVQLVQSGAEAKKPKSSVYKSCKASGDTFNSFPISWVROAPGQGLEWMGGIIPFGSTKY 60
DB 1 QVQLVQSGAEVKKPKSSVYKSCKASGDTFNSFPISWVROAPGQGLEWMGGIIPFGTANY 60
OY 61 AOKFGQRYMTADGSTAYVMEINLSRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 120
DB 61 AOKFGQRYMTADGSTAYVMEINLSRSEDTAIYYCARQONGWYEGPLLEPRPDALDIW 120
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 11:01:15 ; Search time 27.8798 Seconds  
(without alignments)  
927.994 Million cell updates/sec

Title: US-09-674-752-23

Perfect score: 688  
Sequence: 1 OVALVOSGAERKPGSSVKV.....EPRPDLDIWMGTTVSS 130

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgnt2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	524.5	76.2	121	15	US-10-269-805-19 Sequence 19, Appl
2	522	75.9	118	12	US-10-300-675-14 Sequence 14, Appl
3	517	75.1	118	12	US-10-300-675-6 Sequence 6, Appl
4	516	75.0	118	12	US-10-300-675-10 Sequence 10, Appl
5	516	75.0	118	12	US-10-300-675-12 Sequence 12, Appl
6	514.5	74.8	124	11	US-09-880-748-1881 Sequence 1881, Ap
7	513	74.6	124	11	US-10-269-805-25 Sequence 25, Appl
8	512	74.4	120	15	US-10-125-687-1 Sequence 1, Appl
9	512	74.4	120	15	US-10-125-687-1 Sequence 1, Appl
10	511	74.3	120	15	US-09-880-748-1509 Sequence 1509, Ap
11	509.5	74.1	637	14	US-10-047-542-47 Sequence 47, Appl
12	508.5	73.9	253	11	US-09-880-748-1880 Sequence 1880, Ap
13	508	73.8	254	11	US-09-880-748-1866 Sequence 1866, Ap
14	507.5	73.8	125	15	US-10-269-805-35 Sequence 35, Appl
15	506.5	73.6	121	15	US-10-269-805-9 Sequence 9, Appl

16	504	73.3	270	9	US-09-976-118-2	Sequence 2, Appl
17	502.5	73.0	248	11	US-09-880-748-1733	Sequence 1733, Ap
18	502.5	73.0	248	11	US-09-880-748-1734	Sequence 1734, Ap
19	501.5	72.9	245	15	US-10-151-882-15	Sequence 15, Appl
20	501.5	72.9	248	11	US-09-880-748-1718	Sequence 1718, Ap
21	501.5	72.9	248	11	US-09-880-748-1879	Sequence 1879, Ap
22	500	72.7	257	11	US-09-880-748-1553	Sequence 1553, Ap
23	498.5	72.5	248	11	US-09-880-748-1732	Sequence 1732, Ap
24	498.5	72.5	248	11	US-09-880-748-1732	Sequence 1732, Ap
25	498.5	72.5	248	11	US-09-880-748-1732	Sequence 1732, Ap
26	497.5	72.3	248	11	US-10-308-917-191	Sequence 1737, Ap
27	497.5	72.3	248	11	US-09-880-748-1741	Sequence 1741, Ap
28	497.5	72.3	250	11	US-09-880-748-2066	Sequence 1745, Ap
29	497	72.2	254	11	US-09-880-748-1450	Sequence 1756, Ap
30	495.5	72.0	248	11	US-09-880-748-1727	Sequence 1756, Ap
31	495.5	72.0	248	11	US-09-880-748-1727	Sequence 1756, Ap
32	493.5	71.7	251	11	US-09-880-748-1756	Sequence 1756, Ap
33	492.5	71.6	123	15	US-10-269-805-3	Sequence 3, Appl
34	492	71.5	120	15	US-10-269-805-15	Sequence 3, Appl
35	492	71.5	248	11	US-09-880-748-1955	Sequence 1717, Ap
36	491.5	71.4	248	11	US-09-880-748-1955	Sequence 1955, Ap
37	490.5	71.3	123	15	US-10-269-805-17	Sequence 1717, Ap
38	490.5	71.3	239	15	US-10-151-882-23	Sequence 23, Appl
39	490	71.2	252	11	US-09-880-748-1665	Sequence 1666, Ap
40	490	71.2	253	11	US-09-880-748-1813	Sequence 1813, Ap
41	489.5	71.1	253	11	US-09-880-748-1813	Sequence 1813, Ap
42	489	71.1	120	15	US-10-269-805-37	Sequence 37, Appl
43	488.5	70.9	248	11	US-10-151-882-17	Sequence 17, Appl
44	488	70.9	250	15	US-09-880-748-7	Sequence 7, Appl
45	486.5	70.7	242	11	US-09-880-748-1915	Sequence 1915, Ap

## ALIGNMENTS

RESULT 1  
US-10-269-805-19  
; Sequence 19, Application US/10269805  
; Publication No. US20030124129A1  
; GENERAL INFORMATION:  
; APPLICANT: OLIVER, JONATHAN D.  
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS  
; FILE REFERENCE: A-7722  
; CURRENT APPLICATION NUMBER: US/10/269,805  
; PRIOR FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 60/328,604  
; PRIOR FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-269-805-19

Query Match 76.2%, Score 524.5; DB 15; Length 121;  
Best Local Similarity 78.5%; Pred. No. 7e-41;  
Matches 102; Conservative 9; Mismatches 10; Indels 9; Gaps 1;

QY	1	OVALVOSGAERKPGSSVKVSCRAKSGDTFNSPISTWRQAPGGLMGGIIPFGSTKY	60
DB	1	OVALVOSGAERKPGSSVKVSCRAKSGDTFNSPISTWRQAPGGLMGGIIPFGSTKY	60
QY	61	AOKRQGVMTADGSTSTAYMELNSRSEDTATYYCARQNGGMYEGPPLPEPRDLDI	120
DB	61	AOKRQGVMTADGSTSTAYMELNSRSEDTATYYCARQNGGMYEGPPLPEPRDLDI	120
QY	121	GOGMTVSS 130	
DB	121	GOGMTVSS 121	

RESULT 2

DR WPI: 2002-114799/15.

XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for  
PT the diagnosis and treatment of cancers and immune disorders -  
XX  
XX  
PS Claim 1: Page 2470-2471, 3148pp; English.

XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent  
CC the antibodies and fragments of the antibodies described in the method  
CC of the invention.

XX Sequence 248 AA;

SQ Query Match 73.0%; Score 502.5; DB 23; Length 248;

Best Local Similarity 75.2%; Pred. No. 2.8e-40;

Matches 100; Conservative 9; Mismatches 13; Indels 11; Gaps 2;

QY 1 QVQLVSGAEAKKPKSSVKVSCAKASGDTFNSPISWVROAPGQGLEWGGITPIFGSTY 60  
DB 1 QVQLVSGAEVKKPKSSVKVSCAKASGDTFSSVYISWVROAPGQGLEWGGITPIFGTANY 60  
QY 61 AQKFGQRYVTMTADGSTSTAMELNSLRSEDTAIIYCARQONG---GWYEGPLLEPRPDAL 117  
DB 61 AQKFGQRYVTITADESTSTAMELSLRSEDTAVYICARMEYDILTYGOG-----YF 112  
QY 118 DIWGQGTWTVSS 130  
DB 113 DYWGQGTTLTVSS 125

Search completed: December 30, 2003, 10:54:29  
Job time : 41.903 secs

PT treating cancer -  
 XX  
 PS Claim 3; Fig 2; 51pp; English.  
 CC The present invention relates to human anti-epidermal growth factor  
 CC receptor single-chain antibodies (anti-EGFR-scFvs) isolated from a  
 CC human IgM phage display library using EGFR as antigen. Two isolates  
 CC with different amino acid sequences were identified. The  
 CC anti-EGFR-scFvs are useful for treating cancer, and for the  
 CC diagnostic location and assessment of tumor growth, where the  
 CC anti-EGFR-scFv is radiolabelled. The present sequence represents  
 CC human anti-EGFR single-chain antibody isolated from clone pSEX81-63.  
 XX  
 SQ Sequence 270 AA;  
 Query Match 73.3%; Score 504; DB 23; Length 270;  
 Best Local Similarity 74.6%; Pred. No. 2.2e-40;  
 Matches 100; Conservative 10; Mismatches 12; Indels 12; Gaps 2;  
 QY 1 QVQLVSGAFAKPGSSVYKSCASGDTFNSPISWVROAPGQGLEMMGIIPIFGSTRY 60  
 Db 1 QVQLVSGAEVKKRQGSVKVSKASGTFSSYALISWVROAPGQGLEMMGIIPIFGTANY 60  
 QY 61 AQKFGKRVITMTADGSTSTAYMELNSLRSDTAIYYCARQO---NGWYEGPLEPRDPA 116  
 Db 61 AQKFGKRVITMTADESTSTAYMELNSLRSDTAIYYCARPDYVYGGSGY-----PNW 112  
 QY 117 LDWGGGTMTVYSS 130  
 Db 113 FDPWGGTIVTVSS 126  
 RESULT 14  
 ABR01518  
 ID ABR01518 standard; Protein; 229 AA.  
 AC ABR01518;  
 XX  
 DT 16-APR-2003 (first entry)  
 XX  
 DE Human anti-TIMP-1 antibody heavy chain #16.  
 XX  
 KW Human; antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VCDDR3;  
 KW matrix metalloproteinase; MMP; variable heavy chain; VCDDR3; hepatotropic;  
 KW variable light chain; cytototoxic; nephrotropic; cardiac; liver fibrosis;  
 KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;  
 KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;  
 KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200286085-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 24-APR-2002; 2002WO-US12801.  
 XX  
 PR 24-APR-2001; 2001US-285683P.  
 XX  
 PA (FARB) BAYER CORP.  
 PA (MORP-) MORPHOSYS AG.  
 XX  
 PI Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;  
 XX  
 XX WPI; 2003-129114/12.  
 DR N-PSDB; AB274789.  
 XX  
 PT New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1)  
 PT antibodies, for diagnosing or ameliorating the symptoms of a disorder  
 PT in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate  
 PT hypertrophy or lung cancer  
 PS Claim 20; Page 158-159; 228pp; English.

XX  
 CC The invention relates to a novel purified preparation of a human  
 CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)  
 CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of  
 CC TIMP-1. The antibody comprises a variable heavy chain (VH)CDR3 region and  
 CC a variable light chain (VL)CDR3 region. An antibody preparation of the  
 CC invention has hepatotropic, cytotoxic, nephrotropic and cardiac  
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting  
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver  
 CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary  
 CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic  
 CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon  
 CC cancer. The antibody is also useful for detecting a TIMP-1 in a test  
 CC preparation, or in diagnosing a disorder in which a TIMP-1 level is  
 CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy  
 CC chain regions of a human anti-TIMP-1 antibody of the invention.  
 XX  
 SQ Sequence 229 AA;  
 Query Match 73.0%; Score 502.5; DB 24; Length 229;  
 Best Local Similarity 75.8%; Pred. No. 2.6e-40;  
 Matches 100; Conservative 10; Mismatches 13; Indels 9; Gaps 2;  
 QY 1 QVQLVSGAFAKPGSSVYKSCASGDTFNSPISWVROAPGQGLEMMGIIPIFGSTRY 60  
 Db 1 QVQLVSGAEVKKRQGSVKVSKASGTFSSYALISWVROAPGQGLEMMGIIPIFGTANY 60  
 QY 61 AQKFGKRVITMTADGSTSTAYMELNSLRSDTAIYYCAR--QNGWYEGPLEPRDPA 118  
 Db 61 AQKFGKRVITMTADESTSTAYMELNSLRSDTAIYYCARSDGSYHYVHPY-----FD 113  
 QY 119 IWGGGTMTVYSS 130  
 Db 114 VWGGGTIVTVSS 125  
 RESULT 15  
 ABP45722  
 ID ABP45722 standard; Protein; 248 AA.  
 AC ABP45722;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human Blys binding scFv SEQ ID 1733.  
 XX  
 KW Blye; B lymphocyte stimulator; TNF superfamily; human; cytotoxic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antineutritic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200202641-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 15-JUN-2001; 2001WO-US19110.  
 XX  
 PR 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX PA Edwards BM, Main SH, Vaughan TJ;  
 XX PI WPI: 2001-282031/29.  
 XX DR N-PSDB; AAS03455.  
 XX PT Panel of specific binding members of antibody molecules which bind to  
 XX PT whole adipocytes is used in the treatment of obesity and obesity  
 XX PT related diseases -  
 XX PS Claim 1; Page 127; 182pp; English.  
 XX AAU02301-AAU02635, and AAU02641-AAU02748 represent the amino acid  
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light  
 CC chain, and heavy chain complementarity determining regions (CDR) of the  
 CC invention. The antibodies can be used in the treatment of obesity and  
 CC obesity related diseases. The antibodies can be used to deliver drugs or  
 CC pro-drugs directly to the fat mass of an obese patient or the antibody  
 CC can be used as a therapeutic itself. Antibodies binding specifically to  
 CC adipocytes can be used to activate the immune system to destroy the cells  
 CC by complement mediated lysis. The antibodies may be labeled with a  
 CC detectable label such as radiolabel, fluorescent or chemical group and  
 CC used in methods of diagnosis in human subjects e.g. to determine the  
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or  
 CC determine the presence or level of adipocytes in a cell or tissue sample.  
 CC The antibodies can be used as an alternative means of treatment for obese  
 CC patients other than undergoing surgery to remove excess fat. Antibodies  
 CC for different types of fat deposits can also be produced e.g. intra-  
 CC abdominal fat associated with heart disease.  
 CC SQ Sequence 125 AA;  
 XX  
 XX Query Match 73.3%; Score 504.5; DB 22; Length 125;  
 XX Best Local Similarity 75.9%; Pred. No. 8.4e-41;  
 XX Matches 101; Conservative 10; Mismatches 11; Indels 11; Gaps 2;  
 QY 1 QVQLVSGAEAKKPGSSVYKVCCKASGDTFNSPISWYRQAPGQLEWVGIIPIFGSTKY 60  
 D1 1 QVQLVSGAEVKKPGSSVKVSCKASGTFSSYALSWRQAPGQLEWVGIIPIFGTANY 60  
 QY 61 AOKRQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRD---AL 117  
 D1 61 AOKRQGRVTITADGSTSTAYMELSLRSEDTAYVYCARAS-----LNLMPDPTWAF 112  
 QY 118 DIMGGTMTVTSS 130  
 D1 113 DIMGRGTLVTSS 125  
 DB  
 XX RESULT 12  
 XX AAB36083  
 XX ID AAB36083 standard; Protein; 249 AA.  
 XX AC AAB36083;  
 XX DT 16-FEB-2001 (first entry)  
 XX DE Recombinant human antibody scFv TN11.  
 XX KW Human; antibody scFv; TN11; Tenascin-C; TN-C; domain C-containing TNC;  
 XX KM CTN-C.  
 XX OS Homo sapiens.  
 XX PA W0200063699-A1.  
 XX PN W0200063699-A1.  
 XX PD 26-OCT-2000.  
 XX PF 19-APR-2000; 2000MO-EP03550.  
 XX PR 20-APR-1999; 99IT-FT00094.

XX (PHIL-) PHILOGEN SRL.  
 XX PA Zardi L;  
 XX PI WPI: 2000-687225/67.  
 XX DR N-PSDB; AAC67868.  
 XX PT Ligands used for diagnosis and treatment of human neoplasias, are  
 XX PT capable of identifying the tenascin-C isoform containing domain C of  
 XX PT tenascin-C -  
 XX PS Disclosure; Page 5-6; 31pp; English.  
 XX  
 XX The present sequence is a recombinant human antibody scFv. Antibody  
 CC TN1 reacts with the long form of human Tenascin-C (TN-C). The epitope  
 CC recognized by TN1 is located inside domain C of TN-C. TN1 is therefore  
 CC only capable of recognizing TN-C isoforms containing domain C (CTN-C).  
 CC TN1 is useful for detecting the presence of TN-C isoforms in vitro or  
 CC in vivo for diagnosing pathologies expressing the CTN-C isoforms of TN-C.  
 CC It is useful for the preparation of formulations for the treatment of  
 CC human neoplasias.  
 CC SQ Sequence 249 AA;  
 XX  
 XX Query Match 73.3%; Score 504.5; DB 21; Length 249;  
 XX Best Local Similarity 76.9%; Pred. No. 1.8e-40;  
 XX Matches 100; Conservative 9; Mismatches 14; Indels 7; Gaps 1;  
 QY 1 QVQLVSGAEAKKPGSSVYKVCCKASGDTFNSPISWYRQAPGQLEWVGIIPIFGSTKY 60  
 D1 1 QVQLVSGAEVKKPGSSVKVSCKASGTFSSYALSWRQAPGQLEWVGIIPIFGTANY 60  
 QY 61 AOKRQGRVTMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRDALDIW 120  
 D1 61 AOKRQGRVTITADGSTSTAYMELSLRSEDTAYVYCARSRRTITFGC-----GAFDIW 113  
 QY 121 GGGTMTVTSS 130  
 D1 114 GRGTMTVTSS 123  
 DB  
 XX RESULT 13  
 XX AAU97198  
 XX ID AAU97198 standard; protein; 270 AA.  
 XX AC AAU97198;  
 XX DT 27-AUG-2002 (first entry)  
 XX DE Human anti-EGFR single-chain antibody isolated from clone pSEX81-63.  
 XX KW Human; anti-epidermal growth factor receptor single-chain antibody;  
 XX KM anti-EGFR-scFv; IGM; cancer; tumour growth; clone pSEX81-63; cytostatic.  
 XX OS Homo sapiens.  
 XX PA W02000230984-A1.  
 XX PN W02000230984-A1.  
 XX PD 18-APR-2002.  
 XX PF 12-OCT-2001; 2001MO-US31857.  
 XX PR 13-OCT-2000; 2000US-240353P.  
 XX (UABR-) UAB RES FOUND.  
 XX RA Raesch KP, Curiel DT, Bonner JA;  
 XX WPI: 2002-463261/49.  
 XX Novel human anti-epidermal growth factor receptor single-chain antibody  
 XX useful for diagnostic location and assessment of tumour growth, and in

DR WPI; 2002-114799/15.  
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 XX  
 PS Claim 1; Page 2645-2646; 3148pp; English.  
 XX  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytotoxic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antineuritic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS  
 CC and so may be used to detect and quantitate the presence of BLyS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BLyS. They may also be  
 CC administered to treat diseases associated with aberrant BLyS expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX  
 SO Sequence 253 AA:  
 Query Match 73.9%; Score 508.5; DB 23; Length 253;  
 Best Local Similarity 74.6%; Pred. No. 7.6e-41;  
 Matches 100; Conservative 11; Mismatches 12; Indels 11; Gaps 2;  
 OY 1 QVOLVSGAEAKKPGSSVYVSCKASGDTFNSFPISWVRQAPQGLEWNGIIPFGSTKY 60  
 DB 1 QVOLVSGAEVKKPGSSVYVSCKASGDTFSSVAISMVRQAPQGLEWNGIIPFGTANY 60  
 OY 61 AQFGQRYVTMTADGSTSTAYMELNSLRSEDTAIYYCARQO-----GCWYEGPLLEPPDA 116  
 DB 61 AQFGQRYVTITADGSTSTAYMELNSLRSEDTAVYVCARESHYDILTYGYSNP-----S 113  
 OY 117 LDIMWQGTMTVYSS 130  
 DB 114 FDIWGRGTMTVYSS 127  
 RESULT 10  
 ABP45855  
 ID ABP45855 standard; Protein; 254 AA.  
 AC ABP45855;  
 XX  
 XX 19-AUG-2002 (first entry)  
 DT  
 DE Human BLyS binding scFv SEQ ID 1866.  
 XX  
 KW BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antineuritic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 XX MO200202641-A1.  
 XX  
 PD 10-JAN-2002.  
 PF  
 PF 15-JUN-2001; 2001WO-US19110.  
 XX  
 XX 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX WPI; 2002-114799/15.  
 DR  
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 XX  
 PS Claim 1; Page 2628-2629; 3148pp; English.  
 XX  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytotoxic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antineuritic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS  
 CC and so may be used to detect and quantitate the presence of BLyS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BLyS. They may also be  
 CC administered to treat diseases associated with aberrant BLyS expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX  
 SO Sequence 254 AA:  
 Query Match 73.8%; Score 508; DB 23; Length 254;  
 Best Local Similarity 71.4%; Pred. No. 8.5e-41;  
 Matches 100; Conservative 10; Mismatches 8; Indels 22; Gaps 2;  
 OY 1 QVOLVSGAEAKKPGSSVYVSCKASGDTFNSFPISWVRQAPQGLEWNGIIPFGSTKY 60  
 DB 1 QVOLVSGAEVKKPGSSVYVSCKASGDTFSSVAISMVRQAPQGLEWNGIIPFGTANY 60  
 OY 61 AQFGQRYVTMTADGSTSTAYMELNSLRSEDTAIYYCARQO-----GCWYEGPLL 110  
 DB 61 AQFGQRYVTITADGSTSTAYMELNSLRSEDTAVYVCARESHYDILTYGYPGGMF----- 115  
 OY 111 ERRPDLADIWQGTMTVYSS 130  
 DB 116 -----DPWKGRTLVYSS 128  
 RESULT 11  
 AAU02555  
 ID AAU02555 standard; Protein; 125 AA.  
 AC AAU02555;  
 XX  
 XX 29-AUG-2001 (first entry)  
 DT  
 DE Anti-adipocyte monoclonal antibody heavy chain, FAT 41.  
 XX  
 KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;  
 KW heart disease; complementarity determining region; CDR.  
 XX  
 OS Homo sapiens.  
 XX  
 XX MO200127279-A1.  
 XX  
 PD 19-APR-2001.  
 PF  
 PF 11-OCT-2000; 2000WO-GB03900.  
 XX  
 XX 12-OCT-1999; 99US-0158612.

Sequence 220 AA;

1 QVQLVSGAEAKKPGSSVKVSCKASGDTFNSFPISWVRAPGCGLEWMGGIIPIFGSTR

61 A Q K F G R V T M A D G S T S T A Y M E I N S L R S E D T A I Y Y C A R Q O N G W Y E G P L L E P R D A L D I W 120

QY 121 GQGTMTVSS 130

Db 107 GQGLTVSS 116

RESULT 8  
ABP45498  
ID ABP45498 standard; Protein; 253 AA

AC ABP45498;

DT 19-AUG-2002 (first entry)

Human BLYS binding scFv SEQ ID 1509.

KM Blys: B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
KM immunosuppressive; immunostimulant; immunomodulatory; antineoplastic;  
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency  
KM systemic lupus erythematosus; rheumatoid arthritis; COVID; AIDS;  
KM common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 16-MAR-2001; 2001US-276248P.

PR 25-MAY-2001; 2001US-293499P

PA (HUMA-) HUMAN GENOME SCI INC

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 AUGUST 21, 1962  
 AUGUST 21, 1962  
 AUGUST 21, 1962

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524
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the diagnosis and treatment of cancers and immune disorders -

Claim 1; Page 2203-2204; 3148pp; English.

AA	Sequence	253 AA;
SQ		

Query Match 74.3%; Score 511; DB 23; length 253

Best Local Similarity 72.1%; Pred. No. 4.4e-41;  
Matches 101; Conservative 9; Mismatches 8; Indels 22; Gaps 2

1 QVQLVQSGAEAKKPPGSSVKVCSKASGDTFNSFPISWYQAPGGGLEMMGIIPIFGSTKY 60

Db 1 QVQLVSGAEVKKPKSSVKSCASGTFSSYAISWVRQAPGGLEWMGGIIPITGANY 60

61 A Q K F G R V I M T A D G S T I S T A Y M E L N S L R S E D T A I Y Y C A R Q ----- N G S W Y E G P L L 110

DB 61 A Q K F Q G R V I I T A D K S I S T A Y M E L S S L R S E D I A V Y Y C A R E Q G Y D I L I G Y Y P E G W F ----- 115

QY 111 EPRDALDIWGQGTMTVSS 130

Db 116 -----DPWGKGTMTVSS 128

RESULT 9  
ABP45869  
ID ABP45869 standard; Protein; 253 AA

AC ABP45869 ;

DT 19-AUG-2002 (first entry)

Human BLYS binding scFv SEQ ID 1880.

KM Blygs; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KM immunosuppressive; immunostimulant; immunomodulatory; anti-neumatic;  
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency  
 KM systemic lupus erythematosus; rheumatoid arthritis; COVID; AIDS;  
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.

## OS Homo sapiens

PN WO200202641-A1

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 16-MAR-2001; 2001US-276248P.

PR 25-MAY-2001; 2001US-293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

XX

XX

CC with high affinity against a wide range of antigens and having no or  
 CC minimum immunogenicity to human subjects treated with antibody  
 CC therapeutics. This sequence represents a protein region of an antibody  
 CC relating to the novel antibody library construction method of the  
 CC invention.

CC Sequence 120 AA;

Query Match 74.4%; Score 512; DB 24; Length 120;  
 Best Local Similarity 76.9%; Pred. No. 1.5e-41;  
 Matches 100; Conservative 9; Mismatches 11; Indels 10; Gaps 1;

QY 1 QVQLVSGAEEKPGSSVVKSCASGDTFNSPFIWVRQAPGQGLEWMGIIPIFGSTKY 60  
 DB 1 QVQLVSGAEVKKPSSSVKSCASGDTFSSYAISWVRQAPGQGLEWMGIIPIFGTANY 60  
 QY 61 AOKFQGRVMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRPDLDIW 120  
 DB 61 AOKFQGRVITITADESTSTAYMELNSLRSEDTAVYICARWGQDGFY-----AMDYW 110  
 QY 121 GGGTMTVVS 130  
 DB 111 GGGTLTVSS 120

# RESULT 6

ABJ18718  
 ID ABJ18718 standard; Protein; 120 AA.

AC ABJ18718;

DT 06-MAR-2003 (first entry)

DE Antibody library related VH protein region 1DMA.

KW Library; recombinant antibody; clustering variable region; in silico;  
 KM immunogenicity; antibody therapeutic.

OS Unidentified.

PN WO200284277-A1.

XX 24-OCT-2002.

PF 17-APR-2002; 2002WO-US12202.

PR 17-APR-2001; 2001US-284407P.

PA (ABMA-) ABMAXIS INC.

XX Luo P;

DR WPI; 2003-093043/08.

PT Constructing a library of recombinant antibodies useful as source of  
 PT antibody candidates for screening antigens comprises clustering  
 PT variable regions of antibodies having known 3-dimensional structures  
 PT into structural ensembles -

PS Disclosure; Fig 13B; 119pp; English.

XX The invention relates to a novel method for the construction of a library  
 CC of recombinant antibodies. The novel method comprises clustering variable  
 CC regions of a collection of antibodies having known 3D structures into at  
 CC least two families of structural ensembles, each comprising at least two  
 CC different antibody sequences but with substantially identical main chain  
 CC conformations. The method is useful for constructing a library of  
 CC artificial antibodies in silico which provides a structurally diverse and  
 CC yet functionally more relevant source of antibody candidates which can  
 CC then be screened for binding a wide variety of target molecules,  
 CC including small molecules, and biomacromolecules such as proteins,  
 CC peptides and nucleic acids. The libraries constructed are useful as a  
 CC source of antibody candidates for further screening for novel antibodies

CC with high affinity against a wide range of antigens and having no or  
 CC minimum immunogenicity to human subjects treated with antibody  
 CC therapeutics. This sequence represents a protein region of an antibody  
 CC relating to the novel antibody library construction method of the  
 CC invention.

CC Sequence 120 AA;

Query Match 74.4%; Score 512; DB 24; Length 120;  
 Best Local Similarity 76.9%; Pred. No. 1.5e-41;  
 Matches 100; Conservative 9; Mismatches 11; Indels 10; Gaps 1;

QY 1 QVQLVSGAEEKPGSSVVKSCASGDTFNSPFIWVRQAPGQGLEWMGIIPIFGSTKY 60  
 DB 1 QVQLVSGAEVKKPSSSVKSCASGDTFSSYAISWVRQAPGQGLEWMGIIPIFGTANY 60  
 QY 61 AOKFQGRVMTADGSTSTAYMELNSLRSEDTAIYYCARQONGWYEGPLLEPRPDLDIW 120  
 DB 61 AOKFQGRVITITADESTSTAYMELNSLRSEDTAVYICARWGQDGFY-----AMDYW 110  
 QY 121 GGGTMTVVS 130  
 DB 111 GGGTLTVSS 120

# RESULT 7

ABR01538  
 ID ABR01538 standard; Protein; 220 AA.

AC ABR01538;

DT 16-APR-2003 (first entry)

DE Human anti-TIMP-1 antibody heavy chain #36.

XX Human; antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VLDLR3;  
 KM matrix metalloproteinase; MMP; variable heavy chain; VHCDR3; hepatocellular;  
 KM variable light chain; cytoskeletal; nephrotropic; cardiac; liver fibrosis;  
 KM alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;  
 KM lupus nephritis; glomerulosclerotic renal disease; lung cancer;  
 KM idiopathic pulmonary fibrosis; benign prostatic hypertrophy; colon cancer.

XX Homo sapiens.

OS WO200286085-A2.

PN 31-OCT-2002.

PD 24-APR-2002; 2002WO-US12801.

PR 24-APR-2001; 2001US-285683P.

PA (FARB-) BAYER CORP.

XX (MORP-) MORPHOSYS AG.

XX Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;

XX WPI; 2003-129114/12.

DR N-PSDB; AB274809.

PT New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1)  
 PT antibodies, for diagnosing or ameliorating the symptoms of a disorder  
 PT in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate  
 PT hypertrophy or lung cancer -

PS Claim 20; Page 173; 228pp; English.

XX The invention relates to a novel purified preparation of a human  
 CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)  
 CC and neutralizes a matrix metalloproteinase (MMP)-inhibiting activity of  
 CC TIMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and  
 CC a variable light chain (VLC)DR3 region. An antibody preparation of the  
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiac



PS Claim 1; Page 2646-2647; 3148bp; English.

XX This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytosolic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS  
 CC and so may be used to detect and quantitate the presence of BLyS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BLyS. They may also be  
 CC administered to treat diseases associated with aberrant BLyS expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.

SO Sequence 244 AA;

Query Match 74.8%; Score 514.5; DB 23; Length 244;  
 Best Local Similarity 76.9%; Pred. No. 1.9e-41;  
 Matches 100; Conservative 9; Mismatches 12; Indels 9; Gaps 1;

OY 1 OVQVQSGAEAKKPGSSVYKSCASGDTFNSPFIISWROAPQGGLMMGIIPIFGSTKY 60  
 DB 1 OVQVQSGAEVKKPGSSVYKSCASGDTFSSYAIISWROAPQGGLMMGIIPIFGTANY 60  
 OY 61 AOKFGQRTMTADGSTAYAMELNSLRSEDTAIYYCARQNGWYEGPLERPDALDIW 120  
 DB 61 AOKFGQRTVITADKSTAYAMELSLRSDTAIVYICARDGSGSY-----DAFDIW 111  
 OY 121 GCGTMTVYSS 130  
 DB 112 GKGTMVTVSS 121

RESULT 4

AAW27550  
 ID AAW27550 standard; Protein; 120 AA.

AAW27550;

23-JAN-1998 (first entry)

Human Ab heavy chain variable region VH1A consensus.

Human; antibody; preparation; library; VH1A; variable region;  
 heavy chain; consensus.

Homo sapiens.

MO9708320-A1.

06-MAR-1997.

19-AUG-1996; 96WO-EP03647.

18-AUG-1995; 95EP-0113021.

(MORP-) MORPHOSYS GES PROTEINOPTIMERUNG MBH.

Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;

WPI; 1997-179277/16.

N-PSDB; AAT87948.

Preparation of human derived antibody gene library - using synthetic  
 consensus sequences, and signal consensus antibody gene as universal  
 framework for highly diverse antibody libraries

PS Example 1; Fig 5A; 436bp; English.

XX The present sequence is the human antibody heavy chain  
 CC variable region synthetic sequence VH1A, used in the preparation of  
 CC a human derived antibody gene library.

SO Sequence 120 AA;

Query Match 74.4%; Score 512; DB 18; Length 120;  
 Best Local Similarity 76.9%; Pred. No. 1.5e-41;  
 Matches 100; Conservative 9; Mismatches 11; Indels 10; Gaps 1;

OY 1 OVQVQSGAEAKKPGSSVYKSCASGDTFNSPFIISWROAPQGGLMMGIIPIFGSTKY 60  
 DB 1 OVQVQSGAEVKKPGSSVYKSCASGDTFSSYAIISWROAPQGGLMMGIIPIFGTANY 60  
 OY 61 AOKFGQRTMTADGSTAYAMELNSLRSEDTAIYYCARQNGWYEGPLERPDALDIW 120  
 DB 61 AOKFGQRTVITADKSTAYAMELSLRSDTAIVYICARDGSGDY-----AMDYW 110  
 OY 121 GCGTMTVYSS 130  
 DB 111 GCGTLTVYSS 120

RESULT 5

ABJ18672  
 ID ABJ18672 standard; Protein; 120 AA.

ABJ18672;

06-MAR-2003 (first entry)

Antibody library related heavy variable chain protein region SEQ ID No 1.

Library; recombinant antibody; clustering variable region; in silico;  
 immunogenetic; antibody therapeutic.

Unidentified.

MO200284277-A1.

24-OCT-2002.

17-APR-2002; 2002WO-US12202.

17-APR-2001; 2001US-284407P.

(ABMA-) ABMAXIS INC.

Luo P;

WPI; 2003-093043/08.

Constructing a library of recombinant antibodies useful as source of  
 antibody candidates for screening antigens comprises clustering  
 variable regions of antibodies having known 3-dimensional structures  
 into structural ensembles

Disclosure; Page 98-99; 119pp; English.

The invention relates to a novel method for the construction of a library  
 of recombinant antibodies. The novel method comprises clustering variable  
 regions of a collection of antibodies having known 3D structures into at  
 least two families of structural ensembles, each comprising at least two  
 different antibody sequences but with substantially identical main chain  
 conformations. The method is useful for constructing a library of  
 artificial antibodies in silico which provides a structurally diverse and  
 yet functionally more relevant source of antibody candidates which can  
 then be screened for binding a wide variety of target molecules,  
 including small molecules, and biomacromolecules such as proteins,  
 peptides and nucleic acids. The libraries constructed are useful as a  
 source of antibody candidates for further screening for novel antibodies



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 41.8197 Seconds  
(without alignments)  
493.415 Million cell updates/sec

Title: US-09-674-752-23

Perfect score: 688  
Sequence: 1 QVVLVSGAEAKKPGSSVKV.....EPRPDALDIWGQMTVTSS 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	688	100.0	130	21	AAV50948 Human anti-factor
2	517	75.1	118	21	ABP45958 Human LfH3 monoclo
3	514.5	74.8	244	23	ABP45870 Human anti-EGFR s1
4	512	74.4	120	18	AAW27550 Human Ab heavy cha
5	512	74.4	120	24	ABJ18672 Antibody library r
6	512	74.4	120	24	ABJ18718 Antibody library r
7	512	74.4	220	24	ABR01538 Human anti-TIMP-1
8	511	74.3	253	23	ABP45498 Human Blys binding
9	508.5	73.9	253	23	ABP45869 Human Blys binding

10	508	73.8	254	23	ABP45855 Human Blys binding
11	504.5	73.3	125	22	AAU02555 Anti adipocyte mon
12	504.5	73.3	249	21	AAB36083 Recombinant human
13	504	73.0	270	23	AAU97198 Human anti-EGFR s1
14	502.5	73.0	229	24	ABR01518 Human anti-TIMP-1
15	502.5	73.0	248	23	ABP45722 Human Blys binding
16	502.5	73.0	248	23	ABP45723 Human Blys binding
17	501.5	72.9	245	24	ABP60521 Human Blys binding
18	501.5	72.9	248	23	ABP45707 Human Blys binding
19	501.5	72.9	248	23	ABP45868 Human anti-TIMP-1
20	500.5	72.7	231	24	ABR01524 Human anti-TIMP-1
21	500.5	72.7	481	13	AAK24442 Sequence of antibo
22	500	72.7	257	23	ABP45542 Human Blys binding
23	499	72.5	222	24	ABR01531 Human anti-TIMP-1
24	498.5	72.5	248	23	ABP45708 Human Blys binding
25	498.5	72.5	248	23	ABP45721 Human Blys binding
26	498.5	72.5	248	23	ABP45726 Human Blys binding
27	497.5	72.3	248	23	ABP45730 Human Blys binding
28	497.5	72.3	250	23	ABP46055 Human Blys binding
29	497	72.2	254	23	ABP45439 Human Blys binding
30	496.5	72.2	219	24	ABR01523 Human anti-TIMP-1
31	495.5	72.0	248	23	ABP45716 Human Blys binding
32	495.5	72.0	248	23	ABP45717 Human Blys binding
33	494.5	71.9	271	22	AAK66039 scfv 1b4 antibody
34	493.5	71.7	245	22	AAK67617 Human leukocyte an
35	493.5	71.7	251	23	ABP45745 Human Blys binding
36	492.5	71.6	115	23	ABK57559 HLA-DR-specific pr
37	492.5	71.6	225	24	ABR01510 Human anti-TIMP-1
38	492.5	71.6	245	22	AAK67618 Human leukocyte an
39	492	71.5	248	23	ABP45944 Human Blys binding
40	491.5	71.4	223	24	ABR01535 Human anti-TIMP-1
41	491.5	71.4	248	23	ABP45706 Human Blys binding
42	491	71.4	220	24	ABR01512 Human anti-TIMP-1
43	490.5	71.3	239	24	ABP60529 APRIL binding scfv
44	490	71.2	252	23	ABP45655 Human Blys binding
45	490	71.2	253	23	ABP45471 Human Blys binding

ALIGNMENTS

RESULT 1	
AAV50948	AAV50948 standard; Protein; 130 AA.
XX	
XX	AAV50948;
XX	
DT	23-MAR-2000 (first entry)
XX	
DB	Human anti-factor VIII antibody VH clone EL-14 encoded protein.
XX	
KW	Human; heavy chain; antibody; factor VIII; hemostatic;
KW	hemophilia A; VH gene.
XX	
OS	Homo sapiens.
XX	
PN	W0958680-A2.
XX	
PD	18-NOV-1999.
XX	
PF	07-MAY-1999; 99WO-NL00285.
XX	
PR	08-MAY-1998; 98EP-0201543.
XX	
PA	(SAND-) STRICHTING SANDUIN BLOEDVOORZIEING.
XX	
P1	Voorberg JJ, Van Den Brink EN, Turenhout EAM;
XX	
DR	WPI; 2000-053102/04.
XX	
PT	New polynucleotide, polypeptide and antibody useful for diagnosing the
PT	presence of neutralizing antibodies against factor VIII and for
PT	treatment of hemophilia A patients with these antibodies -

Db	80	NEKFKGTTTLADSSSTAAYWFLSLTSEDSAVVCFTR--GGGW-----AFDYM	126
QY	121	GGGTMTVSS 130	
		:	
Db	127	GGGTTLTVSS 136	
RESULT 14			
ID	092401	PRELIMINARY; PRT; 142 AA.	
AC	092401		
DT	01-DEC-2001	(TREMBLrel. 19, Created)	
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)	
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)	
DE	V23-D-U-C mu protein (Fragment).		
GN	V23-D-U-C MU.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6;		
RA	Kozono Y., Kozono H., Azuma T.;		
RT	"Direct Maturation of Relative Affinity by Flow Cytometry Reveals		
RT	Affinity Maturation of B Cell Antigen Receptors in Response to (4-		
RT	Hydroxy-3-Nitrophenyl)Acetyl (NP)."		
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB069913; BAB63929.1; .		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_V.		
DR	PIfam; PF00047; Ig; 1.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PSS0835; IG_LIKE; 1.		
FT	NON TER 1 1		
FT	NON TER 142 142		
SO	SEQUENCE 142 AA; 15622 MW; 244265CEAE4A318B CRC64;		
Query Match 55.7%; Score 383.5; DB 11; Length 142;			
Best Local Similarity 57.7%; Pred. No. 3.5e-32;			
Matches 75; Conservative 18; Mismatches 24; Indels 13; Gaps 2;			
QY	1	OYOLVQSGAEAKPPSSSVKVCCKAGDTPFNSPPISWROAPQGLFMGGIPIFGSKY 60	
		:	
Db	1	OYOLQOPGTELVKPPASVYCLSKASGYFTSYMMHWVKORPQGLEWIGINPNSGNTY 60	
		:	
QY	61	AKPGGRVMTADGSTSTAYMELNSLRSEDTAIYYCARQNGWYEGPLLEBPRPALDIW 120	
		::: : : : : : : : : : : : : : : : : : :	
Db	61	NEKFKSKATLTLYDKSSSTAYWQJSLTSEDSAVVYICAR--GW-----EANDYW 107	
		:	
QY	121	GGGTMTVSS 130	
		:	
Db	108	GGGTSTVSS 117	
RESULT 15			
ID	095978	PRELIMINARY; PRT; 157 AA.	
AC	095978		
DT	01-MAY-1999	(TREMBLrel. 10, Created)	
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)	
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)	
DE	VH1 protein precursor (Fragment).		
GN	VH1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
NCBI_OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Peripheral blood;		
RA	Jox A., Zander T., Kuepers R., Irach J., Kanzler H., Kornacker M.,		

RA Bohlen H., Diehl V., Wolf J.:  
RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a  
RT patient with mixed cellularly Hodgkin's disease is associated with  
RT somatic mutations within the unretranslated regions of rearranged and  
RT class switch recombined Ig genes.",  
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AJ005570; CAA06599.1; -.  
DR HSSP; P01772; 2FB4.  
DR InterPro: IPR007110; IG\_1like.  
DR InterPro: IPR003065; IG\_MHC.  
DR InterPro: IPR003595; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PSS00835; IG\_LIKE; 1.  
KM Signal.  
FT SIGNAL. 1 21 POTENTIAL.  
FT NON TER 157 157  
SQ SEQUENCE 157 AA; 17304 MW; 86986EDDA84D8B5 CRC64;

Query Match 55.6%; Score 382.5; DB 4; Length 157;  
Best Local Similarity 60.4%; Pred. No. 5e-32;  
Matches 81; Conservative 10; Mismatches 26; Indels 17; Gaps 3;

Qy 1 QVQLVSGAARAKKPGSGSVKYSCKASGDTFNSFPISTWRQAPGQGLEMMGGIPIFGSTKY 60  
Db 20 QVQLVSGAARAKKPGSGSVKYSCKASGDTFNSFPISTWRQAPGQGLEMMGGIPIFGSTKY 79  
Qy 61 AAKFGQGVITMTAGDSTSTAYMELNSLRSEDTAIVYCARQONGN----YEGPLLEPPDA 116  
Db 80 AAKFGQGLITMTTRNISTTTVMELNSRLRFEDTAVYFCGR--GGRWRSGNYNGH----- 129  
Qy 117 LDIWGQGTMTVYSS 130  
Db 130 ---WGQGTPTVYSS 140

Search completed: December 30, 2003, 11:01:02  
Job time : 32.6816 secs

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Qy      61 AQRFGAVMTADGISTAYVMEINLSRSEDPAIYYCAROONGWYEGSPILLEPRPDALDIW 120
       ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      80 NEFKGKATFTADTSSNTATVMQSILTSSEDSAVYYCARRL-GRMY-----FDWM 127
Qy      121 GGGTMVTYVS 130
       | |||||
Db      128 GAGTTVTYVS 137

RESULT 11
ID      09GYZ2          PRELIMINARY;           PRT;         119 AA.
AC      09GYZ2;
DT      01-MAR-2001 (TREMBLrel. 16, Created)
DT      01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
        (Fragment) .
OC      Schistosoma japonicum (Blood fluke).
OC      Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC      Schistosomatidae; Schistosomatidae; Schistosoma.
OX      NCBI_TaxId=6182;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Song X.T., Feng Z.O., Guan X.H.;
RT      "Amplification, cloning and sequence analysis of the heavy chain
RT      variable region gene of monoclonal anti-idiotypic antibody NP30 of
RL      Schistosoma japonicum." ;
RL      Submitted (JUN-2000) to the EMBL/genbank/DBAJ databases.
DR      HSBP; AF282622; AAG01452.1; -.
DR      InterPro; IPR007110; IG_Like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_V.
DR      Pfam; PF00047; Igf_1.
DR      SMART; SM00406; IgV_1.
DR      PROSITE; PS50835; IG_LIKE; 1.
FT      NON_TER 1
FT      NON_TER 1
SQ      SEQUENCE 119 AA; 13567 MW; BA938737FD5FA6AB CRC64;

Query Match      57.0%; Score 392.5; DB 5; Length 119;
Best Local Similarity 60.8%; Pred. No. 3.2e-33;
Matches 79; Conservative 14; Mismatches 26; Indels 11; Gaps 1;

Qy      1 QVLTQSAEAKPKGSSTYKSCSKASGDPTFNFSPIISWRQAQGGLGWNGGIPIIFGSTKY 60
       |||||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1 QVLTSESAAETFRKGASRVKSCASKSGITFYGYNNMWQAQGHGIGLEWIGYINPSRGYTNY 60
Qy      61 AQRFQGRVTMTADGSTAYVMEINLSRSEDPAIYYCAROONGWYEGSPILLEPRPDALDIW 120
       |||||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      61 NQKFEDRYTMTTDDKSFTAYMDLNLSDSADSAVVYCARYYDHY-----CLDYW 109
Qy      121 GGGTMVTYVS 130
       |||||
Db      110 GGCTTVTVSS 119

RESULT 12
ID      09ZIC4          PRELIMINARY;           PRT;         118 AA.
AC      09ZIC4;
DT      01-MAY-1999 (TREMBLrel. 10, Created)
DT      01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Anti-porcine VCM mAb 3F4 heavy chain variable region (Fragment) .
OC      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      STRAIN=Balb/c;

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RA	Mueller U.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA	Matlis L.W., Evans M.J.,
RT	"Humanized porcine VCA-M-specific monoclonal antibodies with chimeric
RT	19G2/G4 constant regions block human leukocyte binding to porcine
RT	endothelial cells."
RL	EMBL, U78801; AAD00293.1; .
DR	EMBL, U78801; AAD00293.1; .
DR	HSSP; P01810; 2FBU.
DR	Interpro; IPR007110; Ig-like.
DR	Interpro; IPR003006; Ig_MHC.
DR	Interpro; IPR003586; Ig_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PSS0835; IG_LIKE; 1.
FT	NON_TER
FT	NON_TER
FT	NON_TER
SQ	SEQUENCE 118 AA; 13036 MW; 90EEC59D31EC4FC CRC64;
Query Match	57.0%; Score 392; DB 11; Length 118;
Beet Local Similarity	57.7%; Pred. No. 3.6e-33;
Matches	75; Conservative 20; Mismatches 23; Indels 12; Gaps 1;
QY	1 QVQLVQSGAEAKKKPGSSVYKVSCKASGDTFNSFPISWROAPGQGLEWMGCIPIFGSTKY 60
DB	1 QVQVVOOSGAEELARPMWASYKLSCKASGYVFNFSYMMQWVQKRGQGLEWIGALIPDDGDSY 60
QY	61 AQRKQGRITMPADGSTFAVMEVLSLSEPTAIRYCAKQONGMYEGFLEPRDALDIW 120
DB	61 TQKRGKATLTADSSSTATWQLSLASEDAVYICARRIVGV-----DYW 108
QY	121 GQGTMVTYSS 130
DB	109 GQGTTLTYS 118

Query	Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
1	QVQLVQSAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPGQGLEMMGILPIFGSTKY	56.5%	Score 388.5	DB 11	Length 481		
20	QVQLVQSAEAKKPGSSVKVSCKASGDTFNSFPISWRQAPGQGLEMMGILPIFGSTKY	59.2%	Pred. No. 4,86-32				
61	AKQFQGRVMTADGSGTSTAYWEINLSRSEDTAIYVCARQNGCMYEGPLLEPPDALDIW						

```
Db 1 EVOLVESGAEVKPKGASVSKVSCASGYTFTGYMHWROAPGQGLEWGMGINPNSWTNY 60
QY 61 AAKFGQRTVMTADGSTAYMELNSLRSEDTAIYYCAROONGS-WYEGPLLEPRPALDI 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AAKFGQRTVMTADGSTAYMELNSLRSEDTAIYYCAROONGS-WYEGPLLEPRPALDI 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 WGGQGTWTVSS 130
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 109 WGGQGTWTVSS 119

RESULT 8
Q96DKO PRELIMINARY; PRT; 496 AA.
AC Q96DKO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ25298.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Gastric mucosa;
RA Ishihashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hotta T., Hirooka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuka T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RA "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK058027; BAB71633.1; -.
DR InterPro: IPR007110; IG_LIKE.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IGv_1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KM Hypothetical protein.
SQ SEQUENCE 496 AA; 53532 MW; C72BE1E247C66FED CRC64;

Query Match 59.4%; Score 409; DB 4; Length 496;
Best Local Similarity 61.9%; Pred. No. 3.6e-34;
Matches 83; Conservative 11; Mismatches 26; Indels 14; Gaps 2;

QY 1 QVQLVDSGAEAKKPGSSVSKVSCASGDTFNSFPISWVROAPGQGLEWGMGIIPIFGSTKY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVHLVDSGAEAKKPGSSVSKVSCASGDTFNSFPISWVROAPGQGLEWGMGIIPIFGAPNY 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AAKFGQRTVMTADGSTAYMELNSLRSEDTAIYYCAROONGS-WYEGPLLEPRPALDI 116
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AAKFGQRTVMTADGSTAYMELNSLRSEDTAIYYCAROONGS-WYEGPLLEPRPALDI 129
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 117 LDIWGGQGTWTVSS 130
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 130 LDIWGGQGTWTVSS 143

RESULT 9
Q9BRVO PRELIMINARY; PRT; 500 AA.
AC Q9BRVO;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
```

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=prostate;
RA Struhsberg R.;
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC005951; AAH05951.1; -.
DR HSSP; P01789; IMCP.
DR InterPro: IPR007110; IG_LIKE.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IGv_1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KM Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF41F2A3CC6D9 CRC64;

Query Match 59.2%; Score 407; DB 4; Length 500;
Best Local Similarity 59.1%; Pred. No. 6e-34;
Matches 81; Conservative 17; Mismatches 23; Indels 16; Gaps 2;

QY 1 QVQLVDSGAEAKKPGSSVSKVSCASGDTFNSFPISWVROAPGQGLEWGMGIIPIFGSTKY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVHLVDSGAEAKKPGSSVSKVSCASGDTFNSFPISWVROAPGQGLEWGMGIIPIFGSTKY 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AAKFGQRTVMTADGSTAYMELNSLRSEDTAIYYCAROONGS-WYEGPLLEPRPALDI 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AAKFGQRTVMTADGSTAYMELNSLRSEDTAIYYCAROONGS-WYEGPLLEPRPALDI 132
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 114 PDALDIWGGQGTWTVSS 130
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 133 --YMDVWGKGTITVTVSS 147

RESULT 10
Q8VCX7 PRELIMINARY; PRT; 613 AA.
AC Q8VCX7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 67.9 kDa protein.
GN IGH-6.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Salivary gland;
RA Struhsberg R.;
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC018315; AAH18315.1; -.
DR MGD; MGI:96448; IGH-6.
DR InterPro: IPR007110; IG_LIKE.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam; PF00047; IG_5.
DR SMART; SM00406; IGv_1.
DR PROSITE; PSS0835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KM Hypothetical protein.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 57.7%; Score 397; DB 11; Length 613;
Best Local Similarity 59.2%; Pred. No. 8.5e-33;
Matches 77; Conservative 19; Mismatches 22; Indels 12; Gaps 2;

QY 1 QVQLVDSGAEAKKPGSSVSKVSCASGDTFNSFPISWVROAPGQGLEWGMGIIPIFGSTKY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVHLVDSGAEAKKPGSSVSKVSCASGDTFNSFPISWVROAPGQGLEWGMGIIPIFGSTKY 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db      20 OMVLQVSGAEKVKGGSSVYKVSCKASGDTFTYRYLWVWQAPQALQEMWGIITPENGNTNY 79
Qy      61 AOKFGQRYVTADGSTSTAYMELNSLRSEDPTAIYVCARQONGWYEGPLLEPRPDALDIW 120
Db      80 AOKFGQRYVTADGSTSTAYMELNSLRSEDPTAIYVCARQONGWYEGPLLEPRPDALDIW 130
Qy      121 GCGTMTVTVSS 130
Db      131 GCGTMTVTVSS 140

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## RESULT 5

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Q96QSO 096QSO PRELIMINARY; PRT; 159 AA.
ID      096QSO
DT      01-DEC-2001 (TREMBlrel. 19, Created)
DT      01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Putative matrix cell adhesion molecule-3.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      (1)
RP      SEQUENCE FROM N.A.
RA      Tilson M.D.;
RT      "Homo sapiens putative microfibrillar protein with Ig-like domain 3
RL      Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR      EMBL; AY039025; AAK2649.1; -.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_v.
PFam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
SQ      SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

```

Query Match 63.1%; Score 434; DB 4; Length 159;  
 Best Local Similarity 61.9%; Pred. No. 2.2e-37;  
 Matches 86; Conservative 18; Mismatches 17; Indels 18; Gaps 2;

```

Qy      1 QVQLVQSGAEAKKPGSSVYKVSCKASGDTFNSPISWVWQAPQALQEMWGIITPFGSTKY 60
Db      20 QVQLVQSGAEVKKPKASVYKVSCKASGYTFSNYYMMVWQAPQAGPEWGVINPSSGSARY 79
Qy      61 AOKFGQRYVTADGSTSTAYMELNSLRSEDPTAIYVCARQ-----QNGWYEGPLLE 111
Db      80 SOKFGRLITRDSTSTAYMELNSLRSDPTAVYFCAREMEITFGGAVSKGFYYG---- 135
Qy      112 PRPDALDIWCGTMTVTVSS 130
Db      136 -----MDVWVGQITVTVSS 149

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## RESULT 6

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ID      09Y298 PRELIMINARY; PRT; 150 AA.
AC      09Y298;
DT      01-NOV-1999 (TREMBlrel. 12, Created)
DT      01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      IGG VH protein precursor (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      (1)
RP      SEQUENCE FROM N.A.
RA      MEDLINE=98322155; PubMed=9657749;
Jacquemlin M.G., Vander Elst L.P.L.;

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RT      "Mechanism and kinetics of factor VIII inactivation: study with an
RT      IgG4 monoclonal antibody derived from a hemophilia A patient with an
RT      inhibitor."
RL      Blood 92:496-506(1998).
DR      EMBL; AJ224083; CAA11829.1; -.
DR      HSSP; P01772; 2FB4.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KM      Signal.
FT      SIGNAL.
FT      NON_TER 150 150 POTENTIAL.
SQ      SEQUENCE 150 AA; 16031 MW; 563D164AB2802D5 CRC64;

```

Query Match 61.7%; Score 424.5; DB 4; Length 150;  
 Best Local Similarity 64.6%; Pred. No. 2e-36;  
 Matches 84; Conservative 10; Mismatches 23; Indels 13; Gaps 1;

```

Qy      1 QVQLVQSGAEAKKPGSSVYKVSCKASGDTFNSPISWVWQAPQALQEMWGIITPFGSTKY 60
Db      20 QVQLVQSGAEVKKPKASVYKVSCKASGYTLTLPVHWQAPQAGKLEWGVSPSSGESIY 79
Qy      61 AOKFGQRYVTADGSTSTAYMELNSLRSEDPTAIYVCARQONGWYEGPLLEPRPDALDIW 120
Db      80 AREFQSVTMTADSTSTAYMELNSLRSDPTAVYCA-----VPDDAPFIW 126
Qy      121 GCGTMTVTVSS 130
Db      127 GCGTMTVTVSS 136

```

## RESULT 7

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ID      09UL94 PRELIMINARY; PRT; 119 AA.
AC      09UL94;
DT      01-MAY-2000 (TREMBlrel. 13, Created)
DT      01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Myosin-reactive immunoglobulin heavy chain variable region
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      (1)
RP      SEQUENCE FROM N.A.
RA      MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M.,
Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus."
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
DR      EMBL; AF035020; AAD56256.1; -.
DR      HSSP; P01810; 2FBJ.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
FT      NON_TER 1 1
FT      NON_TER 119 119
SQ      SEQUENCE 119 AA; 13205 MW; 13B64F5345FA16E CRC64;

```

Query Match 61.1%; Score 420.5; DB 4; Length 119;  
 Best Local Similarity 64.9%; Pred. No. 3.9e-36;  
 Matches 85; Conservative 12; Mismatches 21; Indels 13; Gaps 2;

```

Qy      1 QVQLVQSGAEAKKPGSSVYKVSCKASGDTFNSPISWVWQAPQALQEMWGIITPFGSTKY 60

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Db      1 VOSGAEVKKPGSSVKVSCKASGDTFNSPISWVROAPGQGLEWMGRIIPILGIANYAOKF 60
QY      65 QGRVTMTADGSTSTAYVMEIILSRSEDTAIYYCARQNGG-WYEGPFLPEPPDALDIWGGC 123
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 QGRVTITADGSTSTAYVMEIILSRSEDTAIYYCASSNMGPYV-----FDLWGRG 109
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      124 TMTVTSS 130
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      110 TLVTVSS 116

RESULT 2
Q9UL95 PRELIMINARY; PRT; 125 AA.
ID Q9UL95
AC Q9UL95;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalie N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035019; AAD56255.1; -
DR HSP; P01810; 2FBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match      65.8%; Score 452.5; DB 4; Length 125;
Best Local Similarity 69.2%; Pred. No. 1.9e-39;
Matches 90; Conservative 10; Mismatches 25; Indels 5; Gaps 1;

QY      1 QVOLVOSGAEAKKPGSSVKVSCKASGDTFNSPISWVROAPGQGLEWMGRIIPFGSTKY 60
        :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EVOLVESAEVKKPGASVSKVSCKASGYFTGYVMHWROAPGQGLEWMGWINPNSGCTNY 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 AOKFGQVMTADGSTSTAYVMEIILSRSEDTAIYYCARQNGGWYEGPFLPEPPDALDIW 120
        :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 AOKFGQVMTADGSTSTAYVMEIILSRSEDTAIYYCARQNGGWYEGPFLPEPPDALDIW 115
        :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      121 GGGTMTVSS 130
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      116 GGGTMTVSS 125

RESULT 3
Q9UL92 PRELIMINARY; PRT; 124 AA.
ID Q9UL92
AC Q9UL92;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX      NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalie N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035022; AAD56258.1; -
DR HSP; P01772; 2FBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 1
FT NON_TER 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;

Query Match      64.4%; Score 443; DB 4; Length 124;
Best Local Similarity 70.2%; Pred. No. 1.8e-38;
Matches 92; Conservative 11; Mismatches 20; Indels 8; Gaps 3;

QY      1 QVOLVOSGAEAKKPGSSVKVSCKASGDTFNSPISWVROAPGQGLEWMGRIIPFGSTKY 60
        :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EVOLVESAEVKKPGASVSKVSCKASGYFTSSYVMHWROAPGQGLEWMGIIINFGSTSY 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      61 AOKFGQVMTADGSTSTAYVMEIILSRSEDTAIYYCARQNGGWYEGPFLPEPP-DALDI 119
        :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 AOKFGQVMTADGSTSTAYVMEIILSRSEDTAIYYCARQNGGWYEGPFLPEPP-DALDI 113
        :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      120 WGGTMTVSS 130
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      114 WGGTMTVSS 124

RESULT 4
Q96GAG PRELIMINARY; PRT; 614 AA.
ID Q96GAG
AC Q96GAG;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC009851; AAH09851.1; -
DR InterPro: IPR000005; HTHARAC.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 5.
DR SMART: SM00406; IGV; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
DR KW Hypothetical protein.
SQ SEQUENCE 614 AA; 67921 MW; 55EP536E77AA9BBB CRC64;

Query Match      63.7%; Score 438.5; DB 4; Length 614;
Best Local Similarity 68.5%; Pred. No. 4e-37;
Matches 89; Conservative 8; Mismatches 24; Indels 9; Gaps 1;

QY      1 QVOLVOSGAEAKKPGSSVKVSCKASGDTFNSPISWVROAPGQGLEWMGRIIPFGSTKY 60

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OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Parkind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN mRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC DR EMBL: J00539; AAA8172.1; -
CC DR PIR: A02038; G2M643.
CC DR HSSP: P01810; 2FBJ.
CC DR InterPro: IPR007110; IG_1like.
CC DR InterPro: IPR003006; IG_MHC.
CC DR InterPro: IPR003596; IG_V.
CC DR Pfam: PF00047; IG_1.
CC DR SMART: SM00406; IGV_1.
CC DR PROSITE: PS50835; IG_LIKE; 1.
CC DR Immunoglobulin V region; Signal.
CC KW SIGNAL.
CC FT CHAIN 1 19 IG HEAVY CHAIN V REGION S43.
CC FT DOMAIN 20 49 FRAMEWORK-1.
CC FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 55 68 FRAMEWORK-2.
CC FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 86 117 FRAMEWORK-3.
CC FT DOMAIN 118 122 D SEGMENT.
CC FT DOMAIN 123 137 JH2 SEGMENT.
CC FT DISULFID 41 115 BY SIMILARITY.
CC FT NON_TER 137 137
CC SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF448BEC9 CRC64;

Query Match
Best Local Similarity 51.5%; Score 354; DB 1; Length 137;
Matches 70; Conservative 19; Mismatches 29; Indels 12; Gaps 1;

OY 1 QVQLVQSGAEAKKPGSSVYKSCASGDTFNSFPISWVROAPQGLEWMGIIPIFGSTKY 60
DB 20 QVQLQPGAEFVKPGASVYLSCKASGYFTSYLMHVNRPGRGLEWIGRIDPNSGTTY 79
OY 61 AOKFGRTVMTADGSTAYMELNSLRSEDTAIYYCARQONGWYEGPILPRPDALDIW 120
DB 80 NEHFRSKATLTITDKPSSTAYMQLSLTSEDSAVYCARILGRYF-----DYM 127
OY 121 GGGTMTVSS 130
DB 128 GGGTTLTVSS 137

RESULT 15
HY48_MOUSE
ID HY48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region T8PC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
CC DR PIR: A02033; HVMST7.
CC DR HSSP: P01810; 2FBJ.
CC DR InterPro: IPR007110; IG_1like.
CC DR InterPro: IPR003006; IG_MHC.
CC DR InterPro: IPR003596; IG_V.
CC DR Pfam: PF00047; IG_1.
CC DR SMART: SM00406; IGV_1.
CC DR PROSITE: PS50835; IG_LIKE; 1.
CC DR Immunoglobulin V region; Signal.
CC KW SIGNAL.
CC FT CHAIN 1 20 IG HEAVY CHAIN V REGION T8PC 1017.
CC FT DOMAIN 21 49 FRAMEWORK-1.
CC FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 55 68 FRAMEWORK-2.
CC FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 86 117 FRAMEWORK-3.
CC FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
CC FT DOMAIN 128 138 FRAMEWORK-4.
CC FT DISULFID 41 115 BY SIMILARITY.
CC FT NON_TER 138 138
CC SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match
Best Local Similarity 50.1%; Score 344.5; DB 1; Length 138;
Matches 69; Conservative 21; Mismatches 29; Indels 11; Gaps 2;

OY 1 QVQLVQSGAEAKKPGSSVYKSCASGDTFNSFPISWVROAPQGLEWMGIIPIFGSTKY 60
DB 20 QVQLQPGAEFVKPGASVYLSCKASGYFTSYLMHVNRPGRGLEWIGRIDPNSGTTY 79
OY 61 AOKFGRTVMTADGSTAYMELNSLRSEDTAIYYCARQONGWYEGPILPRPDALDIW 120
DB 80 NEHFRSKATLTITDKPSSTAYMQLSLTPEPRAVYICAR--SDGY-----DMPYTW 128
OY 121 GGGTMTVSS 130
DB 129 GGGTTLTVSS 138

Search completed: December 30, 2003, 10:55:49
Job time : 7.96994 secs

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CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02022; GIMSA.
DR HSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 106 IG-LIKE.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A9FABE CRC64;

Query Match
Best Local Similarity 52.3%; Score 360; DB 1; Length 114;
Matches 74; Conservative 17; Mismatches 23; Indels 12; Gaps 1;

QY 1 QVQLVSGAEAKKPGSSVYKSCASGDTFNSFPISWVRQAPQGLEWMGIIPIFGSTKY 60
DB 1 EVQLQQSGAEIVKASSVYKSCATGTFSSYELVWVRQAPQGLEDDGYISSSSAYPNY 60
QY 61 AOKFGQRYVTADGSTSTAYMELNSLRSEDTAIYYCARQNGGWYEGPLLEPRDADIW 120
DB 61 AOKFGQRYVTITADESTINAYMELSSLRSEDTAVYCAVRVISRYFDG-----W 108
QY 121 GGGTMY 126
DB 109 GGGTIV 114

RESULT 12
HVS1_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DR 01-JAN-1988 (Rel. 06, Created)
DR 01-JAN-1988 (Rel. 06, Last sequence update)
DR 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; Pubmed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02037; MHMS15.
DR HSP; P01810; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 105 V SEGMENT.
FT DOMAIN 106 120 D SEGMENT.
FT DISULFID 22 96 J SEGMENT.
FT NON_TER 120 120 BY SIMILARITY.
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match
Best Local Similarity 52.0%; Score 358; DB 1; Length 120;
Matches 71; Conservative 18; Mismatches 30; Indels 12; Gaps 3;

QY 1 QVQLVSGAEAKKPGSSVYKSCASGDTFNSFPISWVRQAPQGLEWMGIIPIFGSTKY 60
DB 1 QVQLVSGAEIVKASSVYKSCATGTFSSYELVWVRQAPQGLEDDGYISSSSAYPNY 60
```

```
QY 61 AOKFGQRYVTADGSTSTAYMELNSLRSEDTAIYYCARQNGGWYEGPLLEPRDADI 119
DB 61 NEKFKSKATLTVDKSSSATYMQLTPTSEDSAYYYCAR-----WDYEGDNY-----FDV 109
QY 120 WGGTMYTVSS 130
DB 110 WGGTIVTVSS 120

RESULT 13
HVS1_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DR 01-JAN-1988 (Rel. 06, Created)
DR 01-JAN-1988 (Rel. 06, Last sequence update)
DR 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; Pubmed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 104 V SEGMENT.
FT DOMAIN 105 118 D SEGMENT.
FT DISULFID 22 96 J SEGMENT.
FT NON_TER 118 118 BY SIMILARITY.
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match
Best Local Similarity 51.5%; Score 354; DB 1; Length 118;
Matches 71; Conservative 17; Mismatches 30; Indels 12; Gaps 2;

QY 1 QVQLVSGAEAKKPGSSVYKSCASGDTFNSFPISWVRQAPQGLEWMGIIPIFGSTKY 60
DB 1 EVQLQQSGAEIVKASSVYKSCATGTFSSYELVWVRQAPQGLEDDGYISSSSAYPNY 60
QY 61 AOKFGQRYVTADGSTSTAYMELNSLRSEDTAIYYCARQNGGWYEGPLLEPRDADIW 120
DB 61 NOKFKGKATLTVDKSSSATYMLNSLRSEDSAYYYCAR-----GYGY-----DPEDVW 108
QY 121 GGGTMYTVSS 130
DB 109 GGGTIVTVSS 118

RESULT 14
HVS1_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DR 21-JUL-1986 (Rel. 01, Created)
DR 21-JUL-1986 (Rel. 01, Last sequence update)
DR 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86203277; PubMed=3084950;
RA Kojima M., Koide T., Odani S., Ono T.;
RT "Amino acid sequence of the variable region of heavy chain in
RL Immunoglobulin (Mc) having unusual papain cleavage sites.";
Mol. Immunol. 23:169-174(1986).
DR PIR: A02025; HVHMO.
DR HSSP: P01772; 2P84.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-1-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 107 D SEGMENT.
FT DOMAIN 108 125 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 125 125
SQ SEQUENCE 125 AA; 13579 MW; F4C4285D6DF0C8EA CRC64;

Query Match 52.5%; Score 361.5; DB 1; Length 125;
Best Local Similarity 56.3%; Pred. No. 2.6e-30;
Matches 76; Conservative 12; Mismatches 32; Indels 15; Gaps 3;

OY 1 OVQVQSAEAKKPGSSVYKVSCKASGDTFNSFPISWNRQAPGQLEMMGIIPIFGSTKY 60
DB 1 OVQVQSAEAKKPGSSVYKVSCKASGDDFNTYDHWVRQAPRGLEMAVVPSSDRITTY 60
OY 61 AOKFGRYVTADGSTAYVWELNSLRSEDPATYYCARQNGWY-----EGPLLEPRPD 115
DB 61 GPRSGARTVTRDSSTTVYVWELTALISADPATYYCAR---GAHYSDPDDSGTSLGP--- 114
OY 116 ALDIWGQGTMTVSS 130
DB 115 ----WGQGTTLIVSS 125

RESULT 10
HV07_MOUSE STANDARD; PRT; 139 AA.
ID HV07_MOUSE
AC P01751; P01752;
RT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE 1g heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
XX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bohwell A.L.M., Peakind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribut in the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACTIVYL
CC (NPB ANTIBODIES).
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL: J00529; AAA38170.1; .
DR PIR: A90809; MEMS18.
DR PDB: 1A6U; 27-MAY-98.
DR PDB: 1A6W; 15-JUL-98.
DR InterPro: IPR007110; IG-1-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; 3d-structure.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 52.5%; Score 361; DB 1; Length 139;
Best Local Similarity 56.2%; Pred. No. 3.3e-30;
Matches 73; Conservative 17; Mismatches 30; Indels 10; Gaps 2;

OY 1 OVQVQSAEAKKPGSSVYKVSCKASGDTFNSFPISWNRQAPGQLEMMGIIPIFGSTKY 60
DB 20 OVQVQSAEALVYKGSVYKVSCKASGYTFSTYMWVWVQVRGRGLEWVGRIDPNSGCTKY 79
OY 61 AOKFGRYVTADGSTAYVWELNSLRSEDPATYYCARQNGWYEGPLLEPRPDALDIW 120
DB 61 NEKFKSKATLVDPSSSTAYVWELNSLRSEDSAVYICARYD-----SSYFDYW 129
OY 121 GQGTMTVSS 130
DB 130 GQGTTLIVSS 139

RESULT 11
HV00_MOUSE STANDARD; PRT; 114 AA.
ID HV00_MOUSE
AC P01741;
RT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE 1g heavy chain V region (Anti-arsenate antibody).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
XX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RA STRAIN=A/J;
RX MEDLINE=79195438; PubMed=109536;
RA Capra J.D., Nisenson A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
RL mice bearing a cross-reactive idiotype.";
RL J. Immunol. 123:279-284(1979).
CC -1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC REGION SEQUENCE.

```

SQ SEQUENCE 117 AA; 12983 MW; 3CF9ACB4BE447E41 CRC64;

Query Match 53.4%; Score 367.5; DB 1; Length 117;

Best Local Similarity 55.4%; Pred. No. 5.9e-31;

Matches 72; Conservative 18; Mismatches 27; Indels 13; Gaps 2;

DB 1 EVOLQSGAEIVKPGASVMSCKASGYTFTDYMKVKVSHKSLKLEWIGDINPENGTSY 60

DB 61 AOKFGQRTMTADGSTSTAYMELNSLRSEDTAIYYCARQNGWYEGPLLEPRPDALDIW 120

DB 61 NEKFGKATLTVDKSSSTAYMQLSLTSEDSAVYYCARDYD--WY-----FDVW 107

QY 121 GGGTMTVSS 130

DB 108 GAGTTVTSS 117

RESULT 7  
HVL3\_MOUSE  
ID HVL3\_MOUSE STANDARD; PRT; 117 AA.

AC P01757;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region J558.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE.

RA MEDLINE=80078170; PubMed=6765983;

RA Schilling J., Clevinger B., Davie J.M., Hood L.;

RT "Amino acid sequence of homogeneous antibodies to dextran and DNA

RT rearrangements in heavy chain V-region gene segments.";

RL Nature 283:35-40(1980)

CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO

CC WHICH OCCUR IN THE D AND J SEGMENTS.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSSP; P01789; IMCPS.

DR InterPro; IPR007110; Ig\_1like.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_V.

DR Pfam; PF00047; Ig\_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.

KW Immunoglobulin V region.

FT DOMAIN 1 116

FT DISULFID 22 96

FT NON\_TER 117 117

FT SEQUENCE 117 AA; 13024 MW; 292E2AFA4BE447E41 CRC64;

Query Match 53.3%; Score 366.5; DB 1; Length 117;

Best Local Similarity 55.4%; Pred. No. 7.4e-31;

Matches 72; Conservative 18; Mismatches 27; Indels 13; Gaps 2;

DB 1 EVOLQSGAEIVKPGASVMSCKASGYTFTDYMKVKVSHKSLKLEWIGDINPENGTSY 60

DB 61 AOKFGQRTMTADGSTSTAYMELNSLRSEDTAIYYCARQNGWYEGPLLEPRPDALDIW 120

DB 61 NEKFGKATLTVDKSSSTAYMQLSLTSEDSAVYYCARDYD--WY-----FDVW 107

QY 121 GGGTMTVSS 130

DB 108 GAGTTVTSS 117

RESULT 8  
HVL2\_MOUSE  
ID HVL2\_MOUSE STANDARD; PRT; 140 AA.

AC P01746;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region J937 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=A/J;

RA MEDLINE=82152818; PubMed=6801765;

RA Sims J., Rabbits T.H., Estees P., Slaughter C., Tucker P.W.,

RA Capra J.D.;

RT "Somatic mutation in genes for the variable portion of the

RT Immunoglobulin heavy chain.";

RL Science 216:309-311(1982).

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation

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CC EMBL J00493; AAA38128.1; -

DR PIR; A94264; HYMSG7.

DR HSSP; P01810; 2FBU.

DR InterPro; IPR007110; Ig\_1like.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_V.

DR Pfam; PF00047; Ig\_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.

KW Immunoglobulin V region; Hybridoma; Signal.

FT SIGNAL 1 19

FT CHAIN 20 140

FT DOMAIN 20 139

FT NON\_TER 140 140

FT SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5C8 CRC64;

Query Match 52.8%; Score 363.5; DB 1; Length 140;

Best Local Similarity 56.5%; Pred. No. 1.9e-30;

Matches 74; Conservative 18; Mismatches 28; Indels 11; Gaps 2;

DB 1 EVOLQSGAEIVKPGASVMSCKASGYTFTDYMKVKVSHKSLKLEWIGDINPENGTSY 79

DB 61 AOKFGQRTMTADGSTSTAYMELNSLRSEDTAIYYCARQ-NGCWYEGPLLEPRPDALDI 119

DB 80 NEKFGKATLTVDKSSSTAYMQLSLTSEDSAVYFCARSHYGGSYD-----FDY 129

QY 120 WGGGTMTVSS 130

DB 130 WGGGTMTVSS 140

RESULT 9

HVL1\_HUMAN  
ID HVL1\_HUMAN STANDARD; PRT; 125 AA.  
AC P06326;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V-I region Mot.

DE Ig heavy chain V-I region V35 precursor.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88296408; PubMed=2841108;  
 RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,  
 RA Ohno H., Fukuhara S., Honjo T.;  
 RT "Dispersed localization of D segments in the human immunoglobulin  
 RT heavy-chain locus."  
 RL EMBO J. 7:1047-1051(1988).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC -----  
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 CC or send an email to [license@1sb-sib.ch](mailto:license@1sb-sib.ch)).  
 CC -----  
 CC EMBL: X07448; NOT ANNOTATED\_CDS.  
 DR PIR: S00476; HAHU35.  
 DR HSSP: P01772; 2FB4.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding activity; NAS.  
 DR GO: GO:0006955; F:immune response; NAS.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_V.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.  
 FT DOMAIN 20 >117 IG-LIKE.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;  
 Query Match 55.2%; Score 380; DB 1; Length 117;  
 Best Local Similarity 75.5%; Pred. No. 3e-32;  
 Matches 74; Conservative 6; Mismatches 18; Indels 0; Gaps 0;  
 QY 1 QVQLVQSGAEAKKPGSSVYVSCKASGDTFNSPISWVQAQPGQGLEMMGILPIFGSTKY 60  
 DB 20 QVQLVQSGAEVAKKPGASVYVSCKASGYFTFTGYTHMVAQAPGQGLEMMGRINPNSGCTNY 79  
 QY 61 AOKFGQRYVTMTADGSTSTAYMELNSLRSEDTAIYYCAR 98  
 DB 80 AOKFGQRYVTSTRDTSISTAYMELSLRSDDTIVYYCAR 117  
 RESULT 5  
 ID HV03\_MOUSE STANDARD; PRT; 120 AA.  
 AC P01747;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region 36-65.  
 DE Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83131846; PubMed=6186498;  
 RA Silevitz M., Geffer M.L., Brodeur P., Riblet R.,  
 RA Marshak-Rothstein A.;  
 RT "The genetic basis of antibody production: the dominant anti-arsenate

RT idotype response of the strain A mouse.";  
 RL Eur. J. Immunol. 12:1023-1032(1982).  
 CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER  
 CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS  
 CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J  
 CC SEGMENT, JH2.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC -----  
 CC HSSP: P01789; 1MCP.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_V.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Hybridoma.  
 FT DOMAIN 1 111  
 FT NON\_TER 120 120 IG-LIKE.  
 SQ SEQUENCE 120 AA; 13307 MW; F04E4A167B654AF CRC64;  
 Query Match 53.9%; Score 370.5; DB 1; Length 120;  
 Best Local Similarity 57.3%; Pred. No. 3e-31;  
 Matches 75; Conservative 17; Mismatches 26; Indels 13; Gaps 2;  
 QY 2 VQLVQSGAEAKKPGSSVYVSCKASGDTFNSPISWVQAQPGQGLEMMGILPIFGSTKYA 61  
 DB 1 VQLVQSGAEVAKKPGASVYVSCKASGYFTFTGYTHMVAQAPGQGLEMMGRINPNSGCTNY 60  
 QY 62 OKFGQRYVTMTADGSTSTAYMELNSLRSEDTAIYYCARQ--QNGGWYGGPLLEPPDLDI 119  
 DB 61 EKFKGKTLITVDKSSSTAYMELNSLRSEDAVYFCARSVYGGSY-----FDY 109  
 QY 120 WGGCTMTVTS 130  
 DB 110 WGGCTMTVTS 120  
 RESULT 6  
 ID HV12\_MOUSE STANDARD; PRT; 117 AA.  
 AC P01756;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region MOPC 104E.  
 DE Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE AND CARBOHYDRATE-LINKAGE SITE ASN-55.  
 RX MEDLINE=83075344; PubMed=6816276;  
 RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,  
 RA Hood L.E.;  
 RT "Complete amino acid sequence of a mouse mu chain: homology among  
 RT heavy chain constant region domains.";  
 RL Biochemistry 21:5415-5424(1982).  
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA  
 CC PROTEIN HAS ALSO BEEN DETERMINED.  
 CC -1- SIMILARITY: THIS PROTEIN BINDS DEXTRAN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC -----  
 CC HSSP: P01789; 1MCP.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; IGV\_1.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Glycoprotein.  
 FT DOMAIN 1 116  
 FT DISULFID 22 96 IG-LIKE.  
 FT CARBOHYD 55 55 BY SIMILARITY.  
 FT NON\_TER 117 117 N-LINKED (GLCNAC. . .) (COMPLEX).

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QY 6 AAKFGGRVMTADGSTSTAYMELNSRSEDPAIYCAQOQNG--VEGFLLEPRPALD 11
Db 61 AAKFGGRVMTITDESTINRAYMELSSRSEDPAFYCA-----GGYGIS-----PFEYN 109
QY 119 IWGGTMTVSS 130
Db 110 ---GGLTVSS 117

RESULT 2
HVLB_HUMAN
ID HVLB_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region H03 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givoli D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups."
RT Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
DR EMBL; J00240; AAA52988.1; -
DR PIR; A02024; HVHUNG.
DR HSSP; P01772; 2PBA.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; F:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION H03.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1E7 CRC64;

Query Match 59.9%; Score 412; DB 1; Length 117;
Best Local Similarity 82.7%; Pred. No. 1,6e-35;
Matches 81; Conservative 5; Mismatches 12; Indels 0; Gaps 0

QY 1 QVALVSGAEAKKRGSSVKVSCASGDTFNSPFIWROAPQGLIEMGGIIPFGSTKY 60
Db 20 QVALVSGAEVKKRGASVKVSCASGDTFNSYVMHWROAPQGLIEMGGIIPNSGGSITSY 79
QY 61 AAKFGGRVMTADGSTSTAYMELNSRSEDPAIYCAR 98
Db 80 AAKFGGRVMTITDESTINRAYMELSSRSEDPAIYCAR 117

RESULT 3
HVLIC_HUMAN
ID HVLIC_HUMAN STANDARD; PRT; 147 AA.

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AC	P01744;1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 40, Last sequence update)
DT	16-OCT-2001 (Rel. 42, Last annotation update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Ig heavy chain V-I region ND precursor (Fragments).
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=83065234; PubMed=6815655;
RA	Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RL	Bell L.O., Gould H.J.;
RT	"Cloning and sequence determination of the gene for the human
RU	immunoglobulin epsilon chain expressed in a myeloma cell line.";
RP	Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN	[2]
RP	SEQUENCE OF 20-147.
RU	Bennich H.H., Johansson S.G.O., von Bahr-Bjindstrom H.;
RL	(in) Bach M.K. (eds.):
CC	Immediate hypersensitivity: modern concepts and developments, pp.1-36,
CC	Marcel Dekker, New York (1978).
CC	-I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC	PROTEIN.
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR	HSPSP, P01789; IMCP
DR	GO; GO:0005576; C:extracellular; NAS.
DR	GO; GO:0003823; F:antigen binding activity; NAS.
DR	GO; GO:0006955; P:immune response; NAS.
DR	Interpro: IPRO07110; Ig-Like.
DR	Interpro: IPRO03065; IG_MHC.
DR	Interpro: IPRO03596; Ig_V.
DR	Pfam: PF00047; Ig; 1.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
KM	Immunoglobulin V region; signal; Pyrrolidone carboxylic acid.
FT	SIGNAL 1 19
FT	CHAIN 20 147
FT	DOMAIN 20 131
FT	MOD_RES 20 20
FT	DISELIFD 41 115
FT	CONFLICT 21 21 T -> V (IN REF. 2).
FT	CONFLICT 53 54 IH -> HI (IN REF. 2).
FT	CONFLICT 67 68 VG -> GV (IN REF. 2).
FT	CONFLICT 125 125 MISSING (IN REF. 2).
FT	NON_TER 147 147
SO	SEQUENCE 147 AA; 16491 MW; 948PFP72A536C30 CRC64;
Query Match	56.2%; Score 387; DB 1; Length 147;
Best Local Similarity	59.8%; Pred. No. 7.5e-33;
Matches 79; Conservative 14; Mismatches 33; Indels 6; Gaps 2	
OY	1 QVQLVQSGAEAKKGGSSVKVSKCAKSCGTFFNSFWVAQADGCGLEWNGGIPIFGSTRK 60           :           :           :           :           Db 20 OTQLVQSAGAEVRKKGASRVSKCSKSGTFLDISYIHIMIQAGHGHEWGWIPNPGGINY 79           :           :           :           :
OY	61 AQKEQGRVTMTADSGSTAYVELNSLRSEDTAITYICAPQQN--GGWYEGPLIEPPDALD 118           :           :           :           :           Db 80 APRQGRTVMTRDASFSTAIVMDLSRSDSDAVFYCAKSDPFMSDYVFNDY---SYTLDD 135           :           :           :           :
OY	119 IWGGITMYTVSS 130           :           :           :           :
Db	136 VMGGGITVTVSS 147           :           :           :           :
RESULT 4	
ID	HVIG_HUMAN STANDARD; PRT; 117 AA.
AC	P23083;
DT	01-NOV-1991 (Rel. 20, Created)
DT	01-NOV-1991 (Rel. 20, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 6.96994 Seconds  
(without alignments)  
877.119 Million cell updates/sec

Title: US-09-674-752-23

Perfect score: 688

Sequence: 1 QVOLVSGAEVKAKKSSSVKVV.....EPPDLDIMCGTIVTVSS 130

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	420.5	61.1	117	1	HV1A_HUMAN
2	412	59.9	117	1	HV1B_HUMAN
3	387	56.2	147	1	HV1C_HUMAN
4	380	55.2	117	1	HV1G_HUMAN
5	370.5	53.9	120	1	HV03_MOUSE
6	367.5	53.4	117	1	HV12_MOUSE
7	366.5	53.3	117	1	HV13_MOUSE
8	363.5	52.8	140	1	HV02_MOUSE
9	361.5	52.5	125	1	HV1F_HUMAN
10	361	52.5	139	1	HV07_MOUSE
11	360	52.3	114	1	HV00_MOUSE
12	358	52.0	120	1	HV50_MOUSE
13	354	51.5	118	1	HV51_MOUSE
14	345	51.5	137	1	HV11_MOUSE
15	344.5	50.1	138	1	HV48_MOUSE
16	342	49.7	117	1	HV52_MOUSE
17	339.5	49.3	121	1	HV01_MOUSE
18	338	49.1	124	1	HV1E_HUMAN
19	329	47.8	117	1	HV09_MOUSE
20	328	47.7	117	1	HV05_MOUSE
21	324	47.1	117	1	HV06_MOUSE
22	322	46.8	117	1	HV04_MOUSE
23	319	46.4	120	1	HV1H_HUMAN
24	317	46.1	117	1	HV49_MOUSE
25	316	45.9	117	1	HV14_MOUSE
26	314	45.6	117	1	HV10_MOUSE
27	313.5	45.6	121	1	HV3J_HUMAN
28	313.5	45.6	116	1	HV15_MOUSE
29	310.5	45.1	135	1	HV3D_HUMAN
30	310	45.1	136	1	HV16_MOUSE
31	308	44.8	116	1	HV3T_HUMAN
32	308	44.8	122	1	HV3G_HUMAN
33	307	44.6	124	1	HV1D_HUMAN

34	303.5	44.1	119	1	HV3I_HUMAN	P01770 homo sapien
35	303	44.0	122	1	HV3A_HUMAN	P01762 homo sapien
36	303	44.0	122	1	HV3H_HUMAN	P01769 homo sapien
37	301	43.8	114	1	HV3B_HUMAN	P01763 homo sapien
38	301	43.8	120	1	HV3U_HUMAN	P01782 homo sapien
39	295	42.9	126	1	HV3K_HUMAN	P01772 homo sapien
40	292	42.4	114	1	HV01_CANFA	P01784 canis fam1
41	291	42.3	117	1	HV3C_HUMAN	P01764 homo sapien
42	291	42.3	119	1	HV38_MOUSE	P01808 mus musculu
43	286.5	41.6	117	1	HV02_CANFA	P01785 canis fam1
44	286	41.6	119	1	HV40_MOUSE	P01810 mus musculu
45	283.5	41.2	142	1	HV01_RAT	P01805 rattus norv

## ALIGNMENTS

ID	HV1A_HUMAN	STANDARD	PRT	117 AA.
AC	P01742:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ig heavy chain V-I region EU.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waxdal M.J., Edelman G.M.,			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RT	acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RL	Biochemistry 9:3161-3170(1970).			
RN	[2]			
RP	DISULFIDE BOND.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.,			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			
RT	Intrachain disulfide bonds."			
RL	Biochemistry 9:3188-3196(1970).			
CC	-I- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS			
CC	MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.			
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.			
DR	PIR; A90563; G1HUEU.			
DR	HSSP; P01772; 2FB4.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0003823; F:antigen binding activity; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003066; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SMO0406; IGV; 1.			
DR	PROSITE; PS50835; IG-LIKE; 1.			
KW	Immunoglobulin V region; Pyroglutamate carboxylic acid.			
FT	DOMAIN 1 112 IG-LIKE.			
FT	MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.			
FT	DISULFID 22 96			
FT	NON_TER 117 117			
SO	SEQUENCE 117 AA; 12472 MW; 99D60ADAEBD52818 CRC64;			
Qy	Query Match	61.1%; Score 420.5; DB 1; Length 117;		
Db	Best Local Similarity	67.4%; Pred. No. 2,1e-36;		
	Matches	89; Conservative 11; Mismatches 15; Indels 17; Gaps 4;		
	1 QVOLVSGAEVKAKKSSSVKSSCKASGDTFNSFPISWYRQAGGGLWMGGIIPFGSTKY 60			
	1 QVOLVSGAEVKAKKSSSVKSSCKASGDTFNSFPISWYRQAGGGLWMGGIIPFGSTKY 60			



OY 1 QNGWYEGPLLEPRDALDI 20  
 Db 8 QNGWYRVPIKDPLEYLE 27

## RESULT 6

O47755 PRELIMINARY; PRT; 358 AA.  
 AC O47755;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE D-alanine:D-alanine ligase.  
 OS Enterococcus faecium (Streptococcus faecium).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1352;  
 KW

SEQUENCE FROM N.A.  
 RC STRAIN=BM4147;  
 RX MEDLINE=96270057; PubMed=8662022;  
 RA Evers S., Casadewall B., Charles M., Dutka-Malen S., Galimand M.,  
 RA Courvalin P.;  
 RT "Evolution of structure and substrate specificity in D-alanine:D-  
 RT alanine ligases and related enzymes.";  
 RL J. Mol. Evol. 42:706-712(1996).  
 [2]  
 RP SEQUENCE FROM N.A.

RA Gholiaden Y., Prevost M., van Bambeke F., Casadewall B.,  
 RA Tulkens P.M., Courvalin P.;  
 RT "Sequencing of the ddl gene and modeling of the mutated D-alanine:D-  
 RT alanine ligase in glycopeptide-dependent strains of Enterococcus  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U39790; AB017902.2; --  
 DR HSP; P07862; 110V.  
 DR InterPro: IPR000291; Dala\_lig Van.  
 DR InterPro: IPR005905; D ala D ala.  
 DR Pfam: PF01820; Dala\_dala\_ligase; 1.  
 DR TIGRFAMs: TIGR01205; D ala D alsttGR; 1.  
 DR PROSITE: PS00843; DALA\_DALA\_LIGASE\_1; 1.  
 DR PROSITE: PS00844; DALA\_DALA\_LIGASE\_2; 1.  
 KW

Query Match 358 AA; 40247 MW; 0801F31DB1FA9PEC CRC64;  
 Best local Similarity 41.7%; Score 50; DB 2; Length 358;  
 Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 2 QNGWYEGPLLEPRDALDI 21  
 Db 42 KEGOWKGPLETEKPSKDV 61

## RESULT 7

O9F0M3 PRELIMINARY; PRT; 358 AA.  
 AC O9F0M3;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE D-alanine:D-alanine ligase.  
 OS Enterococcus faecium (Streptococcus faecium).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1352;  
 KW

SEQUENCE FROM N.A.

RA STRAIN=A902;  
 RC Gold H.S., Eliopoulos G.M., Moellering R.C. Jr.;  
 RT "D-alanine:D-alanine ligase of Vand Enterococcus faecium A902.";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR HSP; P07862; 110V.

DR InterPro: IPR000291; Dala\_lig Van.  
 DR InterPro: IPR005905; D ala D ala.  
 DR Pfam: PF01820; Dala\_dala\_ligase; 1.  
 DR TIGRFAMs: TIGR01205; D ala D alsttGR; 1.  
 DR PROSITE: PS00843; DALA\_DALA\_LIGASE\_1; 1.  
 DR PROSITE: PS00844; DALA\_DALA\_LIGASE\_2; 1.  
 KW

Query Match 358 AA; 40175 MW; 745E3AC27953C20F CRC64;  
 Best local Similarity 41.7%; Score 50; DB 2; Length 358;  
 Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 2 QNGWYEGPLLEPRDALDI 21  
 Db 42 KEGOWKGPLETEKPSKDV 61

## RESULT 8

O9YBR4 PRELIMINARY; PRT; 403 AA.  
 AC O9YBR4;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE 403AA long hypothetical pyruvate formate lyase activating protein.  
 GN ABE1535.  
 OS Aeropyrum pernix.  
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococciales;  
 OC Desulfurococcaceae; Aeropyrum.  
 OX NCBI\_TaxID=56636;  
 [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=KI;  
 RX MEDLINE=99310339; PubMed=10382966;  
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,  
 RA Hino Y., Takahashi M., Sekine M., Baba S.-I., Ankei A., Kosugi H.,  
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,  
 RA Takamiya M., Maeda S., Funahashi T., Tanaka T., Kudoh Y.,  
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,  
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;  
 RT "Complete genome sequence of an aerobic hyper-thermophilic  
 RT crenarchaeon, Aeropyrum pernix KI.";  
 RL DNA Res. 6:83-101(1999).  
 DR EMBL: AP000061; BAA80534.1; --  
 DR InterPro: IPR001005; Myb\_DNA\_binding.  
 DR PROSITE: PS00334; MYB\_2; 1.  
 KW

Query Match 403 AA; 47103 MW; 6B68528AD393DD0 CRC64;

Best local Similarity 41.7%; Score 50; DB 17; Length 403;  
 Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 2 QNGWYEGPLLEPRDALDI 21  
 Db 108 REGGSYEDIKDARPSIMDV 127

## RESULT 9

O9H685 PRELIMINARY; PRT; 322 AA.  
 AC O9H685;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Hypothetical protein FLJ22501.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 6.75548 Seconds  
(without alignments)  
493.415 Million cell updates/sec

Title: US-09-674-752-29

Perfect score: 120

Sequence: 1 QQNGMYEGPLLEPPDLDI 21

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_19Jun03:\*

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2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*

3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*

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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	120	100.0	21	AAV50956
2	120	100.0	21	AAV50948
3	52	43.3	265	ABG00057
4	51.5	42.9	118	AAU43195
5	51	42.5	132	ABP33553
6	50	41.7	341	AAU35179
7	50	41.7	348	ABP57025
8	50	41.7	358	ABP57024
9	49	40.8	549	ABG99970

10	48	40.0	993	20	AAV49897
11	47	39.2	172	22	AAU23343
12	47	39.2	564	22	ABG24835
13	47	39.2	816	22	ABG24833
14	47	39.2	858	22	ABG04046
15	47	39.2	897	22	ABG25828
16	47	39.2	4150	21	AAV92707
17	47	39.2	7068	22	AAE10142
18	47	39.2	9477	22	AAE10144
19	46	38.3	70	23	ABP04042
20	46	38.3	355	22	AAE09457
21	46	38.3	429	22	ABG22412
22	46	38.3	1062	21	ABG2412
23	46	38.3	1235	21	AAAB41663
24	45.5	37.9	472	22	AAU39938
25	45	37.5	77	22	AAO31758
26	45	37.5	186	21	AAO30871
27	45	37.5	186	21	AAO30872
28	45	37.5	314	21	AAO60963
29	45	37.5	325	21	AAO60961
30	45	37.5	329	21	AAO60962
31	45	37.5	338	21	AAO60961
32	45	37.5	340	21	AAO60870
33	45	37.5	346	21	AAO60870
34	45	37.5	349	21	AAO60869
35	45	37.5	352	21	AAO60869
36	45	37.5	352	21	AAO60880
37	45	37.5	363	21	AAO60880
38	45	37.5	369	21	AAO60879
39	45	37.5	369	21	AAO60879
40	45	37.5	375	21	AAO60879
41	45	37.5	382	21	AAO60878
42	45	37.5	382	21	AAO60878
43	45	37.5	463	22	ABG25348
44	45	37.5	772	22	AAU44927
45	45	37.5	1729	22	AAAB2331

#### ALIGNMENTS

RESULT 1

AAV50956

AAV50956 standard; Protein; 21 AA.

AAV50956;

23-MAR-2000 (first entry)

Human anti-factor VIII antibody VH protein VH EL-14 CDR3 fragment.

Human; heavy chain; antibody; factor VIII; hemostatic;

hemophilia A; VH protein.

OS Homo sapiens.

PN MO958680-A2.

PD 18-NOV-1999.

PP 07-MAY-1999; 99WO-NL00285.

PR 08-MAY-1998; 98EP-0201543.

(SANO-) STICHTING SANQUIN BLOEDVOORZIENTING.

Voorberg JI, Van Den Brink EN, Turenhout EAM;

WPI; 2000-053102/04.

New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies.

XX Example 4; Fig 4C; 61pp; English.  
 PS This invention describes a novel polynucleotide (I) (and complements and  
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence  
 CC coding for a human antibody with factor VIII specificity which has  
 CC hemostatic activity. (I) is useful as a primer or probe for detecting the  
 CC presence of inhibitory antibodies directed against factor VIII. The  
 CC polypeptides of the invention and the antibodies generated from them  
 CC are useful in compositions for neutralizing factor VIII inhibiting  
 CC antibodies in hemophilia A patients. This sequence represents the human  
 CC anti-factor VIII antibody A EL-14 protein CDR3 fragment which is used  
 XX in the method of the invention.

SQ Sequence 21 AA;  
 Query Match 100.0%; Score 120; DB 21; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QONGWYEGPLLEPRPDALDI 21  
 DB 1 QONGWYEGPLLEPRPDALDI 21

RESULT 2  
 ID AAY50948 standard; Protein; 130 AA.  
 XX AAY50948;  
 AC  
 XX 23-MAR-2000 (first entry)  
 DT  
 XX  
 DE Human anti-factor VIII antibody VH clone EL-14 encoded protein.  
 KW Human; heavy chain; antibody; factor VIII; hemostatic;  
 KM hemophilia A; VH gene.  
 XX Homo sapiens.  
 OS  
 XX WO958680-A2.  
 PN  
 XX 18-NOV-1999.  
 PD  
 XX 07-MAY-1999; 99WO-NL00285.  
 PF  
 XX 08-MAY-1998; 98EP-0201543.  
 PR  
 XX (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.  
 PA Voorberg JI, Van Den Brink EN, Turehout EAM;  
 PI WPI; 2000-053102/04.  
 DR  
 XX New polynucleotide, polypeptide and antibody useful for diagnosing the  
 PT presence of neutralizing antibodies against factor VIII and for  
 PT treatment of hemophilia A patients with these antibodies -  
 PS Example 4; Fig 4A; 61pp; English.  
 XX This invention describes a novel polynucleotide (I) (and complements and  
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence  
 CC coding for a human antibody with factor VIII specificity which has  
 CC hemostatic activity. (I) is useful as a primer or probe for detecting the  
 CC presence of inhibitory antibodies directed against factor VIII. The  
 CC polypeptides of the invention and the antibodies generated from them  
 CC are useful in compositions for neutralizing factor VIII inhibiting  
 CC antibodies in hemophilia A patients. This sequence represents the human  
 CC anti-factor VIII antibody clone EL-14 protein which is used in the method  
 XX of the invention.

SQ Sequence 130 AA;

Query Match 100.0%; Score 120; DB 21; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-11;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QONGWYEGPLLEPRPDALDI 21  
 DB 99 QONGWYEGPLLEPRPDALDI 119

RESULT 3  
 ID ABG00057 standard; Protein; 265 AA.  
 XX ABG00057;  
 AC  
 XX 13-FEB-2002 (first entry)  
 DT  
 XX  
 DE Novel human diagnostic protein #48.  
 DE  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KM food supplement; medical imaging; diagnostic; genetic disorder.  
 XX Homo sapiens.  
 OS  
 XX WO200175067-A2.  
 PN  
 XX 11-OCT-2001.  
 PD  
 XX 30-MAR-2001; 2001WO-US08631.  
 PF  
 XX 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX Dymanac RT, Liu C, Tang YT;  
 PI WPI; 2001-639362/73.  
 DR N-PDSB; AAS64244.  
 DR  
 XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -  
 PS Claim 20; SEQ ID No 30416; 103pp; English.  
 XX The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridization probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 265 AA;  
 Query Match 43.3%; Score 52; DB 22; Length 265;  
 Best Local Similarity 69.2%; Pred. No. 7.2;

Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGMYESGPLEPP 16  
 ||| ||| ||| |||  
 Db 24 GGMHESGPLEPP 36

## RESULT 4

AAU43195  
 ID AAU43195 standard; Protein; 118 AA.

AC AAU43195;

DT 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #4091.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
 XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
 XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
 XX dermatological; osteopathic; neuroprotectant.

OS Propionibacterium acnes.

PN WO200181581-A2.

PD 01-NOV-2001.

PF 20-APR-2001; 2001WO-US12865.

PR 21-APR-2000; 2000US-199047P.

PR 02-JUN-2000; 2000US-208847P.

PR 07-JUL-2000; 2000US-216747P.

XX (CORI-) CORIXA CORP.

PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

DR WPI: 2001-616774/71.

DR N-PSDB; AAS59520.

XX Example 1; SEQ ID NO 4390; 1069pp; English.

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic  
 CC polypeptides. The proteins and their associated DNA sequences are used in  
 CC the treatment, prevention and diagnosis of medical conditions caused by  
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.  
 CC P. acnes is also involved in infections of bone, joints and the central  
 CC nervous system, however it is particularly involved in the inflammatory  
 CC lesions associated with acne vulgaris. A method for detecting the  
 CC presence or absence of P. acnes in a patient comprises contacting a  
 CC sample with a binding agent that binds to the proteins of the invention  
 CC and determining the amount of bound protein in the sample. The  
 CC polypeptides may be used as antigens in the production of antibodies  
 CC specific for P. acnes proteins. These antibodies can be used to  
 CC downregulate expression and activity of P. acnes polypeptides and  
 CC therefore treat P. acnes infections. The antibodies may also be used as  
 CC diagnostic agents for determining P. acnes presence, for example, by  
 CC enzyme linked immunosorbent assay (ELISA).  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 118 AA;

Query Match 42.9%; Score 51.5; DB 22; Length 118;  
 Best Local Similarity 71.4%; Pred. No. 3.5;

Matches 10; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 NGGMYESG-PLEPP 15  
 ||| | | | | | | | | |  
 Db 74 NGGMHYESGPLEPP 87

## RESULT 5

ABP33553  
 ID ABP33553 standard; Protein; 132 AA.

AC ABP33553;

DT 09-JUL-2002 (first entry)

DE Human ORF2526 protein, SEQ ID NO:5052.

XX Human; ORF; open reading frame; ORFX; drug screening; diagnosis;  
 XX disease monitoring; cytokine; cell proliferation; cell differentiation;  
 XX immune modulation; haematopoiesis regulation; tissue growth;  
 XX angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;  
 XX chromolytic; tumour inhibition; bodily characteristics; fertility;  
 XX behaviour; cancer; proliferative disorder; neurological disorder;  
 XX cardiovascular disease; immune system disorder; organ transplantation;  
 XX tissue growth disorder; tissue regeneration disorder; diabetes mellitus;  
 XX hypothyroidism; cholesterol ester storage disease; infection; vulnery;  
 XX vasotropic; antipsoriatic; antidiabetic; cytosolic; nocotropic;  
 XX neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;  
 XX cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;  
 XX dermatological; analgesic; virucide; antibacterial; fungicide.

OS Homo sapiens.

PN WO200190366-A2.

PD 29-NOV-2001.

PF 24-MAY-2001; 2001WO-US17076.

PR 24-MAY-2000; 2000US-206690P.

XX (CURA-) CURAGEN CORP.

PI Leach MD, Shinkete RA;

DR WPI: 2002-106200/14.

DR N-PSDB; ABN77579.

XX Novel human polypeptides and polynucleotides useful for diagnosing,  
 XX preventing and treating cardiovascular disease, neurodegenerative,  
 XX hyperproliferative disorders and disorders related to organ  
 XX transplantation -  
 PS Claim 10; Page 1516; 2508pp; English.

CC Sequences ABP31028-ABP35561 represent 4534 novel human proteins  
 CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-  
 CC ABN79587 represent cDNAs encoding them. The invention also encompasses  
 CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively  
 CC referred to as ORFX) proteins, polynucleotides at least 85% identical to  
 CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX  
 CC polynucleotides, the recombinant production of ORFX proteins, antibodies  
 CC specific for ORFX proteins, methods of detecting ORFX proteins, antibodies  
 CC polypeptides, methods of screening for modulators of ORFX expression or  
 CC activity, and methods of screening individuals for a predisposition to an  
 CC ORFX-associated disorder. The ORFX proteins of the invention have a wide  
 CC range of biological activities, such as cytokine, cell proliferation,  
 CC cell differentiation, immune modulation, haematopoiesis regulation,  
 CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/  
 CC chemokinetic activity, haemostatic activity, thrombolytic activity,  
 CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,  
 CC and antifibrotic activity, and may also be involved in the determination  
 CC of bodily characteristics, fertility and behaviour. ORFX proteins,

CC nucleic acids and antibodies may be used in the treatment of cancers,  
CC other proliferative disorders such as psoriasis and benign tumours,  
CC neurological disorders such as epilepsy and Alzheimer's disease,  
CC cardiovascular diseases, immune system disorders, disorders related to  
CC organ transplantation, disorders of tissue growth and regeneration,  
CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol  
CC storage disease, and infectious diseases caused by viral, bacterial,  
CC fungal and other pathogens. ORFX nucleic acids may also be used as a  
CC source of primers and probes, in the detection of ORFX genomic sequences  
CC or transcripts, in the identification and cloning of homologous  
CC sequences, in genetic diagnosis, and in forensic biology. The ORFX  
CC nucleic acids may additionally be used to produce transgenic animals  
CC which may be useful for studying the function and/or activity of ORFX  
CC protein, and in drug screening. The ORFX proteins may also be used as  
CC immunogens to generate specific antibodies, which are useful in the  
CC diagnosis, treatment and monitoring of ORFX-associated diseases.

SO Sequence 132 AA;

Query Match 42.5%; Score 51; DB 23; Length 132;  
Best Local Similarity 64.3%; Pred. No. 4.7;  
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 3 NSGMYEGPLERPRP 16  
Db 24 NSGMYTPTSLCRP 37

RESULT 6

AAU35179 standard; Protein; 341 AA.

AAU35179;

13-FEB-2002 (first entry)

Enterococcus faecalis cellular proliferation protein #466.

Antisense; prokaryotic cellular proliferation protein;

antibiotic; antibacterial; drug design.

Enterococcus faecalis.

WO200170955-A2.

27-SEP-2001.

21-MAR-2001; 2001WO-US09180.

21-MAR-2000; 2000US-191078P.

23-MAY-2000; 2000US-206848P.

26-MAY-2000; 2000US-207727P.

23-OCT-2000; 2000US-242578P.

27-NOV-2000; 2000US-253625P.

22-DEC-2000; 2000US-257931P.

16-FEB-2001; 2001US-269308P.

(ELIT-) ELITRA PHARM INC.

Haselebeck R, Ohlsen KL, Zyckind JW, Wall D, Trawick JD, Carr GJ;

Yamamoto RT, Xu HH;

WPI; 2001-611495/70.

N-PSDB; AAS53038.

New polynucleotides for the identification and development of

antibiotics, comprise sequences of antisense nucleic acids -

Example 3; Seq ID No 10772; 511pp; English.

The invention relates to antisense inhibitors of genes essential to

prokaryotic cellular proliferation, their use in identifying the

genes, their use in the discovery of novel antibiotics, the essential

CC genes themselves and the encoded proteins. The prokaryotes used are  
CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*  
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The  
CC invention is also useful for the identification of potential new targets  
CC for antibiotic development. The antisense nucleic acids can also be used  
CC to identify proteins used in proliferation, to express these proteins,  
CC and to obtain antibodies capable of binding to the expressed proteins.  
CC The proteins can be used to screen compounds in rational drug discovery  
CC programmes. The antisense nucleic acid sequence is also useful to screen  
CC for homologous nucleic acids which are required for cell proliferation in  
CC a wide variety of organisms. The present sequence represents an  
CC essential prokaryotic cellular proliferation protein.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

SO Sequence 341 AA;

Query Match 41.7%; Score 50; DB 22; Length 341;  
Best Local Similarity 40.0%; Pred. No. 20;  
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Oy 2 ONGMYEGPLERPRDLDI 21  
Db 27 KDGQWKGPLSERPQKEV 46

RESULT 7

ABP57025 standard; protein; 348 AA.

ABP57025;

10-APR-2003 (first entry)

Enterococcus faecalis D-Ala-D-Ala ligase enzyme SEQ ID NO:31.

D-Ala-D-Ala ligase; enzyme; bacterial; structure-based drug design;

protein co-ordinate data; D-Ala-D-Ala ligase inhibitor; antibacterial.

Enterococcus faecalis.

WO2003002063-A2.

09-JAN-2003.

28-JUN-2002; 2002WO-US20465.

28-JUN-2001; 2001US-301676P.

(ESSE-) ESSENTIAL THERAPEUTICS INC.

(PLIV) PLIVA DD ZAGREB.

Navia MA, Ala PJ, Griffith JP, Ali JA, Faerman CH, Moe ST;

Magee AS, Connelly PR, Perola E;

WPI; 2003-201458/19.

Evaluating association potential of chemical entity to complex having

binding pocket defined by structural coordinates, by employing

computational unit for entity-pocket fitting operation and analyzing

the results -

Example 8; Fig 10; 115pp; English.

The present invention describes a method (M1) of evaluating the potential

of a chemical entity (CE) to associate with a molecule or molecular

complex comprising a binding pocket (BP) defined by specific structural

coordinates (SC) of D-Ala-D-Ala ligase (LI) E. coli amino acids Lys144,

Glu180, Lys181, Leu183, Glu187, Asp257 and Glu270, by employing a

computational unit to perform a fitting operation between CE and BP

defined by SC and analysing the results of the fitting operation to



01-SEP-2000; 2000US-0229344.  
01-SEP-2000; 2000US-0229345

PR 05-SEP-2000; 2000US-0229509.  
 PR 05-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230437.  
 PR 06-SEP-2000; 2000US-0230438.  
 PR 08-SEP-2000; 2000US-0231242.  
 PR 08-SEP-2000; 2000US-0231243.  
 PR 08-SEP-2000; 2000US-0231244.  
 PR 08-SEP-2000; 2000US-0231413.  
 PR 08-SEP-2000; 2000US-0231414.  
 PR 08-SEP-2000; 2000US-0231415.  
 PR 08-SEP-2000; 2000US-0232080.  
 PR 08-SEP-2000; 2000US-0232081.  
 PR 12-SEP-2000; 2000US-0231968.  
 PR 14-SEP-2000; 2000US-0233297.  
 PR 14-SEP-2000; 2000US-0233398.  
 PR 14-SEP-2000; 2000US-0233399.  
 PR 14-SEP-2000; 2000US-0233400.  
 PR 14-SEP-2000; 2000US-0232401.  
 PR 14-SEP-2000; 2000US-0233063.  
 PR 14-SEP-2000; 2000US-0233064.  
 PR 21-SEP-2000; 2000US-0233065.  
 PR 21-SEP-2000; 2000US-0234223.  
 PR 25-SEP-2000; 2000US-0234274.  
 PR 25-SEP-2000; 2000US-0234997.  
 PR 26-SEP-2000; 2000US-0234998.  
 PR 26-SEP-2000; 2000US-0235464.  
 PR 27-SEP-2000; 2000US-0235464.  
 PR 27-SEP-2000; 2000US-0235834.  
 PR 29-SEP-2000; 2000US-0235836.  
 PR 29-SEP-2000; 2000US-0236327.  
 PR 29-SEP-2000; 2000US-0236357.  
 PR 29-SEP-2000; 2000US-0236368.  
 PR 29-SEP-2000; 2000US-0236369.  
 PR 29-SEP-2000; 2000US-0236370.  
 PR 02-OCT-2000; 2000US-0236802.  
 PR 02-OCT-2000; 2000US-0237037.  
 PR 02-OCT-2000; 2000US-0237038.  
 PR 02-OCT-2000; 2000US-0237039.  
 PR 02-OCT-2000; 2000US-0237040.  
 PR 13-OCT-2000; 2000US-0239935.  
 PR 13-OCT-2000; 2000US-0239937.  
 PR 20-OCT-2000; 2000US-0240960.  
 PR 20-OCT-2000; 2000US-0241221.  
 PR 20-OCT-2000; 2000US-0241785.  
 PR 20-OCT-2000; 2000US-0241786.  
 PR 20-OCT-2000; 2000US-0241787.  
 PR 20-OCT-2000; 2000US-0241808.  
 PR 20-OCT-2000; 2000US-0241809.  
 PR 20-OCT-2000; 2000US-0241826.  
 PR 01-NOV-2000; 2000US-0244617.  
 PR 08-NOV-2000; 2000US-0246474.  
 PR 08-NOV-2000; 2000US-0246475.  
 PR 08-NOV-2000; 2000US-0246476.  
 PR 08-NOV-2000; 2000US-0246477.  
 PR 08-NOV-2000; 2000US-0246478.  
 PR 08-NOV-2000; 2000US-0246523.  
 PR 08-NOV-2000; 2000US-0246524.  
 PR 08-NOV-2000; 2000US-0246525.  
 PR 08-NOV-2000; 2000US-0246526.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246528.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246609.  
 PR 08-NOV-2000; 2000US-0246610.  
 PR 08-NOV-2000; 2000US-0246611.  
 PR 17-NOV-2000; 2000US-0249207.  
 PR 17-NOV-2000; 2000US-0249208.  
 PR 17-NOV-2000; 2000US-0249209.  
 PR 17-NOV-2000; 2000US-0249210.  
 PR 17-NOV-2000; 2000US-0249211.  
 PR 17-NOV-2000; 2000US-0249212.  
 PR 17-NOV-2000; 2000US-0249213.  
 PR 17-NOV-2000; 2000US-0249214.  
 PR 17-NOV-2000; 2000US-0249215.

PR 17-NOV-2000; 2000US-0249216.  
 PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249244.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249246.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249329.  
 PR 17-NOV-2000; 2000US-0249330.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 03-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 11-DEC-2000; 2000US-0251990.  
 PR 05-JAN-2001; 2001US-0259678.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX WPI; 2001-465566/50.  
 DR N-PSDB; AAS41213.  
 DR  
 XX  
 PT Novel polypeptides and polynucleotides useful for diagnosing,  
 PT preventing, treating neutral, immune system, muscular, reproductive,  
 PT pulmonary, cardiovascular, renal, proliferative disorders and cancers  
 PT diseases  
 XX  
 PS Claim 11; SEQ ID No 1339; 1180bp; English.  
 XX  
 CC The present invention relates to the isolation of novel human enzyme  
 CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences  
 CC encoding them. The enzyme polypeptides of the invention may comprise the  
 CC functional classes of oxidoreductases, transferases, hydrolases, lyases,  
 CC isomerases or ligases. The sequences of the invention are useful in the  
 CC diagnosis, treatment, prevention and/or prognosis of a wide range of  
 CC disorders including hyperproliferative disorders (e.g. cancer),  
 CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders  
 CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),  
 CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders  
 CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),  
 CC blood-related disorders (e.g. haemophilia), reproductive disorders  
 CC (e.g. infertility) and infectious disorders (e.g. influenza). The  
 CC polynucleotides of the invention can also be used in gene therapy.  
 CC AAS22915-AAS23814 represent the novel human enzyme polypeptides of the  
 CC invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SO Sequence 172 AA;  
 QY  
 Db 8 EGPLEPPDAID 20  
 56 EPPXLPQGPDAID 68  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Query Match 39.2%; Score 47; DB 22; Length 172;  
 Best Local Similarity 69.2%; Pred. No. 27;  
 RESULT 12  
 ABG24835  
 ID ABG24835 standard; Protein; 564 AA.  
 XX



AC ABG24835;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #24826.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
XX 23-AUG-2000; 2000US-0649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.  
XX N-PSDB; AAS89022.  
DR  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX  
PS Claim 20; SEQ ID No 55194; 103pp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 564 AA;  
XX  
Query Match 39.2%; Score 47; DB 22; Length 564;  
Best Local Similarity 43.8%; Pred. No. 1e+02;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 6 WYEGPLLEPPDALDI 21  
|||:|:|:|:  
Db 163 WYEAIVLAPQPERTLPL 178

RESULT 13  
ABG24833  
ID ABG24833 standard; Protein; 816 AA.  
XX  
AC ABG24833;  
XX

DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #24824.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
XX 23-AUG-2000; 2000US-0649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.  
XX N-PSDB; AAS89020.  
DR  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX  
PS Claim 20; SEQ ID No 55192; 103pp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 816 AA;  
XX  
Query Match 39.2%; Score 47; DB 22; Length 816;  
Best Local Similarity 43.8%; Pred. No. 1.5e+02;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 6 WYEGPLLEPPDALDI 21  
|||:|:|:|:  
Db 97 WYEAIVLAPQPERTLPL 112

RESULT 14  
ABG04046  
ID ABG04046 standard; Protein; 858 AA.  
XX  
AC ABG04046;  
XX  
DT 13-FEB-2002 (first entry)  
XX

XX  
XX

----- PROCEEDING #425619 -----

91 WYEAVVLAPQPETLLPL 106

Job time : 7.83882 sec8

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 11:01:15 ; Search time 4.50366 Seconds  
(without alignments)  
927.994 Million cell updates/sec

Title: US-09-674-752-29

Perfect score: 120  
Sequence: 1 QONGGWYEGPLLEPRPDALDI 21

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgnt2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgnt2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgnt2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgnt2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgnt2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgnt2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
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9: /cgnt2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgnt2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgnt2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgnt2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgnt2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgnt2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgnt2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgnt2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgnt2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgnt2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50.5	42.1	1427	12	US-10-369-493-3841 Sequence 3841, Ap
2	50	41.7	341	9	US-09-815-242-10772 Sequence 10772, A
3	50	41.7	348	15	US-10-186-886-31 Sequence 31, Appl
4	50	41.7	358	15	US-10-186-886-30 Sequence 30, Appl
5	50	41.7	555	15	US-10-156-761-8003 Sequence 8003, Ap
6	47.5	39.6	451	12	US-10-369-493-20793 Sequence 20793, A
7	47	39.2	362	12	US-10-369-493-748 Sequence 748, App
8	46	39.3	4150	11	US-09-808-880-2 Sequence 2, Appl
9	46	38.3	355	12	US-10-203-708-44 Sequence 44, Appl
10	45	37.5	163	15	US-10-156-761-11806 Sequence 11806, A
11	44.5	37.1	76	9	US-09-815-242-11403 Sequence 11403, A
12	44	36.7	358	15	US-10-186-886-29 Sequence 29, Appl
13	44	36.7	492	12	US-10-369-493-22963 Sequence 22963, A
14	44	36.7	583	15	US-10-156-761-12356 Sequence 12356, A
15	43.5	36.2	515	12	US-10-369-493-16825 Sequence 16825, A

	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
US-10-369-493-3841	43	43	43	43	43	43	43	43	43	43	42.5	42.5	42.5	42.5	42.5	42.5	42	42	42	42	42	42	42	42	42	42	42	42	42	42	
Application US/10369493	35.8	35.8	35.8	35.8	35.8	35.8	35.8	35.8	35.8	35.8	35.4	35.4	35.4	35.4	35.4	35.0	35.0	35.0	35.0	35.0	35.0	35.0	35.0	35.0	35.0	35.0	35.0	35.0	35.0	35.0	
Publication No. US20030233675A1	35	35	35	35	35	35	35	35	35	35	34	34	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	
GENERAL INFORMATION:																															
APPLICANT: Cao, Yongwei																															
APPLICANT: Hinkle, Gregory J.																															
APPLICANT: Slater, Steven C.																															
APPLICANT: Goldman, Barry S.																															
APPLICANT: Chen, Xianfeng																															
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF																															
FILE REFERENCE: 38-101520521B																															
CURRENT APPLICATION NUMBER: US/10/369,493																															
CURRENT FILING DATE: 2003-02-28																															
PRIOR FILING DATE: 2002-02-21																															
NUMBER OF SEQ ID NOS: 47374																															
SEQ ID NO 3841																															
LENGTH: 1427																															
TYPE: PRT																															
ORGANISM: Neurospora crassa																															
US-10-369-493-3841																															
Query Match																															
Best Local Similarity																															
Matches																															
10: Conservative																															
1: Mismatches																															
5: Indels																															
1: Gaps																															

RESULT 2  
US-09-815-242-10772  
; Sequence 10772, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:

```

; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: EUTRA.01A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10772
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10772

Query Match
Best Local Similarity 41.7%; Score 50; DB 9; Length 341;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 2 ONGWYEGPLLEPRPDALDI 21
Db 27 KDGQWVGKPLLSERPNKEV 46

RESULT 3
US-10-186-886-31
; Sequence 31, Application US/10186886
; Publication No. US20030119061A1
; GENERAL INFORMATION:
; APPLICANT: Navia, Manuel A.
; APPLICANT: Ala, Paul J.
; APPLICANT: Griffith, James P.
; APPLICANT: All, Janid A.
; APPLICANT: Faerman, Carlos H.
; APPLICANT: Magee, Andrew S.
; APPLICANT: Moe, Scott T.
; APPLICANT: Connolly, Patrick R.
; APPLICANT: Perola, Emanuele
; TITLE OF INVENTION: STRUCTURE-BASED DRUG DESIGN METHODS FOR
; TITLE OF INVENTION: IDENTIFYING D-ALA-D-ALA LIGASE INHIBITORS AS ANTIBACTERIAL
; TITLE OF INVENTION: DRUGS
; FILE REFERENCE: 10283-014001
; CURRENT APPLICATION NUMBER: US/10/186,886
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/301,676
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-186-886-31
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Query Match
Best Local Similarity 41.7%; Score 50; DB 15; Length 348;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 2 ONGWYEGPLLEPRPDALDI 21
Db 42 KDGQWVGKPLLSERPNKEV 61

RESULT 4
US-10-186-886-30
; Sequence 30, Application US/10186886
; Publication No. US20030119061A1
; GENERAL INFORMATION:
; APPLICANT: Navia, Manuel A.
; APPLICANT: Ala, Paul J.
; APPLICANT: Griffith, James P.
; APPLICANT: All, Janid A.
; APPLICANT: Faerman, Carlos H.
; APPLICANT: Magee, Andrew S.
; APPLICANT: Moe, Scott T.
; APPLICANT: Connolly, Patrick R.
; APPLICANT: Perola, Emanuele
; TITLE OF INVENTION: STRUCTURE-BASED DRUG DESIGN METHODS FOR
; TITLE OF INVENTION: IDENTIFYING D-ALA-D-ALA LIGASE INHIBITORS AS ANTIBACTERIAL
; TITLE OF INVENTION: DRUGS
; FILE REFERENCE: 10283-014001
; CURRENT APPLICATION NUMBER: US/10/186,886
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/301,676
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-10-186-886-30

Query Match
Best Local Similarity 41.7%; Score 50; DB 15; Length 358;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 2 ONGWYEGPLLEPRPDALDI 21
Db 42 KDGQWVGKPLLEKPKSKDV 61

RESULT 5
US-10-156-761-8003
; Sequence 8003, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAMIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8003
; LENGTH: 555
; TYPE: PRT
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ORGANISM: Streptomyces avermitilis  
US-10-156-761-8003

Query Match 41.7%; Score 50; DB 15; Length 555;  
Best Local Similarity 58.3%; Pred. No. 55;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QONGWYEGPPL 12  
DB 434 QERGWHRGFVL 445

RESULT 6  
US-10-369-493-20793

Sequence 20793, Application US/10369493  
Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

PRIOR FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 20793

LENGTH: 451

TYPE: PRT

ORGANISM: Rhodospseudomonas palustris

US-10-369-493-20793

Query Match 39.6%; Score 47.5; DB 12; Length 451;  
Best Local Similarity 40.0%; Pred. No. 1e+02;  
Matches 10; Conservative 3; Mismatches 5; Indels 7; Gaps 1;

QY 4 GGMWEG-----PLLEPPDALDI 21  
DB 74 GGYEGFANSALWPLHSRDLIRV 98

RESULT 7  
US-10-369-493-748

Sequence 748, Application US/10369493  
Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

PRIOR FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 748

LENGTH: 362

TYPE: PRT

ORGANISM: Escherichia coli

US-10-369-493-748

Query Match 39.2%; Score 47; DB 12; Length 362;  
Best Local Similarity 43.8%; Pred. No. 98;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 WYEGPPLPPDALDI 21  
DB 178 WYEAIVLAPCPETLPL 193

RESULT 8  
US-09-808-880-2

Sequence 2, Application US/09808880  
Publication No. US20030027287A1

GENERAL INFORMATION:

APPLICANT: Betlach, Mary C.

APPLICANT: Shah, Sanjay Krishnakant

APPLICANT: McDaniel, Robert

APPLICANT: Tang, Li

TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE

FILE REFERENCE: 30062-20029.00

CURRENT APPLICATION NUMBER: US/09/808,880

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: US/09/428,517

PRIOR FILING DATE: 1999-10-28

PRIOR APPLICATION NUMBER: 60/120,254

PRIOR FILING DATE: 1999-02-16

PRIOR APPLICATION NUMBER: 60/106,100

PRIOR FILING DATE: 1998-10-29

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 4150

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Recombinant

US-09-808-880-2

Query Match 39.2%; Score 47; DB 11; Length 4150;  
Best Local Similarity 56.2%; Pred. No. 1.1e+03;  
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 QNGWYEGPPLPPRD 17  
DB 2583 QNRGMDLGRLYDPDPD 2598

RESULT 9  
US-10-203-708-44

Sequence 44, Application US/10203708  
Publication No. US20030149238A1

GENERAL INFORMATION:

APPLICANT: SMITHKLINE BEECHAM CORPORATION

APPLICANT: SMITHKLINE BEECHAM P.L.C.

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GFS0013

CURRENT APPLICATION NUMBER: US/10/203,708

PRIOR FILING DATE: 2002-08-13

PRIOR APPLICATION NUMBER: PCT/US01/04703

PRIOR FILING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: 60/182,172

PRIOR FILING DATE: 2000-02-14

PRIOR APPLICATION NUMBER: 60/186,084

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 46

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 44

LENGTH: 355

TYPE: PRT

ORGANISM: Homo sapiens

US-10-203-708-44

Query Match 38.3%; Score 46; DB 12; Length 355;  
Best Local Similarity 45.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 30, 2003, 10:47:45 ; Search time 2.13241 Seconds  
(without alignments)

416.677 Million cell updates/sec

Title: US-09-674-752-29

Perfect score: 120

Sequence: 1 QQNGWIEGPLEPPALDI 21

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep: \*  
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6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep: \*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	41.7	348	1	US-08-454-196-8 Sequence 8, Appli
2	50	41.7	348	1	US-08-454-196-17 Sequence 17, Appli
3	50	41.7	348	3	US-09-064-033-8 Sequence 8, Appli
4	50	41.7	348	3	US-09-064-033-17 Sequence 17, Appli
5	50	41.7	348	4	US-09-291-046-8 Sequence 8, Appli
6	50	41.7	348	4	US-09-291-046-17 Sequence 17, Appli
7	50	41.7	370	4	US-09-107-532A-5920 Sequence 5920, Ap
8	48	40.0	993	3	US-09-060-410-4 Sequence 4, Appli
9	48	40.0	993	4	US-09-723-458-4 Sequence 4, Appli
10	47	39.2	4150	3	US-09-428-517-2 Sequence 2, Appli
11	46	38.3	605	4	US-09-252-991A-11355 Sequence 11355, A
12	44.5	37.1	76	4	US-09-732-210-1438 Sequence 1438, Ap
13	44	36.7	396	4	US-09-252-991A-20263 Sequence 20263, A
14	43	35.8	35	4	US-09-227-357-409 Sequence 409, App
15	43	35.8	425	4	US-08-556-422A-7 Sequence 7, Appli
16	43	35.8	862	4	US-08-556-422A-2 Sequence 2, Appli
17	42.5	35.4	316	4	US-09-252-991A-22518 Sequence 22518, A
18	42.5	35.4	540	3	US-08-688-988-43 Sequence 43, Appli
19	42.5	35.4	791	4	US-09-252-991A-23201 Sequence 23201, A
20	42.5	35.4	1290	1	US-08-138-641-2 Sequence 2, Appli
21	42.5	35.4	1290	1	US-08-138-641-2 Sequence 2, Appli
22	42	35.0	153	4	US-09-252-991A-30437 Sequence 16, Appli
23	42	35.0	172	1	US-08-471-058-16 Sequence 3, Appli
24	42	35.0	172	1	US-08-471-058-16 Sequence 3, Appli
25	42	35.0	172	3	US-08-471-057-16 Sequence 3, Appli
26	42	35.0	172	3	US-09-113-789-3 Sequence 3, Appli
27	42	35.0	172	4	US-08-470-865-16 Sequence 16, Appli

28	42	35.0	432	4	US-09-252-991A-21794 Sequence 21794, A
29	42	35.0	433	1	US-07-661-610C-2 Sequence 2, Appli
30	42	35.0	519	3	US-09-172-841-55 Sequence 55, Appli
31	42	35.0	519	4	US-08-951-621-55 Sequence 55, Appli
32	42	35.0	888	2	US-08-861-464-6 Sequence 6, Appli
33	42	35.0	888	2	US-08-396-001-6 Sequence 6, Appli
34	42	35.0	888	3	US-09-323-433A-6 Sequence 6, Appli
35	42	35.0	2710	2	US-08-568-459A-12 Sequence 12, Appli
36	42	35.0	2710	2	US-08-487-826B-12 Sequence 12, Appli
37	42	35.0	2710	4	US-09-210-288-12 Sequence 12, Appli
38	42	35.0	3060	2	US-08-487-826B-14 Sequence 14, Appli
39	42	35.0	34.2	1	US-08-248-819A-50 Sequence 50, Appli
40	41	34.2	16	1	US-08-798-897-42 Sequence 42, Appli
41	41	34.2	16	2	US-08-337-646A-68 Sequence 68, Appli
42	41	34.2	16	3	US-08-978-523-42 Sequence 42, Appli
43	41	34.2	16	3	US-08-927-326-68 Sequence 68, Appli
44	41	34.2	17	1	US-08-333-565-14 Sequence 14, Appli
45	41	34.2	17	2	US-08-661-479-14 Sequence 14, Appli

## ALIGNMENTS

RESULT 1  
US-08-454-196-8  
Sequence 8, Application US/08454196  
Patent No. 5770361  
GENERAL INFORMATION:  
APPLICANT: ARTHUR, MICHEL  
APPLICANT: DUTKA-MALEN, SYLVIE  
APPLICANT: EVERS, STEFAN  
APPLICANT: COURVALIN, PATRICE  
TITLE OF INVENTION: PROTEIN CONFERRING AN INDUCIBLE  
TITLE OF INVENTION: RESISTANCE TO GLYCOPOLYMERES, PARTICULARLY IN GRAM-POSITIVE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P. C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/454,196  
FILING DATE: 07-SEP-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 92/15671  
FILING DATE: 18-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 93/08356  
FILING DATE: 07-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 660-101-O PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 348 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-454-196-8

Query Match 41.7%; Score 50; DB 1; Length 348;  
Best Local Similarity 40.0%; Pred. No. 9.2;  
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGWYEGPLLEPPDLDI 21  
Db 42 KDGQWVGPLLSERPNKEV 61

## RESULT 2

US-08-454-196-17  
; Sequence 17, Application US/08454196  
; Patent No. 570361  
; GENERAL INFORMATION:  
; APPLICANT: ARTHUR, MICHEL  
; APPLICANT: DUTKA-MALEN, SYLVIE  
; APPLICANT: EVERS, STEFAN  
; TITLE OF INVENTION: PROTEIN CONFERRING AN INDUCIBLE  
; TITLE OF INVENTION: RESISTANCE TO GLYCOPOLYMERES, PARTICULARLY IN GRAM-POSITIVE  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/454,196  
; FILING DATE: 07-SEP-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 92/15671  
; FILING DATE: 18-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 93/08356  
; FILING DATE: 07-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 660-101-O PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 348 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-454-196-17

Query Match 41.7%; Score 50; DB 1; Length 348;  
Best Local Similarity 40.0%; Pred. No. 9.2;  
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGWYEGPLLEPPDLDI 21  
Db 42 KDGQWVGPLLSERPNKEV 61

RESULT 3  
US-09-064-033-8

; Sequence 8, Application US/09064033  
; Patent No. 6087106  
; GENERAL INFORMATION:  
; APPLICANT: ARTHUR, MICHEL  
; APPLICANT: DUTKA-MALEN, SYLVIE  
; APPLICANT: EVERS, STEFAN  
; TITLE OF INVENTION: PROTEIN CONFERRING AN INDUCIBLE  
; TITLE OF INVENTION: RESISTANCE TO GLYCOPOLYMERES, PARTICULARLY IN GRAM-POSITIVE  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/064,033  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/454,196  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 93/08356  
; FILING DATE: 07-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 660-101-O PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 348 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-064-033-8

Query Match 41.7%; Score 50; DB 3; Length 348;  
Best Local Similarity 40.0%; Pred. No. 9.2;  
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGWYEGPLLEPPDLDI 21  
Db 42 KDGQWVGPLLSERPNKEV 61

## RESULT 4

US-09-064-033-17  
; Sequence 17, Application US/09064033  
; Patent No. 6087106  
; GENERAL INFORMATION:  
; APPLICANT: ARTHUR, MICHEL  
; APPLICANT: DUTKA-MALEN, SYLVIE  
; APPLICANT: EVERS, STEFAN  
; TITLE OF INVENTION: PROTEIN CONFERRING AN INDUCIBLE  
; TITLE OF INVENTION: RESISTANCE TO GLYCOPOLYMERES, PARTICULARLY IN GRAM-POSITIVE  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/064,033  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/454,196  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 93/08356  
; FILING DATE: 07-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 660-101-O PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 348 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-064-033-17

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/064,033  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/454,196  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 93/08356  
FILING DATE: 07-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 660-101-O PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 348 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-064-033-17

Query Match 41.7%; Score 50; DB 3; Length 348;  
Best Local Similarity 40.0%; Pred. No. 9.2;  
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGGWEGPLLEPRPDALDI 21  
DB 42 KDQGWKGPLLSERPNKEV 61

RESULT 5  
US-09-291-046-8  
Sequence 8, Application US/09291046  
Patent No. 6569622  
GENERAL INFORMATION:  
APPLICANT: ARTHUR, MICHEL  
DUTKA-MALEN, SYLVIE  
EVERS, STEFAN  
COURVALIN, PATRICE  
TITLE OF INVENTION: PROTEIN CONFERRING AN INDUCIBLE  
RESISTANCE TO GLYCOPOLYMERIDES, PARTICULARLY IN GRAM-POSITIVE  
BACTERIA  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/291,046  
FILING DATE: 14-Apr-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/454,196  
FILING DATE: <Unknown>  
APPLICATION NUMBER: FR 93/08356  
FILING DATE: 07-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 660-101-O PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 348 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-291-046-8

Query Match 41.7%; Score 50; DB 4; Length 348;  
Best Local Similarity 40.0%; Pred. No. 9.2;  
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGGWEGPLLEPRPDALDI 21  
DB 42 KDQGWKGPLLSERPNKEV 61

RESULT 6  
US-09-291-046-17  
Sequence 17, Application US/09291046  
Patent No. 6569622  
GENERAL INFORMATION:  
APPLICANT: ARTHUR, MICHEL  
DUTKA-MALEN, SYLVIE  
EVERS, STEFAN  
COURVALIN, PATRICE  
TITLE OF INVENTION: PROTEIN CONFERRING AN INDUCIBLE  
RESISTANCE TO GLYCOPOLYMERIDES, PARTICULARLY IN GRAM-POSITIVE  
BACTERIA  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/291,046  
FILING DATE: 14-Apr-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/454,196  
FILING DATE: <Unknown>  
APPLICATION NUMBER: FR 93/08356  
FILING DATE: 07-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 660-101-O PCT



TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 348 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-291-046-17

Query Match 41.7%; Score 50; DB 4; Length 348;  
Best Local Similarity 40.0%; Pred. No. 9.2;  
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGWYEGPLLEPPDALDI 21  
DB 42 KDGQWVGPLLEPPKPKV 61

RESULT 7  
US-09-107-532A-5920  
Sequence 5920, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107.532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-8277  
TELEFAX: (781)893-5007  
INFORMATION FOR SEQ ID NO: 5920:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 370 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...370  
SEQUENCE DESCRIPTION: SEQ ID NO: 5920:  
US-09-107-532A-5920

Query Match 41.7%; Score 50; DB 4; Length 370;

Best Local Similarity 40.0%; Pred. No. 9.8;  
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGWYEGPLLEPPDALDI 21  
DB 54 KEGQWVGPLLEPPKPKV 73

RESULT 8  
US-09-060-410-4  
Sequence 4, Application US/09060410  
Patent No. 6165461  
GENERAL INFORMATION:  
APPLICANT: Cobb, Melanie  
APPLICANT: Hutchinson, Michele  
APPLICANT: Chen, Zhu  
APPLICANT: Berman, Kevin  
TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/060,410  
FILING DATE: 14-Apr-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 860098.421  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 993 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-060-410-4

Query Match 40.0%; Score 48; DB 3; Length 993;  
Best Local Similarity 53.8%; Pred. No. 57;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 GWIEGPLEPPD 17  
DB 888 GWVGPLVTPVPE 900

RESULT 9  
US-09-723-458-4  
Sequence 4, Application US/09723458  
Patent No. 6586242  
GENERAL INFORMATION:  
APPLICANT: Cobb, Melanie  
APPLICANT: Hutchinson, Michele  
APPLICANT: Chen, Zhu  
APPLICANT: Berman, Kevin  
TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:

```

; ADDRESS: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/723,458
; FILING DATE: 27-NOV-98
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,410
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MAKI, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-723-458-4

Query Match      40.0%; Score 48; DB 4; Length 993;
Best Local Similarity 53.8%; Pred. No. 57;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      5 GWYEGPLLEPRPD 17
Db      888 GWYGFVLTVPVE 900

RESULT 10
US-09-428-517-2
; Sequence 2, Application US/09428517
; Patent No. 6251636
; GENERAL INFORMATION:
; APPLICANT: Belilach, Mary C.
; APPLICANT: Shah, Sanjay Krishnakant
; APPLICANT: McDaniel, Robert
; APPLICANT: Tang, Li
; TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 30062-20029.00
; CURRENT APPLICATION NUMBER: US/09/428,517
; CURRENT FILING DATE: 1999-10-28
; EARLIER APPLICATION NUMBER: 60/120,254
; EARLIER FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/106,100
; EARLIER FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4150
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: Oleandolide PKS
US-09-428-517-2

Query Match      39.2%; Score 47; DB 3; Length 4150;
Best Local Similarity 56.2%; Pred. No. 3.9e+02;
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Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      2 QNCGWYEGPLLEPRPD 17
Db      2583 QNRGMDLGRLYDPD 2598

RESULT 11
US-09-252-991A-31355
; Sequence 31355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31355
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31355

Query Match      38.3%; Score 46; DB 4; Length 605;
Best Local Similarity 52.6%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      1 QNCGWYEGPLLEPRPDAL 19
Db      340 QNVGAWYEIRPDPDPLDKL 358

RESULT 12
US-09-732-210-1438
; Sequence 1438, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mitnick, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1438
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-732-210-1438

Query Match      37.1%; Score 44.5; DB 4; Length 76;
Best Local Similarity 36.0%; Pred. No. 11;
Matches 9; Conservative 5; Mismatches 6; Indels 5; Gaps 1;

QY      1 QNCGW-----YEGPLLEPRPDALD 20
Db      27 RRDGMISIGYNNPLSEPKDIDK 51

RESULT 13
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US-09-252-991A-20263
; Sequence 20263, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20263
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20263

Query Match
Best Local Similarity 36.7%; Score 44; DB 4; Length 396;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GNGEPLLEPPD 17
Db 96 GCEHPLSPRE 108

RESULT 14
US-09-227-357-409
; Sequence 409, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
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EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 409
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-409

Query Match
Best Local Similarity 35.8%; Score 43; DB 4; Length 35;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QNGEPLLEPPD 16
Db 20 BGGGWPGRLEPLD 34

RESULT 15
US-08-556-422A-7
; Sequence 7, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: Hall, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSIOTIS, Vasileiki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DPN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; PRIOR FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-556-422A-7

Query Match 35.8%; Score 43; DB 4; Length 425;
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Best Local Similarity 45.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 3; Mismatches 6; Indels 2; Gaps 1;  
Oy 1 QONGGM--YEGPILBPPDA 18  
| : | | | : | | |  
Db 180 QSHTKWRYNGFVFKRPDA 199

Search completed: December 30, 2003, 11:05:33  
Job time : 3.21575 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 ; Search time 2.20471 Seconds  
(without alignments)  
1003.251 Million cell updates/sec

Title: US-09-674-752-30

Sequence: 1 DGGGAGVEDVWSEGEPEYAMDV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR 76: \*  
2: PIR1: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	56.5	42.2	131	2	S26792
3	53	39.6	1264	2	A36858
4	53	39.6	1896	2	B72175
5	53	39.6	1897	2	T28621
6	50.5	37.7	433	2	S26646
7	50	37.3	292	2	T26908
8	49.5	36.9	220	2	E64169
9	49	36.6	509	2	H87389
10	48.5	36.2	166	2	H96940
11	48	35.8	469	2	B70607
12	47.5	35.4	308	2	B47369
13	47.5	35.4	321	2	A47369
14	47.5	35.4	345	1	B41732
15	47.5	35.4	558	2	T40651
16	47	35.1	383	2	C96581
17	47	35.1	812	1	MMECOF
18	47	35.1	860	1	F86349
19	46.5	34.7	126	2	S44107
20	46.5	34.7	431	1	B69092
21	46.5	34.7	1307	2	T35944
22	46	34.3	136	2	A49047
23	46	34.3	136	2	T05080
24	46	34.3	344	2	AG3020
25	46	34.3	345	2	S75745
26	46	34.3	368	2	B98264
27	46	34.3	482	2	G71603
28	46	34.3	528	2	F64580
29	46	34.3	627	2	G88533

30	46	34.3	741	2	I48694	probable transcrip
31	46	34.3	826	1	T02753	S-receptor kinase
32	46	34.3	894	2	C86756	prophage p12 prote
33	45	33.6	172	1	MMVZTH	BamHI-ORF13 protei
34	45	33.6	276	2	G83304	chloroperoxidase P
35	45	33.6	276	2	UC4161	probable chloride
36	45	33.6	419	2	S54100	deacetylcephalosp
37	45	33.6	449	2	AF0820	exodeoxyribonuclea
38	45	33.6	453	2	F71673	exodeoxyribonuclea
39	45	33.6	456	1	NCRC7	exonuclease VII la
40	45	33.6	456	2	C91050	exonuclease VII, 1
41	45	33.6	456	2	H85894	hypothetical prote
42	45	33.6	457	2	B97828	exodeoxyribonuclea
43	45	33.6	459	2	AH0349	anexin VII - mouse
44	45	33.6	463	2	S29170	outer membrane pro
45	45	33.6	528	2	F71931	

#### ALIGNMENTS

##### RESULT 1

PH0954

Ig heavy chain V region (G6+ CUL-HEN) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

C:Accession: PH0954

R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A>Title: Evidence for somatic selection of natural autoantibodies.

A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0954

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-132 <MAR>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-50/Region: framework 2

F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3

F:99-120/Region: complementarity-determining 3

Query Match Best Local Similarity 43.3% Score 58; DB 2; Length 132;

Matches 11; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

Db 8 EDVWSGEPE--YYAMDV 23

104 DDFWSGYNNYYTGMDV 121

##### RESULT 2

S26792

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000

C:Accession: S26792

R:Morfari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.

Eur. J. Immunol. 22, 241-245, 1992

A>Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fan

A:Reference number: S26786; MUID:9211632; PMID:1730251

A:Accession: S26792

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-131 <MOR>

A:Cross-references: EMBL:X61012; NID:932804; PIDN:CAA4346.1; PID:g1335131

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 42.2%; Score 56.5; DB 2; Length 131;  
 Best Local Similarity 56.5%; Pred. No. 0.92;  
 Matches 13; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

OY 1 DGGGAYEDVMSGEYPEYAMDV 23  
 DB 99 DSRGYSYDFWMSG-YFYYYMDV 120

## RESULT 3

A36858  
 G2R protein - variola virus (strain India-1967)

C/Species: variola virus  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 23-Mar-2001

A/Accession: A36858; S46886

R:Binov, V.M.  
 submitted to GenBank, November 1992

A/Reference number: A36859

A/Accession: A36858

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1264 <BLI>

A/Cross-references: GB:X69198

R:Kolykhalov, A.A.; Binov, V.M.; Gylorov, V.V.; Pozdnyakov, S.G.; Chiznikov, V.E.; Frolov, V.V.;

submitted to the EMBL Data Library, April 1992

A/Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P

A/Reference number: S46868

A/Accession: S46866

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1264 <KOL>

A/Cross-references: EMBL:X67117; NID:G516428; PIDN:CAA47538.1; PID:G516447

A/Experimental source: strain India-1967, isolate Ind3

C/Superfamily: variola virus protein G2R

## Query Match

Best Local Similarity 39.6%; Score 53; DB 2; Length 1264;

Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 6 AYEDVMSGEYPEY 18

DB 927 SYEDIKSDMPDY 939

## RESULT 4

B72175

D1SR protein - variola minor virus (strain Garcia-1966)

C/Species: variola minor virus

C/Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 24-Nov-1999

A/Accession: B72175

R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safonov, P.F.; Maesung, R.F.; Lopat

submitted to GenBank, March 1998

A/Description: Analysis of the complete coding sequence of DNA of alacstrim variola minor

A/Reference number: A72150

A/Accession: B72175

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1896 <SHC>

A/Cross-references: GB:Y16780; NID:G5830555; PIDN:CA854796.1; PID:el542752; PID:G5830757

A/Experimental source: strain Garcia-1966

C/Genetics:

A/Gene: D1SR

## Query Match

Best Local Similarity 39.6%; Score 53; DB 2; Length 1896;

Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 6 AYEDVMSGEYPEY 18

DB 1559 SYEDIKSDMPDY 1571

## RESULT 5

T28621

hypothetical protein B22R - variola major virus

C/Species: variola major virus

C/Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000

A/Accession: T28621

R:Maesung, R.F.; Esposto, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aub

Nature 366, 748-751, 1993

A/Title: Potential virulence determinants in terminal regions of variola smallpox viru

A/Reference number: Z20489; PMID:94088747; PMID:8264798

A/Accession: T28621

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1897 <MAS>

A/Cross-references: EMBL:L22579; NID:G623595; PIDN:AAA60931.1; PID:G439100

A/Experimental source: strain Bangladesh 1975

## Query Match

Best Local Similarity 39.6%; Score 53; DB 2; Length 1897;

Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 6 AYEDVMSGEYPEY 18

DB 1560 SYEDIKSDMPDY 1572

## RESULT 6

S26646

transcription factor IIE - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jul-2000

A/Accession: S26646

R:Ohkuma, Y.; Hashimoto, S.; Roeder, R.G.; Horikoshi, M.

Nucleic Acids Res. 20, 5838, 1992

A/Title: Identification of two large subdomains in TFIIE-alpha on the basis of homology

A/Reference number: S26646; MUID:93087200; PMID:1454543

A/Accession: S26646

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-433 <OHK>

A/Cross-references: EMBL:Z14131; NID:G65130; PIDN:CAA78505.1; PID:G65131

## Query Match

Best Local Similarity 37.7%; Score 50.5; DB 2; Length 433;

Matches 10; Conservative 3; Mismatches 9; Indels 3; Gaps 1;

OY 2 GGGAYEDVMSGEYPEY---YAMDV 23

DB 227 GASGTOKEWSSKSPSYEDLYTQDV 251

## RESULT 7

T26908

hypothetical protein Y45F10A.1 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000

A/Accession: T26908

R:McMurray, A.

submitted to the EMBL Data Library, January 1998

A/Reference number: Z20285

A/Accession: T26908

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-292 <WIL>

A/Cross-references: EMBL:AL021488; PIDN:CAA16365.1; GSPDB:GN00022; GSP:Y45F10A.1

A/Experimental source: clone Y45F10A

C/Genetics:

A/Gene: GSP:Y45F10A.1

A/Map position: 4

A/Intons: 228/2; 261/3

C/Superfamily: Caenorhabditis elegans hypothetical protein Y45F10A.1

## Query Match

Best Local Similarity 37.3%; Score 50; DB 2; Length 292;

```
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 127
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-125
```

```
Query Match      73.8%; Score 524.5; DB 12; Length 127;
Best Local Similarity 78.9%; Pred. NO. 1.4e-42;
Matches 105; Conservative 6; Mismatches 15; Indels 7; Gaps 3;
```

```
Qy 1 QVQLQSATEVKKPKGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGMSISGNTDY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGAEVKKKQASVKSCKASGYTFSTYGISWVRQAPGQGLEWMGMSISGNTNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 AOKFQGRVTMTTDSRRTAYMELSLRSDDTAVYYCARDGGGAYEDVWSGEY-PEYYAM 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKLQGRVTMTTDSRTAYMELSLRSDDTAVYYCARD-----HYVD--SSDYLYYYGCL 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 120 DVMGGQTTVTYSS 132
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 DVMGGQTTVTYSS 127
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 6
US-09-880-748-1674
; Sequence 1674, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1674
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1674
```

```
Query Match      73.7%; Score 524; DB 11; Length 252;
Best Local Similarity 78.0%; Pred. NO. 3.2e-42;
Matches 103; Conservative 7; Mismatches 16; Indels 6; Gaps 2;
```

```
Qy 1 QVQLQSATEVKKPKGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGMSISGNTDY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGAEVKKKQASVKSCKASGYTFSTYGISWVRQAPGQGLEWMGMSISGNTDNTY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 AOKFQGRVTMTTDSRRTAYMELSLRSDDTAVYYCARDGGGAYEDVWSGEYPEYYAM 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKLQGRVTMTTDSRTAYMELSLRSDDTAVYYCAR-----GAYDYLITGYYP--YGM 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 VMGQGTIVTVSS 132
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 VMGQGTIVTVSS 126
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 7

```
US-09-880-748-1921
; Sequence 1921, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1921
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1921
```

```
Query Match      73.6%; Score 523; DB 11; Length 251;
Best Local Similarity 74.6%; Pred. NO. 4e-42;
Matches 103; Conservative 5; Mismatches 14; Indels 16; Gaps 2;
```

```
Qy 1 QVQLQSATEVKKPKGASMKVSCMASGYPFTSYDISWVRQAPGQGLEWMGMSISGNTDY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGAEVKKKQASVKSCKASGYTFSTYGISWVRQAPGQGLEWMGMSISGNTNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 AOKFQGRVTMTTDSRRTAYMELSLRSDDTAVYYCAR-----DGGGAYEDVWSGEYP 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKLQGRVTMTTDSRTAYMELSLRSDDTAVYYCARVTVSSSGGY----- 111
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 115 BYVAMDVYMGQGTIVTVSS 132
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 112 -YGMADVYMGQGTIVTVSS 128
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 8
US-09-880-748-973
; Sequence 973, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 973
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-973
```

```
Query Match      73.3%; Score 521.5; DB 11; Length 259;
```

Best Local Similarity 74.5%; Pred. No. 5.8e-42;  
Matches 102; Conservative 8; Mismatches 18; Indels 9; Gaps 2;

Qy 1 QVOLLQSAATEVKKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEMMGMIISYSGNTDY 60  
Db 1 QVOLLQSGAEVKKKPGASVKSCKASGYFTSYGISWVRQAPGQGLEMMGMIISAYNGNTY 60  
Qy 61 AOKFGQAVTMTTDSRTTAYMELRLSRSDTAAYVYCARDDGGGAYEDVWSGEYPEYVYAM 117  
Db 61 AOKLQGRVTMTTDTSTSTAYMELRLSRSDTAAYVYCARDDGGGAYEDVWSGEYPEYVYAM 116  
Cy 118 --AMDVWGQGTMTVSS 132  
Db 117 SDAFDIWGQGTMTVSS 133

## RESULT 9

US-09-880-748-1777  
Sequence 1777, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1777  
LENGTH: 253  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-1777

Query Match  
Best Local Similarity 73.1%; Score 520; DB 11; Length 253;  
Matches 100; Conservative 12; Mismatches 18; Indels 2; Gaps 2;

Qy 1 QVOLLQSAATEVKKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEMMGMIISYSGNTDY 60  
Db 1 EVOLLQSGAEVKKKPGASVKSCKASGYFTSYGISWVRQAPGQGLEMMGMIISAYNGNTY 60  
Qy 61 AOKFGQAVTMTTDSRTTAYMELRLSRSDTAAYVYCARDDGGGAYEDVWSGEYPEYVYAM 120  
Db 61 AOELOGRVMTTDTSTSTAYMELRLSRSDTAAYVYCAR--GDFGDI--DILGYYFPVYVYAMD 118  
Qy 121 VMGQGTMTVSS 132  
Db 119 VMGQGTMTVSS 130

## RESULT 10

US-09-880-748-1778  
Sequence 1778, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1778  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-1778

Query Match  
Best Local Similarity 72.4%; Score 514.5; DB 11; Length 248;  
Matches 100; Conservative 9; Mismatches 16; Indels 7; Gaps 2;

Qy 1 QVOLLQSAATEVKKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEMMGMIISYSGNTDY 60  
Db 1 QVOLLQSGAEVKKKPGASVKSCKASGYFTSYGISWVRQAPGQGLEMMGMIISAYNGNTY 60  
Qy 61 AOKFGQAVTMTTDSRTTAYMELRLSRSDTAAYVYCARDDGGGAYEDVWSGEYPEYVYAM 120  
Db 61 AOKLQGRVTMTTDTSTSTAYMELRLSRSDTAAYVYCAR-----SYDILTYFP--FGMD 113  
Qy 121 VMGQGTMTVSS 132  
Db 114 VMGQGTMTVSS 125

## RESULT 11

US-09-880-748-1610  
Sequence 1610, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1610  
LENGTH: 257  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-1610

Query Match  
Best Local Similarity 72.4%; Score 514.5; DB 11; Length 257;  
Matches 104; Conservative 6; Mismatches 18; Indels 7; Gaps 3;

Qy 1 QVOLLQSAATEVKKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEMMGMIISYSGNTDY 60  
Db 1 QVOLLQSGAEVKKKPGASVKSCKASGYFTSYGISWVRQAPGQGLEMMGMIISAYNGNTY 60  
Qy 61 AOKFGQAVTMTTDSRTTAYMELRLSRSDTAAYVYCARDDGGGAYEDVWSGEYPEYVYAM 117  
Db 61 AOELOGRVMTTDTSTSTAYMELRLSRSDTAAYVYCARDTLTG---YDILTYFP--YPPYYV 116



QY 118 AMDWGGTIVTSS 132  
 |||||  
 Db 117 DMDVWGRTLVTVSS 131

## RESULT 12

US-09-880-748-1425  
 ; Sequence 1425, Application US/09880748  
 ; Publication No. US20030059937A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
 ; FILE REFERENCE: PFS23  
 ; CURRENT APPLICATION NUMBER: US/09/880,748  
 ; PRIOR FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: 60/212,210  
 ; PRIOR FILING DATE: 2000-06-15  
 ; PRIOR APPLICATION NUMBER: 60/240,816  
 ; PRIOR FILING DATE: 2000-10-17  
 ; PRIOR APPLICATION NUMBER: 60/276,248  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/277,379  
 ; PRIOR FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/293,499  
 ; PRIOR FILING DATE: 2001-05-25  
 ; NUMBER OF SEQ ID NOS: 3239  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1425  
 ; LENGTH: 249  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-880-748-1425

Query Match Best Local Similarity 72.2%; Score 513; DB 11; Length 249;  
 Matches 103; Conservative 8; Mismatches 13; Indels 10; Gaps 4;

QY 1 QVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVRQAPQGGLMMGMISYSGNTDY 60  
 |||||  
 Db 1 QVQLVSGAEVKKPKGASVAVSCASGYFTSYGISWVRQAPQGGLMMGMISAVNGNTNY 60  
 QY 61 AOKFGQRYMTTDTSRRTAYMELSLRSDDTAVYYCARDGGAEDVWVGSEYEPY--A 118  
 |||||  
 Db 61 AOKLQGRVMTTDTSTAYMELSLRSDDTAVYYCAR---GGNY-DLTG---YIIGA 112  
 QY 119 MDWGGTIVTSS 132  
 |||||  
 Db 113 PDWGGTIVTVSS 126

## RESULT 13

US-09-880-748-1576  
 ; Sequence 1576, Application US/09880748  
 ; Publication No. US20030059937A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
 ; FILE REFERENCE: PFS23  
 ; CURRENT APPLICATION NUMBER: US/09/880,748  
 ; PRIOR FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: 60/212,210  
 ; PRIOR FILING DATE: 2000-06-15  
 ; PRIOR APPLICATION NUMBER: 60/240,816  
 ; PRIOR FILING DATE: 2000-10-17  
 ; PRIOR APPLICATION NUMBER: 60/276,248  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/277,379  
 ; PRIOR FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/293,499  
 ; PRIOR FILING DATE: 2001-05-25  
 ; NUMBER OF SEQ ID NOS: 3239  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1576

; LENGTH: 257  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-880-748-1576

Query Match Best Local Similarity 72.1%; Score 512.5; DB 11; Length 257;  
 Matches 101; Conservative 8; Mismatches 21; Indels 3; Gaps 2;

QY 1 QVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVRQAPQGGLMMGMISYSGNTDY 60  
 |||||  
 Db 1 QVQLVSGAEVKKPKGASVAVSCASGYFTSYGISWVRQAPQGGLMMGMISAVNGNTNY 60  
 QY 61 AOKFGQRYMTTDTSRRTAYMELSLRSDDTAVYYCARDGGAEDVWVGSEYEPY--A 119  
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 Db 61 POKLQGRVMTTDTSTAYMELSLRSDDTAVYYCAR--GRSLYDILTGIVYARDYGM 118  
 QY 120 DWGGTIVTVSS 132  
 |||||  
 Db 119 DMDGRTIVTVSS 131

## RESULT 14

US-09-880-748-1562  
 ; Sequence 1562, Application US/09880748  
 ; Publication No. US20030059937A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
 ; FILE REFERENCE: PFS23  
 ; CURRENT APPLICATION NUMBER: US/09/880,748  
 ; PRIOR FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: 60/212,210  
 ; PRIOR FILING DATE: 2000-06-15  
 ; PRIOR APPLICATION NUMBER: 60/240,816  
 ; PRIOR FILING DATE: 2000-10-17  
 ; PRIOR APPLICATION NUMBER: 60/276,248  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/277,379  
 ; PRIOR FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/293,499  
 ; PRIOR FILING DATE: 2001-05-25  
 ; NUMBER OF SEQ ID NOS: 3239  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1562  
 ; LENGTH: 251  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-880-748-1562

Query Match Best Local Similarity 71.8%; Score 510.5; DB 11; Length 251;  
 Matches 101; Conservative 7; Mismatches 17; Indels 7; Gaps 2;

QY 1 QVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVRQAPQGGLMMGMISYSGNTDY 60  
 |||||  
 Db 1 QVQLVSGAEVKKPKGASVAVSCASGYFTSYGISWVRQAPQGGLMMGMISAVNGNTNY 60  
 QY 61 AOKFGQRYMTTDTSRRTAYMELSLRSDDTAVYYCARDGGAEDVWVGSEYEPY--A 120  
 |||||  
 Db 61 AOKLQGRVMTTDTSTAYMELSLRSDDTAVYYCAR---MEYDILTGIVYGYGYP--D 113  
 QY 121 VWGGTIVTVSS 132  
 |||||  
 Db 114 YWGGTIVTVSS 125

## RESULT 15

US-09-880-748-1452  
 ; Sequence 1452, Application US/09880748  
 ; Publication No. US20030059937A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.



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OM protein - protein search, using bw model

Run on: December 30, 2003, 10:47:45 ; Search time 13.4037 Seconds

(without alignments)  
416.677 Million cell updates/sec

Title: US-09-674-752-25

Perfect score: 711

Sequence: 1 QVQLQSGATEVKRPGASMKV.....YPEYAMDVWGQTTVTSS 132

Scoring table:

BLOSUM62

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	485	68.2	120	4	US-09-025-769B-36 Sequence 36, Appl
2	485	68.2	120	4	US-09-025-769B-59 Sequence 59, Appl
3	484.5	68.1	117	4	US-09-025-769B-52 Sequence 22, Appl
4	478.5	67.3	121	1	US-08-264-093-3 Sequence 3, Appl
5	476.5	67.0	129	2	US-08-561-521-45 Sequence 45, Appl
6	476.5	67.0	129	4	US-08-525-539A-77 Sequence 77, Appl
7	476.5	67.0	129	5	PCT-US95-01219-45 Sequence 45, Appl
8	476	66.9	128	1	US-08-202-047-22 Sequence 22, Appl
9	476	66.9	128	3	US-08-964-690-22 Sequence 22, Appl
10	471.5	66.3	125	3	US-09-199-149-3 Sequence 3, Appl
11	464	65.3	120	2	US-08-652-816A-19 Sequence 19, Appl
12	452.5	63.6	139	3	US-08-933-983-21 Sequence 21, Appl
13	450	63.3	117	3	US-08-545-809A-105 Sequence 105, Appl
14	448	63.0	139	1	US-08-253-877C-19 Sequence 19, Appl
15	448	63.0	139	2	US-08-452-164A-19 Sequence 19, Appl
16	448	63.0	139	3	US-08-603-024-18 Sequence 18, Appl
17	448	63.0	139	4	US-08-450-809-14 Sequence 14, Appl
18	447	62.9	123	6	US-09-049-672A-13 Sequence 13, Appl
19	444	62.4	120	4	US-09-025-769B-35 Sequence 35, Appl
20	444	62.4	120	4	US-09-025-769B-57 Sequence 57, Appl
21	443.5	62.4	119	2	US-08-561-521-10 Sequence 10, Appl
22	443.5	62.4	119	5	PCT-US95-01219-10 Sequence 10, Appl
23	440.5	62.0	119	4	US-09-438-954-41 Sequence 41, Appl
24	440.5	62.0	146	1	US-08-276-852-155 Sequence 155, App
25	440.5	62.0	146	1	US-08-899-575-155 Sequence 155, App
26	440.5	62.0	146	1	US-08-899-575-155 Sequence 155, App
27	440.5	62.0	146	5	PCT-US95-08743-155 Sequence 155, App

28	438	61.6	116	2	US-08-561-521-41 Sequence 41, Appl
29	438	61.6	116	5	PCT-US95-01219-41 Sequence 41, Appl
30	438	61.6	135	1	US-08-137-117D-102 Sequence 102, App
31	438	61.6	135	2	US-08-436-717-102 Sequence 102, App
32	436.5	61.4	119	1	US-08-300-386A-65 Sequence 65, Appl
33	436.5	61.4	119	3	US-08-931-645-65 Sequence 65, Appl
34	436.5	61.4	119	5	PCT-US95-11235-65 Sequence 65, Appl
35	435.5	61.3	119	2	US-08-561-521-12 Sequence 12, Appl
36	435.5	61.3	119	5	PCT-US95-01219-12 Sequence 12, Appl
37	434.5	61.1	123	1	US-08-477-877B-94 Sequence 94, Appl
38	434.5	61.1	123	2	US-08-472-281A-94 Sequence 94, Appl
39	434.5	61.1	123	2	US-08-477-989B-94 Sequence 94, Appl
40	433.5	61.0	140	3	US-08-836-561-63 Sequence 63, Appl
41	433.5	61.0	140	4	US-09-434-122-63 Sequence 63, Appl
42	433	60.9	135	1	US-08-137-117D-100 Sequence 100, App
43	433	60.9	135	2	US-08-436-717-100 Sequence 100, App
44	432	60.8	135	1	US-08-137-117D-112 Sequence 112, App
45	432	60.8	135	2	US-08-436-717-112 Sequence 112, App

#### ALIGNMENTS

RESULT 1  
US-09-025-769B-36  
Sequence 36, Application US/09025769B  
Parent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Illeg, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-36  
Query Match 68.2%; Score 485; DB 4; Length 120;  
Best Local Similarity 72.7%; Pred. No. 5.3e-39;  
Matches 96; Conservative 7; Mismatches 17; Indels 12; Gaps 1;



APPLICANT: Michael D. Dan  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO  
CELL CYCLE-INDEPENDENT GLIOMA SURFACE  
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE  
TITLE OF INVENTION: ANTIGEN  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ridout & Maybee  
STREET: 2300 Richmond-Adelaide Centre  
STREET: 101 Richmond Street West  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5H 2J7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS-DOS 6.00  
SOFTWARE: ASCII Editor  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/264,093  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA: No. 5639863 applicable  
ATTORNEY/AGENT INFORMATION:  
NAME: Lake, James R.  
REGISTRATION NUMBER: 31081  
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 868-1482  
TELEFAX: (416) 362-0823  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
STRANDEDNESS: not applicable  
TOPOLOGY: linear  
US-08-264-093-3

Query Match 67.3%; Score 478.5; DB 1; Length 121;  
Best Local Similarity 72.0%; Pred. No. 2,2e-38;  
Matches 95; Conservative 11; Mismatches 15; Indels 11; Gaps 3;

QY 1 QVQLQSGATEYVKKPGKASVKSCMASGYPTFTSYDISWVRAQPGQGLEMMGWISISYSGNTDY 60  
DB 1 QVQLVQSGAEYVKKPGASVKSCKASGYTFTYGLSWVRAQPGQGLEMMGWISAHNGTNS 60  
QY 61 AOKFGGRVTMTTDSRRTAYMELRSRSDPTAVYYCARDGCGGAYEDVWSGEYPEYYAM 120  
DB 61 AOKFGGRVSMTTDTSTSTAYMEVRLSRSDPTAVYYCARVG-----VW--DLNLYF--D 109  
QY 121 VMGQGTIVTVSS 132  
DB 110 YMGQGTIVTVSS 121

RESULT 5  
US-08-561-521-45  
Sequence 45, Application US/08561521  
Patent No. 5840299  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Legier, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
TITLE OF INVENTION: Adhesion Molecule VIA-4  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourlie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA

ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/561,521  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/186,269A  
FILING DATE: 25-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 129 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-561-521-45

Query Match 67.0%; Score 476.5; DB 2; Length 129;  
Best Local Similarity 71.4%; Pred. No. 3,7e-38;  
Matches 95; Conservative 11; Mismatches 22; Indels 5; Gaps 2;

QY 1 QVQLQSGATEYVKKPGKASVKSCMASGYPTFTSYDISWVRAQPGQGLEMMGWISISY-SGNTD 59  
DB 1 QVQLVQSGAEYVKKPGASVKSCKASGYTFTSYAISWVRAQPGQGLEMMGWINPYGNGDTN 60  
QY 60 YAKQFGGRVTMTTDSRRTAYMELRSRSDPTAVYYCARDGCGGAYEDVWSGEYPEYYAM 119  
DB 61 YAKQFGGRVTMTTDSRRTAYMELRSRSDPTAVYYCARARVGGGCGYRGD----YXF 116  
QY 120 DVMGQGTIVTVSS 132  
DB 117 DVMGQGTIVTVSS 129

RESULT 6  
US-08-525-539A-77  
Sequence 77, Application US/08525539A  
Patent No. 6309636  
GENERAL INFORMATION:  
APPLICANT: DO COUTO, FERNANDO J.R.  
APPLICANT: CERTANT, ROBERTO L.  
APPLICANT: PETERSON, JERRY A.  
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE  
TITLE OF INVENTION: M63 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND  
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/525,539A  
FILING DATE: 14-SEP-1995

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LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-45

Query Match          67.0%; Score 476.5; DB 5; Length 129;
Best Local Similarity 71.4%; Pred. No. 3.7e-36;
Matches 95; Conservative 11; Mismatches 22; Indels 5; Gaps 2

QY 1 QVOLLQSATVKKPKGASMKVSCMASGYPTSYDISWYRQAPGGGLEWNGWISY-SCGNTD 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVSGAEVKKPKGASVKKVSKASGVTFTFSIALSWRQAPGGGLEWNGWLNIPYNGDITN 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 YAQKFGKRVTTMTDTSRRRTAYMEIURLSRDDTAVYCCARDGGGGAVEDVMSGEYPEYYAM 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YAQKFGKRVTTMTDTSRRRTAYMEIURLSRDDTAVYCCARDGGGGAVEDVMSGEYPEYYAM 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 DWMGQGTYYVSS 132
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Db 117 DWMGQGTLYTVSS 129
   |||||:|||||

RESULT 8
US-08-202-047-22
; Sequence 22, Application US/08202047
; Patent No. 5800815
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
; APPLICANT: BENDIG, Mary M.
; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202.047
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION: /label= HUMAN_1
US-08-202-047-22

```

RESULT 9  
 US-08-964-690-22  
 : Sequence 22, Application US/08964690  
 : Patent No. 6033667  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: CHESNUT, Robert W.  
 : APPLICANT: POLEY, Margaret J.  
 : APPLICANT: PAULSON, James C.  
 : APPLICANT: JONES, S. Tarran  
 : APPLICANT: SALDANHA, Jose W.  
 : APPLICANT: BENDIG, Mary M.  
 :  
 : TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses  
 :  
 : NUMBER OF SEQUENCES: 45  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESS: Townsend and Townsend Kourie and Crew  
 : STREET: One Market Plaza, Stewart Tower, Suite 2000  
 : CITY: San Francisco  
 : STATE: California  
 : COUNTRY: USA

Query Match	66.9%	Score 476;	DB 3;	Length 128;
Best Local Similarity	71.4%;	Pred. No. 4.1e-38;		
Matches 95;	Conservative 11;	Mismatches 21;	Indels 6;	Gaps 2

RESULT 10  
 US-09-199-149-3  
 Sequence 3, Application US/09199149  
 Patent No. 6160099  
 GENERAL INFORMATION:  
 APPLICANT: Jonak, Zdenka L.  
 APPLICANT: Taylor, Alexander H.  
 APPLICANT: Trull Jr., Stephen H.  
 APPLICANT: Johnson, Kyung O.  
 TITLE OF INVENTION: Humanized Monoclonal Antibodies  
 FILE REFERENCE: P50860  
 CURRENT APPLICATION NUMBER: US/09/199,149  
 CURRENT FILING DATE: 1998-11-24  
 NUMBER OF SEQ ID NOS: 37  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 3  
 LENGTH: 125  
 TYPE: PRT  
 ORGANISM: Kabat VH subgroup I  
 US-09-199-149-3

RESULT 11  
 US-08-652-816A-19  
 ; Sequence 19, Application US/08652816A  
 ; Patent No. 5872215  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Osbourn, JK  
 ; APPLICANT: Allen, DJ  
 ; APPLICANT: McCafferty, JG  
 ; TITLE OF INVENTION: Specific binding members, materials and  
 ; TITLE OF INVENTION: methods.  
 ; NUMBER OF SEQUENCES: 53  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: United States of America  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,816A  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.4  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.8  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9525004.9  
FILING DATE: 07-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02240  
FILING DATE: 02-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/244,597  
FILING DATE: 01-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33308  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-652-816A-19

Query Match 65.3%; Score 464; DB 2; Length 120;  
Best Local Similarity 71.2%; Pred. No. 5.2e-37;  
Matches 94; Conservative 5; Mismatches 21; Indels 12; Gaps 2;

QY 1 QVQLQSGATEYVKKPGASMKVSCMASGYPTSYDISWVRQAPGQGLEWMGNIISYSGNTDY 60  
DB 1 QVTLQSSGAIEYKPKGSPVKVSKASGYFTAYGNWVRQAPGQGLEWM-WISAYSGNTKY 59  
QY 61 AAKFGQGVMTTDTSRRTAYMELRSLSDDTAYVYCCARDGGGAYEDVMSGEYPERYAMD 120  
DB 60 AAKFGQGVMTTDTSRRTAYMELRSLSDDTAYVYCCARDGGGAYEDVMSGEYPERYAMD 120  
QY 121 VMGGGTTVTYSS 132  
DB 109 VMGGGTTVTYSS 120

RESULT 12  
US-08-933-983-21  
Sequence 21, Application US/08933983  
Patent No. 6114506  
GENERAL INFORMATION:  
APPLICANT: REED, GUY L.  
APPLICANT: HARRIS, LINDA  
APPLICANT: BAJORATH, JURGEN  
APPLICANT: MATSUEDA, GARY  
APPLICANT: HSU, MEI-YIN  
APPLICANT: NOVOTNY, JIRI  
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS: 81  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVENUE, N.W. SUITE 600  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,983  
FILING DATE: 19-SEP-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026,356  
FILING DATE: 20-SEP-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: GOLDSTEIN, JORGE A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0609.4320002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 139 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-933-983-21

Query Match 63.6%; Score 452.5; DB 3; Length 139;  
Best Local Similarity 65.2%; Pred. No. 7.5e-36;  
Matches 86; Conservative 14; Mismatches 19; Indels 13; Gaps 2;

QY 1 QVQLQSGATEYVKKPGASMKVSCMASGYPTSYDISWVRQAPGQGLEWMGNIISYSGNTDY 60  
DB 21 QVTLQSSGAIEYKPKGASVSKISCKASGYFTYGNWVRQAPGQGLEWMGNIINRSGSPY 80  
QY 61 AAKFGQGVMTTDTSRRTAYMELRSLSDDTAYVYCCARDGGGAYEDVMSGEYPERYAMD 120  
DB 81 AAEFRKGRFTFLDTSTAYLFIKLSRSDTAYVFCAR-----W---VPGTYAMD 127  
QY 121 VMGGGTTVTYSS 132  
DB 128 VMGGGTTVTYSS 139

RESULT 13  
US-08-545-809A-105  
Sequence 105, Application US/08545809A  
Patent No. 6096878  
GENERAL INFORMATION:  
APPLICANT: Honjo, Tasuku  
APPLICANT: Matsuda, Fumihiko  
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE  
NUMBER OF SEQUENCES: 145  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/08/545,809A  
FILING DATE: 27-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/Jp93/00603  
FILING DATE: 10-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 06501/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-545-809A-105

Query Match 63.3%; Score 450; DB 3; Length 117;  
Best Local Similarity 86.7%; Pred. No. 1,1e-35;  
Matches 85; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVOLLQATVEVKKPGASMKVSCMASGYPTSTYDISWVROAPQGLEMMGMISYSGNTDY 60  
DB 20 QVLLVQSGAEVKKPGASVKVSCKASGYTFSTYDISWVROAPQGLEMMGMISYSGNTDY 79  
QY 61 AOKFGRYVTMTDTSRTAYMELSLRSDDTAVYYCAR 98  
DB 80 AOKLQGRVTMTDTSRTAYMELSLRSDDTAVYYCAR 117

RESULT 14  
US-08-253-877C-19  
Sequence 19, Application US/08253877C  
Patent No. 5773001  
GENERAL INFORMATION:  
APPLICANT: Hamann, Philip R.  
APPLICANT: Hinman, Lois  
APPLICANT: Hollander, Irwin  
APPLICANT: Holcomb, Ryan  
APPLICANT: Halleck, William  
APPLICANT: Tsou, Hwei-Ru  
APPLICANT: Weiss, Martin J.  
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor  
TITLE OF INVENTION: Agents and Intermediates for Their Synthesis  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/253,877C  
FILING DATE: 03-JUN-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 32,368  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-831-3246  
TELEFAX: 201-831-3305  
INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:  
LENGTH: 139 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-253-877C-19

Query Match 63.0%; Score 448; DB 1; Length 139;  
Best Local Similarity 65.2%; Pred. No. 2e-35;  
Matches 86; Conservative 13; Mismatches 21; Indels 12; Gaps 1;

QY 1 QVOLLQATVEVKKPGASMKVSCMASGYPTSTYDISWVROAPQGLEMMGMISYSGNTDY 60  
DB 20 QVLLVQSGAEVKKPGASVKVSCKASGYTFSTYDISWVROAPQGLEMMGMISYSGNTDY 79  
QY 61 AOKFGRYVTMTDTSRTAYMELSLRSDDTAVYYCARDDGGGAYEDVSGEYPEYYAMD 120  
DB 80 NEKRGRTVTDTSRTAYMELSLRSDDTAVYYCARDDGGGAYEDVSGEYPEYYAMD 127  
QY 121 VMGGQTVTVSS 132  
DB 128 VMGGQTVTVSS 139

RESULT 15  
US-08-452-164A-19  
Sequence 19, Application US/08452164A  
Patent No. 5877296  
GENERAL INFORMATION:  
APPLICANT: Hamann, Philip R.  
APPLICANT: Hinman, Lois  
APPLICANT: Hollander, Irwin  
APPLICANT: Holcomb, Ryan  
APPLICANT: Halleck, William  
APPLICANT: Tsou, Hwei-Ru  
APPLICANT: Weiss, Martin J.  
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor  
TITLE OF INVENTION: Agents and Intermediates for Their Synthesis  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Home Products Corporation  
STREET: One Campus Drive  
CITY: Parsippany  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/452,164A  
FILING DATE: 26-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 32,368-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-2158  
TELEFAX: 201-683-4117  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 139 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-452-164A-19

Query Match 63.0%; Score 448; DB 2; Length 139;

Best Local Similarity 65.2%; Pred. No. 2e-35; Matches 86; Conservative 13; Mismatches 21; Indels 12; Gaps 1;

```

OY      1 QVQLQSATEVKKPGASMKVSCMASGYPTTSYDISWVROAPGQGLEMMGMSISYSGNTDY 60
      |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      20 QIQVQSGAEVKKPGSSVSKVSCKASGYFTDYINMMROAPGQGLEMMGMDPGSGNTKY 79
      |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY      61 AQFQGRVTMTDTSRRTAYMELRSLRSDDTAVYCGARDGGGAYEDVWSGEYPEYYAMD 120
      |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      80 NEKFKGRVTITVDTSNTAYMELSLRSEDTAFYFCARE-----KTTYYYAMD 127
      |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY      121 VMGGGTTVTVSS 132
      |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      128 YWGQGTIVTVSS 139
      |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

```

Search completed: December 30, 2003, 11:05:31  
Job time : 13.4871 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 (Search time 9.39399 Seconds  
(without alignments)  
1003.251 Million cell updates/sec

Title: US-09-674-752-27  
Perfect score: 521  
Sequence: 1 QVOLLQSAIEVKKKGASMKV.....AYMELRLSRSDPTAVYYCAR 98

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	456	87.5	98	2	S26919 Ig heavy chain V r
2	453	86.9	129	2	S36260 Ig heavy chain V r
3	451	86.6	122	2	S36271 Ig heavy chain V r
4	450	86.4	124	2	S19665 Ig heavy chain V r
5	432	82.9	131	2	S21924 Ig heavy chain V r
6	428	82.1	160	2	PI0105 anti-PR2 erythrocy
7	420	80.6	111	2	S21925 Ig heavy chain V r
8	407	78.1	98	2	S26918 Ig heavy chain V r
9	407	78.1	117	2	S18553 Ig heavy chain V r
10	407	78.1	136	2	S31600 Ig heavy chain V r
11	405	77.7	125	2	S68170 Ig heavy chain V r
12	401	77.0	98	2	S26938 Ig heavy chain V r
13	401	77.0	117	2	S31680 Ig heavy chain V r
14	401	77.0	117	2	S18551 Ig heavy chain V r
15	401	77.0	135	2	S49530 anti-5m antibody V
16	400	76.8	118	2	S36265 Ig heavy chain V r
17	397	76.2	104	2	S69899 Ig heavy chain V r
18	397	76.2	127	2	S34014 Ig heavy chain V r
19	393	75.4	98	2	S26912 Ig heavy chain V r
20	393	75.4	129	2	S46333 Ig heavy chain V r
21	391	75.0	117	2	S18552 Ig heavy chain V r
22	390	74.9	132	2	S31596 Ig heavy chain V r
23	389	74.7	110	2	PH1670 Ig heavy chain V r
24	389	74.7	123	2	D33548 Ig heavy chain V-1
25	388	74.5	98	2	S26920 Ig heavy chain V r
26	387	74.3	117	2	PH0371 Ig gamma chain pre
27	383	73.5	117	1	HVHUNG Ig heavy chain pre
28	383	73.5	148	2	S29257 Ig heavy chain V r
29	382	73.3	114	2	PH1667 Ig heavy chain V r

30	382	73.3	118	2	PH1666 Ig heavy chain V r
31	381	73.1	142	2	A32483 Ig heavy chain V r
32	380	72.9	171	2	S23623 Ig heavy chain V r
33	379	72.7	98	2	PH0871 Ig heavy chain V r
34	378	72.6	119	2	PH0295 Ig heavy chain V-D
35	377	72.4	116	2	S31667 Ig heavy chain V r
36	377	72.4	117	1	HVH035 Ig heavy chain pre
37	377	72.4	120	2	S31999 Ig heavy chain V r
38	377	72.4	135	2	B32274 Ig heavy chain pre
39	376	72.2	126	2	I44151 Ig heavy chain V r
40	372	71.4	98	2	S24680 Ig heavy chain V1
41	370	71.0	98	2	S26921 Ig heavy chain V r
42	369	70.8	104	2	PH1665 Ig heavy chain V r
43	369	70.8	109	2	PH1668 Ig heavy chain V r
44	367	70.4	98	2	S26915 Ig heavy chain V r
45	367	70.4	116	2	S31698 Ig heavy chain pre

#### ALIGNMENTS

RESULT 1  
S26919  
Ig heavy chain V region (DP-14) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #ext\_change 23-Jul-1999  
R:Accession: S26919  
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of  
A:Reference number: S26885; MID:93021117; PMID:1404388  
A:Accession: S26919  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-98 <TOM>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 456; DB 2; Length 98;  
Best Local Similarity 87.8%; Pred. No. 1.7e-39;  
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLLQSAIEVKKKGASMKVSCASGYPTSYDISVVRQAPQGLFVNGHISYNGNTNY 60  
DB 1 QVOLLQSAIEVKKKGASMKVSCASGYPTSYDISVVRQAPQGLFVNGHISYNGNTNY 60  
QY 61 AOKFQGRVTMTTDTSRRTAVMELRLSRSDPTAVYYCAR 98  
DB 61 AOKFQGRVTMTTDTSRRTAVMELRLSRSDPTAVYYCAR 98

RESULT 2  
S36260  
Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #ext\_change 23-Jul-1999  
R:Accession: S36260  
R:Griffiths, A.D.; Malngvict, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
EMBO J. 12, 725-734, 1993  
A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
A:Reference number: S36256; MID:93178448; PMID:7679990  
A:Accession: S36260  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-129 <GR1>  
A:Cross-references: EMBL:218651; NID:g33124; PIDN:CAA79303.1; PID:g9339903  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.9%; Score 453; DB 2; Length 129;





S68170

Query Match	77.7%;	Score 405;	DB 2;	Length 125;
Best Local Similarity	-76.5%;	Pred. No. 3.5e-34;		
Matches 75; Conservative	9;	Mismatches 14;	Indels 0;	Gaps 0

**Dy**     **1** QVOLLQSATEVVKKPGASMKVSCMASGYPFTSYDISWVRAPQGGLEWGMSAYNGNTHY     60  
     :**:** | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
**Dd**     **1** EVKLIHQSGAELKKPGASVKVCCKTSGTFSSYNINMWQAPEGQGIEWGMNSVDNCKTRY     60

Dy 61 A Q F G R V T M T D T S R R T A I W E L K R S D D T A V Y C A R 98  
| | | | | : | | | |  
Db 61 A Q F G R V T M T D T S T A I W E L R S L T T D D T A V Y C T R 98

S26938

1g heavy chain/region (DP-75) - human (fragment)  
 C.Species: Homo sapiens (man)  
 C.Date: 22-Nov-1993 #sequence\_revision 17-Nov-1995 #text\_change 23-Jul-1999  
 C.Accession: S26938  
 R.Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
 Mol. Biol. 227 776-798 1992

**A1:** Title: The repertoire of human germ-line V(H) sequences reveals about fifty groups of A1: Reference number: S26885; MUID:93021117; PMID:1404388  
A1: Accession: S26938  
A1: Status: not available

A;Molecule type: DNA  
A;Residues: 1-98 <TOM>  
A;Cross-references: EMBL:Z14071; NID:g332969; PIDN:CAA78451.1; PID:g332970

C Superfamily: Immunoglobulin V region; immunoglobulin homology  
 Keywords: heterodimer; immunoglobulin  
 15-98/Domain: immunoglobulin homology <IMM>

Query Match	77.0%	Score 401	DB 2	Length 98
Best Local Similarity	77.6%	Pred. No. 6.8e-34		
Matches 76; Conservative	7	Mismatches 15	Indels 0	Gaps 0

**dy**

1 QVQLLSATPEYKKPGASMKYSQMASTGYPFTSYDISWTRAPCGGLEWGWISAYNGNTHY 600  
||| : || | || || || || || || || || || || || || || || || || || ||  
**db** 1 QVQLVSAGAEVKKPKGASVKYSCKASTGTFTGYMHWVRQPAGQGLEMGWINPNSGCTNY 600  
||| : || | || || || || || || || || || || || || || || || || || ||

61 AQRQGRVMTTDSRTAAMELSLRSDTAIVYCAR 98  
|||||  
61 AQRFQGRVTMRDTSISTAYMELSLRSDDAVYYCAR 98

## 31680

```

9 heavy chain V region - human
;Species: Homo sapiens (man)
;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

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C/Accession: S31680  
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
Submitted to the EMBL Data Library, June 1992  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A/Reference number: S31585  
A/Accession: S31680

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-117 <CUI>  
A:Cross-references: EMBL:214213; NID:g37795; PIDD:CAA76582.1; PID:g37796  
A:Genetics:

A;Introns: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match	77.0%	Score 401;	DB 2;	Length 117;
Best Local Similarity	77.6%	Pred. No. 8.2e-34;		
Matches	76;	Conservative	8;	Mismatches 14; Indels 0; Gaps 0

[illegible]

**Dy**    61 A Q K E G R V M T T D S R F A Y M E I R L S L S D D P T A V Y C A R    98  
         ||||| : |||||  
**Db**    80 A Q K E G R V M T R D T S I S T A Y V E L S R L S D D T A V Y C A R    117

\$18551

I9 heavy chain V region precursor (VI-2) - human (fragment)  
 C1Species: Homo sapiens (man)  
 C1date: 13-Jan-1995 #sequence \_revision 06-Jun-1997 #text\_change 23-Jul-1999  
 C1Accession: S18551; S23625  
 C1Chen, R.Y. 1985

A:reference number: S18551; NCBI:accession number: F06792  
EMBL J. 10 3641-3645, 1991  
A:reference number: S18551; NCBI:accession number: F06792  
EMBL J. 10 3641-3645, 1991  
A:reference number: S18551; NCBI:accession number: F06792  
EMBL J. 10 3641-3645, 1991

A/Molecule type: DNA  
A/Residues: 1-117 <SH1>  
A/Cross-references: ENBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:a378333

A:Reference number: S23623: MUIP-92156804: PMID-1740665

A;Accession: 533625  
A;Molecule type: DNA  
A;Residues: 1-117 <OLE>  
A;Cross-references: EMBL: Y59704. NID: 012557. BION: CNA43307.1. STD: -  
A;References: -

**C1:Genetics:**  
A:introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
**Keywords:** heterotrimer; immunoglobulin

F1-19/Domains: signal sequence #status predicted <SIG>  
F1-20-117/Product: Ig heavy chain V region (V1-2) #status predicted <MAT>  
F1-34-117/Domains: immunoglobulin homology <IMM>

Query Match	77.0%	Score 401;	DB 2;	Length 117;
Best Local Similarity	77.6%	Pred. No. 8.2e-34;		
Matches	76;	Conservative	15;	Indels 0; Gaps 0

10 VQVLLVDSALEVKKRPGASMKVSCMSAGYPTFSYDLSWVRQAPGGGLEWVGWISAYNNTHTY 60  
 ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
 20 QVQLVDSGAELVKRPGASVKVSCKASGYTFTGYTHMIVRQAPGGGLEWVGWISAYNNTHTY 79

61 AAKFQGRMTMDTSRRAYAMELSLSDDTAYYYCAR 98  
 |||||  
 80 AAKFQGRVTMDTSISTAYMEISRLSSDDTAYYYCAR 111

## RESULT 15

S49530  
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human  
C:Species: Homo sapiens (man)  
C:Date: 01-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 23-Jul-1999  
C:Accession: S49530  
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.  
Submitted to the EMBL Data Library, October 1994  
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.  
A:Reference number: S48797  
A:Accession: S49530  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-135 <MAH>  
A:Cross-references: EMBL:Z46348; NID:G560839; PIDN:CA466467.1; PID:G560840  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:34-117/Domain: immunoglobulin homology <IMH>

Query Match	77.0%;	Score 401;	DB 2;	Length 135;
Best Local Similarity	77.6%;	Pred. No. 9.6e-34;		
Matches	76;	Conservative	7;	Mismatches 15; Indels 0; Gaps 0;

QY 1 QVOLLQSATEYKKPGASMKVSCMASGYPFTSYDLSWVRAPGCGLEWVCISAYNANTHY 60  
|||:|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
DB 20 QVQLVDSGAELVKKPGASVSKVSCASGYFTGYNHMWRQAPQGGLSEMWGVINPNSSGTNY 79

OY		61	AQFQGRVTMTTDTSRRTAYMELRSLRSDDTA	VYYCAR	98
Db		80	AQFQGRVTMTTRDTSISTAYMELSRLSRDDTA	VYYCAR	117

Search completed: December 30, 2003, 11:03:14  
Job time : 9.39399 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 5.25426 Seconds  
(without alignments)  
877.119 Million cell updates/sec

Title: US-09-674-752-27

Perfect score: 521

Sequence: 1 QVQLVQSGAEVKKRQASGAVK...AYNELRLRSDDTAIVYCAR 98

Scoring table:

BLOSUM62

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	383	73.5	117	1	HV1B_HUMAN
2	377	72.4	117	1	HV1G_HUMAN
3	359	68.9	147	1	HV1C_HUMAN
4	340	65.3	117	1	HV52_MOUSE
5	331	63.5	117	1	HV1A_HUMAN
6	326	62.6	114	1	HV00_MOUSE
7	326	62.6	117	1	HV14_MOUSE
8	326	62.6	120	1	HV03_MOUSE
9	325	62.4	117	1	HV04_MOUSE
10	324	62.2	140	1	HV02_MOUSE
11	319	61.2	117	1	HV51_MOUSE
12	315	60.5	118	1	HV06_MOUSE
13	314	60.3	117	1	HV06_MOUSE
14	314	60.3	120	1	HV50_MOUSE
15	313	60.1	117	1	HV05_MOUSE
16	313	60.1	117	1	HV12_MOUSE
17	313	60.1	117	1	HV12_MOUSE
18	307	58.9	139	1	HV07_MOUSE
19	300	57.6	136	1	HV15_MOUSE
20	298	57.2	117	1	HV3C_HUMAN
21	297	57.0	117	1	HV10_MOUSE
22	297	57.0	117	1	HV10_MOUSE
23	295	56.6	117	1	HV49_MOUSE
24	294	56.4	138	1	HV48_MOUSE
25	292	56.0	121	1	HV3J_HUMAN
26	290	55.7	125	1	HV1F_HUMAN
27	289	55.5	117	1	HV5E_MOUSE
28	284	54.5	119	1	HV3I_HUMAN
29	282	54.1	121	1	HV01_MOUSE
30	275.5	52.9	120	1	HV1H_HUMAN
31	274	52.6	119	1	HV3P_HUMAN
32	274	52.6	122	1	HV3G_HUMAN
33	272	52.2	136	1	HV1E_MOUSE

34	270	51.8	122	1	HV3A_HUMAN	P01762	homo	sapien
35	270	51.8	122	1	HV3H_HUMAN	P01769	homo	sapien
36	269	51.6	114	1	HV3B_HUMAN	P01763	homo	sapien
37	268	51.4	119	1	HV3M_HUMAN	P01774	homo	sapien
38	266	51.1	117	1	HV54_MOUSE	P18525	mus	muscultu
39	265.5	51.0	97	1	HV5E_MOUSE	P18527	mus	muscultu
40	265.5	51.0	116	1	HV05_CARAU	P19181	carabablu	a
41	265	50.9	119	1	HV3L_HUMAN	P01773	homo	sapien
42	264	50.7	126	1	HV02_HUMAN	P01772	homo	sapien
43	263.5	50.6	117	1	HV03_CARAU	P01785	canis	famil
44	263	50.5	117	1	HV03_CARAU	P19180	carabablu	a
45	261.5	50.2	115	1	HV3F_HUMAN	P01767	homo	sapien

## ALIGNMENTS

## RESULT 1

HV1B\_HUMAN STANDARD: PRT; 117 AA.  
ID HV1B\_HUMAN  
AC P01743;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-I region Hg3 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83144026; PubMed=6298778;  
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;  
RT "Evolutionary aspects of immunoglobulin heavy chain variable region  
RT (VH) gene subgroups.";  
RT Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).  
RL -1 SIMILARITY: Contains 1 immunoglobulin-like domain.  
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CC  
CC EMBL; J08240; AAA52988.1; -  
CC PIR; A02024; HVALHG.  
CC HSSP; P01772; 2FB4.  
CC DR GO; GO:0005576; C:extracellular; NAS.  
CC DR GO; GO:0003823; P:antigen binding activity; NAS.  
CC DR GO; GO:0006955; P:immune response; NAS.  
CC DR InterPro; IPR007110; Ig-like.  
CC DR InterPro; IPR003006; Ig\_MHC.  
CC DR InterPro; IPR003596; Ig\_V.  
CC DR SMART; SM00406; IGV; 1.  
CC DR Pfam; PF00047; IGV; 1.  
CC DR PROSITE; PSS0835; IG\_LIKE; 1.  
CC KM Immunoglobulin V region; Signal.  
CC FT CHAIN 1 19  
CC FT DOMAIN 20 117 IG HEAVY CHAIN V-I REGION Hg3.  
CC FT NON\_TER 117 IG-LIKE.  
CC ST SEQUENCE 117 AA; 12946 MW; 205F92FC60CD1FE7 CRC64;

Query Match Best Local Similarity 73.5%; Score 383; DB 1; Length 117;  
Matches 74; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVKKRQASGAVK...PFTSYDLSMTVRAPGGLLEWVGIMATVNGTTHY 60  
Db 20 QVQLVQSGAEVKKRQASGAVK...PFTSYDLSMTVRAPGGLLEWVGIMATVNGTTHY 79



QY 61 AOKFOGRVTMTDTSRTAYMELSLRSDDTAVYYCAR 98  
 Db 80 AOKFOGRVTMTDTSRTAYMELSLRSDDTAVYYCAR 117

## RESULT 2

HVLG\_HUMAN

ID HV1G\_HUMAN STANDARD; PRT; 117 AA.

AC P21083;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-I region V35 precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=8296408; PubMed=2841108;

RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.O.,

RT Ohno H., Fukushima S., Honjo T.,

RT "Dispersed localization of D segments in the human immunoglobulin

heavy-chain locus.";

RL EMBO J. 7:1047-1051 (1988).

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

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DR PIR: X07448; -; NOT\_ANNOTATED\_CDS.

DR EMBL: S00476; HVHJ35.

DR HSSP: P01772; 2P84.

DR GO: GO:0005576; C:extracellular; NAS.

DR GO: GO:0003823; F:antigen binding activity; NAS.

DR GO: GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; IG-1-like.

DR InterPro: IPR003006; IG\_MHC.

DR InterPro: IPR003596; IG\_V.

DR Pfam: PF00047; Ig\_1.

DR SMART: SM00406; Igv\_1.

DR PROSITE: PS50835; IG-LIKE; 1.

KM Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.

FT DOMAIN 20 &gt;117 IG-LIKE.

FT NON\_TER 117 117

SO SEQUENCE 117 AA; 13009 MW; BE6ICE63F8CE97BD CRC64;

Query Match 72.4%; Score 377; DB 1; Length 117;

Best Local Similarity 74.5%; Pred. No. 5, 1e-37;

Matches 73; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 QVQLQSATEVKKKSGAMKYSCKASGYPTSYDSWTRQAPGQGLEWVGMSAYNGNTHY 60

Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMHWVRQAPGQGLEWVGIRINPNSGCTNY 79

QY 61 AOKFOGRVTMTDTSRTAYMELSLRSDDTAVYYCAR 98

Db 80 AOKFOGRVTMTDTSRTAYMELSLRSDDTAVYYCAR 117

RESULT 3

HVLG\_HUMAN

ID HV1G\_HUMAN STANDARD; PRT; 147 AA.

AC P01744;

DT 21-JUL-1986 (Rel. 01, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

QY 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-I region ND precursor (Fragments).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.  
 RX MEDLINE=83065234; PubMed=6815656;  
 RA Kenten J.H., Moigard H.V., Houghton M., Derbyshire R.B., Viney J.,  
 RA Bell L.O., Gould H.J.,  
 RT "Cloning and sequence determination of the gene for the human  
 RT immunoglobulin epsilon chain expressed in a myeloma cell line."  
 RT Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665 (1982).

RP SEQUENCE OF 20-147.

RA Bennich H.H., Johanson S.G.O., von Bahr-Lindstrom H.;

RL (In) Bach M.K. (ed.);

RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,  
 Marcel Dekker, New York (1978).CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA  
 CC PROTEIN.

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DR PIR: X07448; -; NOT\_ANNOTATED\_CDS.

DR EMBL: S00476; HVHJ35.

DR HSSP: P01789; 1MCP.

DR GO: GO:0005576; C:extracellular; NAS.

DR GO: GO:0003823; F:antigen binding activity; NAS.

DR GO: GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; IG-1-like.

DR InterPro: IPR003006; IG\_MHC.

DR InterPro: IPR003596; IG\_V.

DR Pfam: PF00047; Ig\_1.

DR SMART: SM00406; Igv\_1.

DR PROSITE: PS50835; IG-LIKE; 1.

KM Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.

FT SIGNAL 1 19

FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.

FT DOMAIN 20 131 IG-LIKE

FT DISULFID 21 115 PYRROLIDONE CARBOXYLIC ACID.

FT CONFLICT 21 21 T -&gt; V (IN REF. 2).

FT CONFLICT 53 54 IH -&gt; HI (IN REF. 2).

FT CONFLICT 67 68 VG -&gt; GV (IN REF. 2).

FT CONFLICT 125 125 MISSING (IN REF. 2).

FT NON\_TER 147 147

SO SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 68.9%; Score 359; DB 1; Length 147;

Best Local Similarity 67.3%; Pred. No. 8, 3e-35;

Matches 66; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 1 QVQLQSATEVKKKSGAMKYSCKASGYPTSYDSWTRQAPGQGLEWVGMSAYNGNTHY 60

Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMHWVRQAPGQGLEWVGIRINPNSGCTNY 79

QY 61 AOKFOGRVTMTDTSRTAYMELSLRSDDTAVYYCAR 98

Db 80 AOKFOGRVTMTDTSRTAYMELSLRSDDTAVYYCAR 117

RESULT 4

HVS2\_MOUSE

ID HV52\_MOUSE STANDARD; PRT; 117 AA.

AC P06327;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region VH58 A1/A4 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=85099340; PubMed=2578321;  
 RA Yancopoulos G.D., Alt F.W.;  
 RT "Developmentally controlled and tissue-specific expression of  
 RL unexpressed VH gene segments."; Cell 40:271-281(1985).

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DR EMBL: M13787; AAA3849.1; -  
 DR PIR: A02029; HVMSA1.  
 DR HSSP: P01810; 2FBJ.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF00047; IG\_1.  
 DR SMART: SM00406; IG; 1.  
 DR PROSITE: PS50835; IG LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.  
 FT DOMAIN 20 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DISULFID 41 115 FRAMEWORK-3.  
 FT NON\_TER 117 117 BY SIMILARITY.  
 SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 65.3%; Score 340; DB 1; Length 117;  
 Best Local Similarity 62.2%; Pred. No. 1e-32;  
 Matches 61; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 1 QVQLQSATEVKKRPGASMKVSCMASGYPTSYDISWVROAPQGLEWVGMSAYNGNTY 60  
 DB 20 QVQLQSGPELVKPGALVKISCKASGYFTSYDINWVKRPGQGLEWIGVPGSGSTKY 79  
 QY 61 AOKFQGRVTMTTDSRRTAIMELSRSDPTAVYYCA 98  
 DB 80 NEKFKGKATLTADKSSSTAYMOLSSITSENSAVYFCAR 117

RESULT 5

HVLA\_HUMAN STANDARD; PRT; 117 AA.  
 AC P01742;

DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-1 region EU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE.  
 RX MEDLINE=71064024; PubMed=5489771;  
 RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
 RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino  
 RL acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; J.  
 RN Biochemistry 9:3161-3170(1970).  
 [2]

RP DISULFIDE BOND.  
 RX MEDLINE=71064027; PubMed=4923144;  
 RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.

RT Intrachain disulfide bonds";  
 RL Biochemistry 9:3168-3196(1970).  
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS  
 CC MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR: A90563; GHUED.  
 DR HSSP: P01772; 2FBJ.  
 DR GO: GO:0005576; Extracellular; NAS.  
 DR GO: GO:0003823; Antigen binding activity; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF00047; IG; 1.  
 DR SMART: SM00406; IG; 1.  
 DR PROSITE: PS50835; IG LIKE; 1.  
 DR Immunoglobulin V region; Pyrolydine carboxylic acid.  
 FT DOMAIN 1 112 IG-LIKE.  
 FT MOD\_RES 1 112 PYRROLIDONE CARBOXYLIC ACID.  
 FT DISULFID 22 96  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12472 MW; 99D60ADAE8D52818 CRC64;

Query Match 63.5%; Score 331; DB 1; Length 117;  
 Best Local Similarity 68.0%; Pred. No. 1.2e-31;  
 Matches 66; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

QY 1 QVQLQSATEVKKRPGASMKVSCMASGYPTSYDISWVROAPQGLEWVGMSAYNGNTY 60  
 DB 1 QVQLVQSGAEVKKRGGSSVSKVSCASGCTFSASAIWVROAPQGLEWVGIVPMFCPPNY 60  
 QY 61 AOKFQGRVTMTTDSRRTAIMELSRSDPTAVYYCA 97  
 DB 61 AOKFQGRVTMTTDSRRTAIMELSRSDPTAVYYCA 97

RESULT 6

HV00\_MOUSE STANDARD; PRT; 114 AA.  
 AC P01741;

DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region (Anti-arsenate antibody).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE.  
 RX MEDLINE=79195438; PubMed=109536;  
 RA Capra J.D., Nisonoff A.;  
 RT "Structural studies on induced antibodies with defined idiotypic  
 RT specificities. VII. The complete amino acid sequence of the heavy  
 RT chain variable region of anti-p-azophenylarsenate antibodies from A/J  
 RT mice bearing a cross-reactive idiotype."; J.  
 RL Immunol. 123:279-284(1979).  
 CC -1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF  
 CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V  
 CC REGION SEQUENCE.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR: A02022; GIMSAA.  
 DR HSSP: P01772; 2FBJ.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF00047; IG; 1.  
 DR SMART: SM00406; IG; 1.  
 DR PROSITE: PS50835; IG LIKE; 1.  
 DR Immunoglobulin V region.  
 FT DOMAIN 1 106 IG-LIKE.  
 FT NON\_TER 114 114

SEQUENCE 114 AA; 12555 MW; 99DB8F0B6A69F4BE CRC64;

Query Match  
Best Local Similarity 62.6%; Score 326; DB 1; Length 114;  
Matches 62; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

QY 1 QVQLQSATEVKKPKGASMKVSCASGYPTSYDISVNRQAPQGLEWGMISAVNGNTHY 60  
DB 1 EVQLQSGAEIVKAGSSVMSKCAIGYTTSTELTAVRQAPQGLELDGISSSSAYPNY 60  
QY 61 AOKFQGRVTMTDTSRTAYMELRSLSRSDTAIVYCAR 97  
DB 61 AOKFQGRVTITADESTINAYMELSLRSRSDTAIVYCAR 97

RESULT 7

HYV4\_MOUSE  
ID HYV4\_MOUSE STANDARD; PRT; 117 AA.  
AC P01758;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region 108A precursor.  
GN IGH-VJ558.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81245215; PubMed=6789211;  
RA Givol D., Zakut R., Eitron K., Rechavi G., Ram D., Cohen J.B.;  
RT "Diversity of germ-line immunoglobulin VH genes";  
RL Nature 292:426-430(1981).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
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CC  
CC EMBL: J00488; AAA38519.1; .  
CC PIR: A02041; HWS8A.  
CC HSSP: P01810; ZFBJ.  
CC MGD: MGI:96486; Igh-VJ558.  
CC InterPro: IPR007110; Ig-like.  
CC InterPro: IPR003006; Ig\_MHC.  
CC InterPro: IPR003596; Ig\_v.  
CC Pfam: PF00047; Ig; 1.  
CC SMART: SM00406; IGV; 1.  
CC PROSITE: PS50835; IG\_LIKE; 1.  
CC Immunoglobulin V region; Signal.  
CC SIGNAL 1 19  
CC CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.  
CC DOMAIN 20 >117 IG-LIKE.  
CC NON\_TER 117 117  
CC SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match  
Best Local Similarity 62.6%; Score 326; DB 1; Length 117;  
Matches 59; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 QVQLQSATEVKKPKGASMKVSCASGYPTSYDISVNRQAPQGLEWGMISAVNGNTHY 60  
DB 20 EVQLQSGAEIVKAGSSVMSKCAIGYTTSTELTAVRQAPQGLELDGISSSSAYPNY 60  
QY 61 AOKFQGRVTMTDTSRTAYMELRSLSRSDTAIVYCAR 98  
DB 80 NOKFKSKATLTVDNSSSTAYMELSLTSEDSAVYCAR 117

RESULT 8

HYV3\_MOUSE  
ID HYV3\_MOUSE STANDARD; PRT; 120 AA.  
AC P01747;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region 36-65.  
GN Mus musculus (Mouse)  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8131846; PubMed=6186498;  
RA Stekevitz M., Gelfer M.L., Brodeur P., Riblet R.,  
RA Marshak-Rothstein A.;  
RT "The genetic basis of antibody production: the dominant anti-arsenate  
RT idotype response of the strain A mouse";  
RL Eur. J. Immunol. 12:1023-1032(1982).  
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER  
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS  
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J  
CC SEGMENT. JH2.  
CC  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC  
CC HSSP: P01789; IMCP.  
CC InterPro: IPR007110; Ig-like.  
CC InterPro: IPR003006; Ig\_MHC.  
CC InterPro: IPR003596; Ig\_v.  
CC Pfam: PF00047; Ig; 1.  
CC SMART: SM00406; IGV; 1.  
CC PROSITE: PS50835; IG\_LIKE; 1.  
CC Immunoglobulin V region; Hybridoma.  
CC DOMAIN 1 111 IG-LIKE.  
CC NON\_TER 120 120  
CC SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match  
Best Local Similarity 60.8%; Score 326; DB 1; Length 120;  
Matches 59; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 2 VQLQSATEVKKPKGASMKVSCASGYPTSYDISVNRQAPQGLEWGMISAVNGNTHY 61  
DB 1 VQLQSGAEIVKAGSSVMSKCAIGYTTSTELTAVRQAPQGLELDGISSSSAYPNY 60  
QY 62 AOKFQGRVTMTDTSRTAYMELRSLSRSDTAIVYCAR 98  
DB 61 EKFKGKTLTVDKSSSTAYMELSLTSEDSAVYCAR 97

RESULT 9

HYV4\_MOUSE  
ID HYV4\_MOUSE STANDARD; PRT; 117 AA.  
AC P01748;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region 23 precursor.  
GN Mus musculus (Mouse).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6;  
RX MEDLINE=81234546; PubMed=6789376;  
RA Botwell A.L.M., Paakind M., Rech M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NpD family of  
RT antibodies: somatic mutation evident in a gamma 2a variable region";  
RL Cell 24:625-637(1981).  
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY

CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.  
 DR PIR: A02030; HWS23.  
 DR HSSP: P01810; 2FBJ.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG-LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.  
 FT DOMAIN 20 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON TER 117 117  
 SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;  
 Query Match 62.4%; Score 325; DB 1; Length 117;  
 Best Local Similarity 62.2%; Pred. No. 5.9e-31;  
 Matches 61; Conservative 15; Mismatches 22; Indels 0; Gaps 0;  
 QY 1 QVQLQSATEVKKRPGASMKVSCMASGYPTSDISWVROAPGGGLEWGMISAYNGNTY 60  
 DB 20 QVQLQPGTBLVKGASVSKSCASGYTFTSYMMHWKORPGGLEWIGINPNNGNTY 79  
 QY 61 AAKFGQVMTTDTSRRTAYMELRLSRSDTAVYYCAR 98  
 DB 80 NEKFKSKTTLVVDKSSSTAYTQLSSLTSEDSAVYYCAR 117  
 RESULT 10  
 ID HV02\_MOUSE STANDARD; PRT; 140 AA.  
 AC P01746;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region 93GT precursor.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A/7;  
 RX MEDLINE=82152818; PubMed=6801765;  
 RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,  
 RT "Somatic mutation in genes for the variable portion of the  
 immunoglobulin heavy chain.";  
 RT Science 216:309-311(1982).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC -----  
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 CC -----  
 CC EMBL: J00493; AAA8128.1; -  
 DR PIR: A94264; HYMSG7.  
 DR HSSP: P01810; 2FBJ.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV\_1.

DR PROSITE: PS50835; IG-LIKE; 1.  
 DR Immunoglobulin V region; Hyridoma; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93GT.  
 FT DOMAIN 20 139 IG-LIKE.  
 FT NON TER 140 140  
 SQ SEQUENCE 140 AA; 15514 MW; 25A4CB8E31DA5CE8 CRC64;  
 Query Match 62.2%; Score 324; DB 1; Length 140;  
 Best Local Similarity 59.2%; Pred. No. 9.5e-31;  
 Matches 58; Conservative 20; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 QVQLQSATEVKKRPGASMKVSCMASGYPTSDISWVROAPGGGLEWGMISAYNGNTY 60  
 DB 20 EVQLQDSAEELVKGASVSKSCASGYTFTSYGMHWKORPGGLEWIGINPNNGNTY 79  
 QY 61 AAKFGQVMTTDTSRRTAYMELRLSRSDTAVYYCAR 98  
 DB 80 NEKFKSKTTLVVDKSSSTAYTQLSSLTSEDSAVYYCAR 117  
 RESULT 11  
 ID HV09\_MOUSE STANDARD; PRT; 117 AA.  
 AC P01753; P11271;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region 186-1 precursor.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=81234548; PubMed=6788376;  
 RA Botchwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NPB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
 RT Cell 24:625-637(1981).  
 CC -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY  
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.  
 CC PIR: D90809; HWS61.  
 DR HSSP: P01810; 2FBJ.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV\_1.  
 DR PROSITE: PS50835; IG-LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.  
 FT DOMAIN 20 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON TER 117 117  
 SQ SEQUENCE 117 AA; 12890 MW; 16191A086CB17F5A CRC64;  
 Query Match 60.2%; Score 319; DB 1; Length 117;  
 Best Local Similarity 60.2%; Pred. No. 2.9e-30;  
 Matches 59; Conservative 15; Mismatches 24; Indels 0; Gaps 0;  
 QY 1 QVQLQSATEVKKRPGASMKVSCMASGYPTSDISWVROAPGGGLEWGMISAYNGNTY 60  
 DB 20 QVQLQPGTBLVKGASVSKSCASGYTFTSYMMHWKORPGGLEWIGINPNNGNTY 79  
 QY 61 AAKFGQVMTTDTSRRTAYMELRLSRSDTAVYYCAR 98



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OY 1 QVOLLQSAATEVKKPKGASMKVSCMASGYPTSYDISWVRQAPGGLWGWISAYNGNTHY 60
DB 1 QVOLLQPTTELVRKPGASVNLSCKASGTYFTSYMMHWRGQGLWGTGINSNGSTNY 60
OY 61 AQKFGQRTVMTTDSRTTAYMELRSLRSDDTAVYYCAR 98
DB 61 NEKRSKATLTVDKSSSTAYVQLSTPSEDSAVYYCAR 98

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OY 61 AQKFGQRTVMTTDSRTTAYMELRSLRSDDTAVYYCAR 98
DB 80 NQKFKDKA TLTVDKSSSTAYVQLSTPSEDSAVYYCAR 117

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Search completed: December 30, 2003, 10:55:49  
Job time : 5.25426 secs

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RESULT 15
HV05_MOUSE
ID HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig heavy chain V region 3 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botchwell A.L.M., Paskind M., Reich M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981)
CC -1 MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
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CC -----
DR EMBL; J00536; AAA38605.1; -
DR PIR; A02031; HVMS3.
DR HSSP; P01810; 2FBJ.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immuglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 19
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON TER 117
SQ SEQUENCE 117 AA; 13016 MM; 427C861C53975EDC CRC64;

```

Query Match 60.1%; Score 313; DB 1; Length 117;  
Best Local Similarity 59.2%; Pred. No. 1.5e-29;  
Matches 58; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

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OY 1 QVOLLQSAATEVKKPKGASMKVSCMASGYPTSYDISWVRQAPGGLWGWISAYNGNTHY 60
DB 20 QVOLLQPGALVLRGSSVSKASGTYFTSYMMHWRGQGLWGTGINSNGSTNY 79

```



Db 1 EVOLVESGAEEVKKPGASVAVSCASGYTFTGYMHWROAPGQGLEWGMWINSNGTNY 60  
 QY 61 AOKFGQGVMTTDTSRRTAYMELRSRSDDTAVYYCAR 98  
 DB 61 AOKFGQGVMTTDTSRRTAYMELRSRSDDTAVYYCAR 98

## RESULT 2

Q9UL94 PRELIMINARY; PRT; 119 AA.

AC Q9UL94; 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN 1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL: AF035020; AAD56258.1; -.  
 DR HSSP; P01810; 2PB4.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 FT NON-TER 1  
 FT 119  
 SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345FA16E CRC64;

Query Match 73.7%; Score 384; DB 4; Length 119;  
 Best Local Similarity 73.5%; Pred. No. 8.9e-35;  
 Matches 72; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVQLQSATEYVKKPGASMKVSCMASGYPTFTSYDISWVROAPGQGLEWGMWINSNGTNY 60  
 DB 1 EVOLVESGAEEVKKPGASVAVSCASGYTFTGYMHWROAPGQGLEWGMWINSNGTNY 60  
 QY 61 AOKFGQGVMTTDTSRRTAYMELRSRSDDTAVYYCAR 98  
 DB 61 AOKFGQGVMTTDTSRRTAYMELRSRSDDTAVYYCAR 98

## RESULT 3

Q9BRV0 PRELIMINARY; PRT; 500 AA.

AC Q9BRV0; 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN 1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RA Strausberg R.;  
 RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC005951; AA05951.1; -.  
 DR HSSP; P01789; IMCP.  
 DR InterPro; IPR07110; Ig-like.

DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR Hypothetical protein.  
 SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 73.3%; Score 382; DB 4; Length 500;  
 Best Local Similarity 72.4%; Pred. No. 8.2e-34;  
 Matches 71; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 QVQLQSATEYVKKPGASMKVSCMASGYPTFTSYDISWVROAPGQGLEWGMWINSNGTNY 60  
 DB 20 QVQLVSGAEVMSPGASVAVSCKTSGYAHTYSLIMVWROAPGQGLEWGMWINSNGTNY 79  
 QY 61 AOKFGQGVMTTDTSRRTAYMELRSRSDDTAVYYCAR 98  
 DB 80 AOKFGQGVMTTDTSRRTAYMELRSRSDDTAVYYCAR 117

## RESULT 4

Q9UL92 PRELIMINARY; PRT; 124 AA.

AC Q9UL92; 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN 1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL: AF035022; AAD56258.1; -.  
 DR HSSP; P01772; 2PB4.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 FT NON-TER 1  
 FT 124  
 SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 72.6%; Score 378; DB 4; Length 124;  
 Best Local Similarity 73.5%; Pred. No. 4.3e-34;  
 Matches 72; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVQLQSATEYVKKPGASMKVSCMASGYPTFTSYDISWVROAPGQGLEWGMWINSNGTNY 60  
 DB 1 EVOLVESGAEEVKKPGASVAVSCASGYTFTGYMHWROAPGQGLEWGMWINSNGTNY 60  
 QY 61 AOKFGQGVMTTDTSRRTAYMELRSRSDDTAVYYCAR 98  
 DB 61 AOKFGQGVMTTDTSRRTAYMELRSRSDDTAVYYCAR 98

## RESULT 5

Q96GAG PRELIMINARY; PRT; 614 AA.

ID Q96GAG  
 AC Q96GAG;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)



DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DB 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RA Strauberg R.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC009851; AAK09851.1; -  
DR InterPro; IPR000005; HTHARC.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00041; HTH\_ARAC\_FAMILY\_1; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KM Hypothetical protein.  
SQ SEQUENCE 614 AA; 67921 MW; 558F536E77AA9BBB CRC64;  
  
Query Match 71.2%; Score 371; DB 4; Length 614;  
Best Local Similarity 70.4%; Pred. No. 1.7e-32;  
Matches 69; Conservative 12; Mismatches 17; Indels 0; Gaps 0;  
  
QY 1 QVQLLOSATEYVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWVGMISAYNGNTHY 60  
DB 20 QVQLVSGAEVKKRQGSFSSVCSKASGYTFTYTLKVRQAPQALEMGMITPFGNINNY 79  
61 AOKFGQRYVTMTDTSRRTAYMELSLRSDDTAVYYCAR 98  
80 AOKFQDRVITITDRSMTATYMLSLRSEDYAVYYCAR 117  
DB  
  
RESULT 6  
Q96QSO PRELIMINARY; PRT; 159 AA.  
ID 096QSO  
AC 096QSO;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DB 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DE Putative matrix cell adhesion molecule-3.  
DE Putative matrix cell adhesion molecule-3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA Tilson M.D.;  
RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3  
mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3)."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY039025; AAK82649.1; -  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;  
  
Query Match 69.7%; Score 363; DB 4; Length 159;  
Best Local Similarity 69.4%; Pred. No. 2.6e-32;  
Matches 68; Conservative 13; Mismatches 17; Indels 0; Gaps 0;  
  
QY 1 QVQLLOSATEYVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWVGMISAYNGNTHY 60  
DB 20 QVQLVSGAEVKKRQGSFSSVCSKASGYTFTSNNYMNVRQAPGQGPWMGVINPSGGSARY 79

QY 61 AOKFGQRYVTMTDTSRRTAYMELSLRSDDTAVYYCAR 98  
DB 80 AOKFQDRVITITDRSMTATYMLSLRSEDYAVYYCAR 117  
DB  
  
RESULT 7  
Q9GYZ2 PRELIMINARY; PRT; 119 AA.  
ID 09GYZ2  
AC 09GYZ2;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DB 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region  
DE (Fragment).  
OS Schistosoma japonicum (Blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigidae;  
OC Schistosomatoidea; Schistosomatidae; Schistosoma.  
OX NCBI\_TaxID=6182;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA Song X.T., Feng Z.O., Guan X.H.;  
RT "Amplification, cloning and sequence analysis of the heavy chain  
variable region gene of monoclonal anti-idiotypic antibody NP30 of  
Schistosoma japonicum."  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF282622; AAG01452.1; -  
DR HSP; P01772; 2PB4.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT 119 119  
SQ SEQUENCE 119 AA; 13567 MW; BA893873FDSFA6AB CRC64;  
  
Query Match 68.7%; Score 358; DB 5; Length 119;  
Best Local Similarity 68.4%; Pred. No. 6.7e-32;  
Matches 67; Conservative 14; Mismatches 17; Indels 0; Gaps 0;  
  
QY 1 QVQLLOSATEYVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWVGMISAYNGNTHY 60  
DB 1 QVQLVSGAEVKKRQGSFSSVCSKASGYTFTGYNNVRQAPGQGLEWVGMISAYNGNTHY 60  
61 AOKFGQRYVTMTDTSRRTAYMELSLRSDDTAVYYCAR 98  
61 AOKFQDRVITITDRSMTATYMLSLRSDDTAVYYCAR 98  
DB  
  
RESULT 8  
Q8WY24 PRELIMINARY; PRT; 497 AA.  
ID 08WY24  
AC 08WY24;  
DT 01-MAR-2002 (Tremblrel. 20, Created)  
DB 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
DE SMC6, a protein.  
DE SMC6 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA Zheng S., Shao X., Cao J., Geng L., Pang Y., Dong Q.;  
RT "Identification and characterization of SMC6, a Ig-like gene which is  
down-regulated in colorectal cancer."  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF283666; AAL36987.1; -  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig; 4.

DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR NCBI; PS00290; IG\_MHC; 1.  
SO SEQUENCE 497 AA; 5365 MW; F24D08DFA5A63E5 CRC64;

Query Match  
Best Local Similarity 68.5%; Score 357; DB 4; Length 497;  
Matches 65; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

Qy 1 QVQLQSATEVKKPGASKVKSCMASGYPTSYDISWVRQAPGQGLEWVGMISAVNGNTHY 60  
Db 20 QGELQSQSGAEVTKPKASVAVSCASGYTFIADINWVRQAPGQGLEWVGWNPQTGNTF 79  
Qy 61 AQKFGRYMTTDSRTAYMELRLSDDTAVYYCA 98  
Db 80 AQKFGRLTFSDTISINIAVMYLSLSTEDSHYFCAR 117

## RESULT 9

Q9UL89 PRELIMINARY; PRT; 116 AA.  
AC Q9UL89;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
DE Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalls N.N., Berney S.M.,  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."  
RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
RL EMBL; AF035025; AAD56261.1; -.  
DR HSSP; P01810; 2FBJ.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON TER 1  
FT NON TER 116  
SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

Query Match  
Best Local Similarity 72.0%; Score 340; DB 4; Length 116;  
Matches 67; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy 5 LOSATEVKKPGASKVKSCMASGYPTSYDISWVRQAPGQGLEWVGMISAVNGNTHY 64  
Db 1 VQSGAEVKKKSSSVKSCASGGTFSYALSWVRQAPGQGLEWVGRIIPILGIANVYAKKF 60  
Qy 65 QGRVMTTDSRTAYMELRLSDDTAVYYCA 97  
Db 61 QGRVTTADKSTSTAYMELSLSEDTAVYYCA 93

## RESULT 10

Q925S3 PRELIMINARY; PRT; 147 AA.  
AC Q925S3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE MRP3  
SO Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN (1)

RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX PubMed=1181679;  
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,  
SU C.;  
RT "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice."  
RT World J. Gastroenterol. 6:709-717(2000).  
RN (2)

RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Cui D., Zeng G., Yan X., Li X., Su C.;  
RT "Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain."  
RT Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
RL EMBL; AF240166; AAK43731.1; -.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

Query Match  
Best Local Similarity 64.7%; Score 337; DB 11; Length 147;  
Matches 63; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

Qy 1 QVQLQSATEVKKPGASKVKSCMASGYPTSYDISWVRQAPGQGLEWVGMISAVNGNTHY 60  
Db 3 QVQLHQSPEVVKPKASVKLSCKASGYFTSYDIDWVRQGTGQGLEWIGMIFPEGSTEV 62  
Qy 61 AQKFGRYMTTDSRTAYMELRLSDDTAVYYCA 98  
Db 63 NEKFGKATLSVDSSSTAYMELRLTSEDSAVYFCAR 100

## RESULT 11

Q91WT1 PRELIMINARY; PRT; 481 AA.  
AC Q91WT1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical 52.1 kDa protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN (1)

RP SEQUENCE FROM N.A.  
RC TISSUE=Colon;  
RA Straubeberg R.;  
RL Submitted (SRP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC013480; AAH13490.1; -.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KM Hypothetical protein.  
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match  
Best Local Similarity 64.3%; Score 335; DB 11; Length 481;  
Matches 62; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

QY 1 QVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVRQAPQGQGLEWYGMISAVYNGNTHY 60  
 Db 20 QVQLQSGPELVKPKASVSKISCKASGYFTSYIHMMVGRPGQGLWIGMILPPDGNTRY 79  
 QY 61 AOKFGQRYVTMTDTSRRRTAYMELRLSRSDDTAVYYCAR 98  
 Db 80 NEKFKGKATLTVDKSSSTAYMFLSLTSEDSAVYFCTR 117

## RESULT 12

QY298 PRELIMINARY: PRT; 150 AA.  
 AC QY298:

DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE IGG VH protein precursor (fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98322155; PubMed=9657749;  
 RA Jacquemin M.G., Vander Elst L.P.U.,  
 RT "Mechanism and kinetics of factor VIII inactivation: study with an  
 RT IGG4 monoclonal antibody derived from a hemophilia A patient with  
 RT inhibitor."  
 RL Blood 92:496-506 (1998).  
 DR EMBL; AJ224083; CAA11829.1; -.  
 DR HSSP; P01772; 2PB4.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT SIGNAL.  
 FT NON\_TER  
 FT SIGNAL.  
 FT NON\_TER  
 SQ SEQUENCE 150 AA; 16031 MW; 563D164AB2280ZDS CRC64;

Query Match 64.1%; Score 334; DB 4; Length 150;  
 Best Local Similarity 67.0%; Pred. No. 4e-29;  
 Matches 65; Conservative 8; Mismatches 24; Indels 0; Gaps 0;

QY 1 QVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVRQAPQGQGLEWYGMISAVYNGNTHY 60  
 Db 20 QVQLQSGPELVKPKASVSKISCKASGYFTSYIHMMVGRPGQGLWIGMILPPDGNTRY 79  
 QY 61 AOKFGQRYVTMTDTSRRRTAYMELRLSRSDDTAVYYCAR 97  
 Db 80 NEKFKGKATLTVDKSSSTAYMFLSLTSEDSAVYFCTR 116

## RESULT 13

QY298 PRELIMINARY: PRT; 480 AA.  
 AC QY298:

DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Similar to expressed sequence A1893585.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Breast tumor;  
 RA Strauberg R.;

RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC029188; AAH29188.1; -.  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003597; IG-cl.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 4.  
 DR SMART; SM00409; IGV; 3.  
 DR SMART; SM00407; IGV; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 4.  
 DR PROSITE; PSS0290; IG\_MHC; 2.  
 SQ SEQUENCE 480 AA; 51645 MW; 8690A63C669CDBED CRC64;

Query Match 63.5%; Score 331; DB 11; Length 480;  
 Best Local Similarity 60.2%; Pred. No. 3.4e-28;  
 Matches 59; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

QY 1 QVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVRQAPQGQGLEWYGMISAVYNGNTHY 60  
 Db 20 QVQLQSGPELVKPKASVSKISCKASGYFTSYIHMMVGRPGQGLWIGMILPPDGNTRY 79  
 QY 61 AOKFGQRYVTMTDTSRRRTAYMELRLSRSDDTAVYYCAR 98  
 Db 80 NEKFKGKATLTVDKSSSTAYMFLSLTSEDSAVYFCTR 117

## RESULT 14

QY298 PRELIMINARY: PRT; 123 AA.  
 AC QY298:

DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Anti-DNA heavy chain (fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C3H/HeJ-Ipr; PubMed=8814271;  
 RA Wlodek M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gilkerson G.S.;  
 RT "Differences in V kappa gene utilization and VH CDR3 sequence among  
 RT anti-DNA from C3H-Ipr mice and lupus mice with nephritis."  
 RL Eur. J. Immunol. 26:2225-2233 (1996).  
 DR EMBL; U59154; AAB02916.1; -.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam; PF00047; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT NON\_TER  
 FT NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 123 AA; 13806 MW; CC0037A806E9911B CRC64;

Query Match 63.3%; Score 330; DB 11; Length 123;  
 Best Local Similarity 60.2%; Pred. No. 8.6e-29;  
 Matches 59; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY 1 QVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVRQAPQGQGLEWYGMISAVYNGNTHY 60  
 Db 1 EQQLQSGPELVKPKASVSKISCKASGYFTSYIHMMVGRPGQGLWIGMILPPDGNTRY 60  
 QY 61 AOKFGQRYVTMTDTSRRRTAYMELRLSRSDDTAVYYCAR 98  
 Db 61 SOKFKGKATLTVDKSSSTAYMFLSLTSEDSAVYFCTR 98

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RESULT 15
O9DBL4      PRELIMINARY;      PRT;      473 AA.
AC      O9DBL4;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      1810060009RIK protein.
GN      IGH-1 OR 1810060009RIK.
OS      Mus musculus (mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Pancreas;
RX      MEDLINE=21085660; PubMed=11217851;
RA      Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA      Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleisemann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA      Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA      Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA      Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaudo M.F.,
RA      Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Guenichon S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA      Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
RA      Wyshaw-Boris A., Yoshida K., Haegawa Y., Kawaji H., Kohzuki S.,
RA      Hayashizaki Y.;
RT      "Functional annotation of a full-length mouse cDNA collection.";
RL      Nature 409:685-690(2001).
DR      EMBL; AK007918; BAB25349.1; -.
DR      HSSP; P01842; 7PAB.
DR      MGD; MGI:96443; Igh-1.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; Ig; 4.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PSS0835; IG_LIKE; 4.
DR      PROSITE; PS00290; IG_MHC; 1.
DR      PROSITE; PS00290; IG_MHC; 1.
SQ      SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

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Query Match      63.3%; Score 330; DB 11; Length 473;
Best Local Similarity 61.2%; Pred. No. 4,3e-28;
Matches 60; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

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OY      1 QVOLLGATEVKKPKGASMKVSCMASGYPTSYDISWVRQAPGQGLEWVGWISAYNGNTHY 60
      |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB      20 QVQLKQSGAELVKGASVKISCKASGYFTDYINWVKRPGQGLEWIGKIGPGSGSTYY 79
      |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
OY      61 AQKQGRVMTTDTSRRTAYMELSLRSDPTAVYYCAR 98
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB      80 NEKFKGKATLTADKSSSTAYWQLSLTSEDSAVYFCAR 117
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

```

Search completed: December 30, 2003, 11:01:02  
 Job time : 23.883 secs



DT 25-FEB-2003 (first entry)  
 XX  
 DE Human liver peptide, SEQ ID No 34543.  
 XX  
 KM Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
 KM hypercholesterolaemia; coronary heart disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157273-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00664.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2001-488898/53.  
 DR  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for  
 PT analysing gene expression in human adult liver -  
 XX  
 PS Claim 27; SEQ ID No 34543; 658pp; English.  
 XX  
 CC The invention relates to a single exon nucleic acid probe (SENP) (I) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver, comprising one of 13109 defined nucleotide sequences given in the  
 CC specification (or complements/fragments). The probe hybridises at high  
 CC stringency to a nucleic acid molecule expressed in the human adult  
 CC liver. (I) may be used for predicting, measuring and displaying gene  
 CC expression in samples derived from human adult liver. The genes  
 CC identified may be involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which  
 CC is associated with coronary heart disease. AB047348-AB059930 represent  
 CC human liver single exon encoded peptides of the invention.  
 CC Note: The sequence information for this patent does not appear in the  
 CC printed specification but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SQ Sequence 104 AA;  
 XX  
 Query Match 87.5%; Score 456; DB 22; Length 104;  
 Best Local Similarity 87.8%; Pred. No. 2.2e-39;  
 Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 XX  
 QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWVRQAPGQGLEWVGWISAYNGNTYH 60  
 DB 4 QVQLVQSGAEVKKPGASVKVSCKASGTTFTSYGISWVRQAPGQGLEWVGWISAYNGNTYH 63  
 QY 61 AOKFGQRYVTMTTDSRTATYMELRSLRSDDTAVYYCAR 98  
 DB 64 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 101  
 XX  
 RESULT 13  
 ABB40538  
 ID ABB40538 standard; Peptide; 104 AA.  
 XX  
 AC ABB40538;  
 XX  
 DT 04-FEB-2002 (first entry)  
 XX  
 DE Peptide #8044 encoded by human foetal liver single exon probe.

XX  
 KM Human; foetal liver; gene expression; single exon nucleic acid probe.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157277-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00669.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2001-483447/52.  
 DR  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for  
 PT analysing gene expression in human fetal liver -  
 XX  
 PS Claim 27; SEQ ID NO 33173; 639pp + sequence listing; English.  
 XX  
 CC The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal  
 CC liver. The single exon nucleic acid probes may be used for predicting,  
 CC measuring and displaying gene expression in samples derived from human  
 CC fetal liver. The present sequence is a peptide encoded by a single exon  
 CC nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SQ Sequence 104 AA;  
 XX  
 Query Match 87.5%; Score 456; DB 22; Length 104;  
 Best Local Similarity 87.8%; Pred. No. 2.2e-39;  
 Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
 XX  
 QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWVRQAPGQGLEWVGWISAYNGNTYH 60  
 DB 4 QVQLVQSGAEVKKPGASVKVSCKASGTTFTSYGISWVRQAPGQGLEWVGWISAYNGNTYH 63  
 QY 61 AOKFGQRYVTMTTDSRTATYMELRSLRSDDTAVYYCAR 98  
 DB 64 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 101  
 XX  
 RESULT 14  
 AAR66311  
 ID AAR66311 standard; Protein; 117 AA.  
 XX  
 AC AAR66311;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 03-AUG-1995 (first entry)  
 XX  
 DE Human immunoglobulin variable heavy chain #17.  
 XX  
 KM Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;  
 KM cosmid; placenta; vector; pJB81; E.coli; mammalian.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9426895-A1.  
 XX

XX Human antibody fragment #46.  
DE XX

XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
KM metastasis; hypervariable region; autoimmune disease; thrombosis;  
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
KM myocardial infarction; retinopathic disease; abnormal platelet function;  
XX sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.

PN WO200253700-A2.

PD 11-JUL-2002.

PF 31-DEC-2001; 2001WO-US49442.

PR 29-DEC-2000; 2000US-258948P.

PR 29-DEC-2000; 2000US-0751181.

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX WPI; 2002-674776/72.

DR Novel isolated epitope present on cancer cells and important in

PT physiological phenomena such as cell rolling, metastasis and

PT inflammation, for treating autoimmune, inflammatory or cardiovascular

PT diseases, and cancer -

PS Disclosure; Page 246-247; 310pp; English.

XX The invention relates to an isolated epitope present on cancer cells and  
CC important in physiological phenomena such as cell rolling, metastasis and  
CC inflammation, where the epitope is capable of being bound by an antibody,  
CC its antigen-binding fragment or its complex comprising at least one  
CC antibody or its binding fragment having a first hypervariable region. The  
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,  
CC platelet-platelet and/or cell-platelet adhesion or aggregation, for  
CC increasing mortality of tumour or leukaemia cells, for increasing the  
CC susceptibility of diseased cells to damage by anti-disease, anti-cancer  
CC or anti-leukaemia agents, or for decreasing the number of tumour or  
CC leukaemia cells in a patient, or in the manufacture of a medicament for  
CC treating diseases such as cancer, leukaemia, autoimmune diseases, and  
CC inflammatory diseases, cardiovascular diseases and other diseases mediated by abnormal  
CC infection, retinopathic diseases and other diseases mediated by abnormal  
CC platelet function and diseases caused by sulphated tyrosine-dependent  
CC protein-protein interactions. This sequence represents a human antibody  
CC fragment of the invention.

XX Sequence 98 AA;

Query Match 87.5%; Score 456; DB 23; Length 98;

Best Local Similarity 87.8%; Pred. No. 2e-39;

Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLLGATATEVKKFGASMKVSCNAGYPTSYDISWVRQAPGGGLEWVGWISAYNGNTY 60  
Db 1 QVOLLGATATEVKKFGASMKVSCNAGYPTSYDISWVRQAPGGGLEWVGWISAYNGNTY 60  
QY 61 AOKFQGRVTMTTDTSTSRITAYMEILRSRSDTAVYYCAR 98  
Db 61 AOKFQGRVTMTTDTSTSRITAYMEILRSRSDTAVYYCAR 98  
61 AOKLQGRVTMTTDTSTSRITAYMEILRSRSDTAVYYCAR 98

RESULT 11  
ABG78171

ID ABG78171 standard; Protein; 98 AA.

XX ABG78171;

XX 15-NOV-2002 (first entry)

XX Human Fv molecule hypervariable region related peptide #46.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytosolic;

KM disulfide Fv; defv; scfv; cancer; carcinoma; sarcoma; leukaemia; adenoma;

KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX Homo sapiens.

PN WO200259264-A2.

PD 01-AUG-2002.

PF 31-DEC-2001; 2001WO-US49440.

PR 29-DEC-2000; 2000US-0751181.

PI (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

XX Plaksin D, Peretz T;

XX WPI; 2002-619166/66.

DR Novel peptide/polypeptide for cancer therapy has Fv molecule, construct

PT or fragment, or construct of fragment with enhanced binding

PT characteristics so as to selectively bind target cell in favour of other

PT cells -

XX Claim 13; Page 169; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv  
CC molecule, a construct or fragments or a construct of a fragment with  
CC enhanced binding characteristics which selectively and/or specifically  
CC binds to a target cell in favour of other cells, where binding is  
CC primarily determined by a first hypervariable region and Fv is a single  
CC chain Fv (scfv) or a disulfide Fv (defv). The peptide, optionally in  
CC association with or attached, coupled, combined, linked or fused to a  
CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
CC the medicament has activity against a diseased cell, preferably a cancer  
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
CC composition for use in inhibiting the growth of a diseased or cancer  
CC cell. This sequence represents a human Fv molecule hypervariable region  
CC related peptide of the invention.

XX Sequence 98 AA;

Query Match 87.5%; Score 456; DB 23; Length 98;

Best Local Similarity 87.8%; Pred. No. 2e-39;

Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLLGATATEVKKFGASMKVSCNAGYPTSYDISWVRQAPGGGLEWVGWISAYNGNTY 60  
Db 1 QVOLLGATATEVKKFGASMKVSCNAGYPTSYDISWVRQAPGGGLEWVGWISAYNGNTY 60  
QY 61 AOKFQGRVTMTTDTSTSRITAYMEILRSRSDTAVYYCAR 98  
Db 61 AOKFQGRVTMTTDTSTSRITAYMEILRSRSDTAVYYCAR 98  
61 AOKLQGRVTMTTDTSTSRITAYMEILRSRSDTAVYYCAR 98

RESULT 12  
ABG55895  
ID ABG55895 standard; Peptide; 104 AA.  
XX ABG55895;  
XX

RESULT 8  
ABP45584  
ID ABP45584 standard; Protein; 250 AA.  
XX  
AC ABP45584;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human BlyS binding scFv SEQ ID 1595.  
XX  
KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US19110.  
XX  
PR 16-JUN-2000; 2000US-212210P.  
XX  
PR 17-OCT-2000; 2000US-240816P.  
XX  
PR 16-MAR-2001; 2001US-276248P.  
XX  
PR 21-MAR-2001; 2001US-277379P.  
XX  
PR 25-MAY-2001; 2001US-293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX  
DR WPI; 2002-114799/15.  
XX  
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for  
PT the diagnosis and treatment of cancers and immune disorders -  
XX  
PS Claim 1; Page 2306-2307; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS  
CC and so may be used to detect and quantitate the presence of BlyS in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of BlyS. They may also be  
CC administered to treat diseases associated with aberrant BlyS expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, and  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method  
XX  
SQ Sequence 250 AA;  
XX  
Query Match 88.3%; Score 460; DB 23; Length 250;  
Best Local Similarity 88.8%; Pred. No. 2.2e-39;  
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 QVOLLQSATVKKPKGASMKVSCMASGYPTSTSYDISWVRQAPQGLQEMWGMISAVNGNTY 60  
DB 1 QVOLLQSAEAEVKKPKGASVSVCKASGYTTSTSYDISWVRQAPQGLQEMWGMISAVNGNTY 60

OY 61 AOKFQGRVTMTTDSRRTAYMELRSLSRSDDTAVYYCAR 98  
DB 61 AOKLQGRVTMTTDTISTATYMELSRLSRSDDTAVYYCAR 98

RESULT 9  
AAV50952  
ID AAV50952 standard; Protein; 98 AA.  
XX  
AC AAV50952;  
XX  
DT 23-MAR-2000 (first entry)  
XX  
DE Human anti-factor VIII antibody VH clone DP-14 protein #2.  
XX  
KW Human; heavy chain; antibody; factor VIII; hemostatic;  
KW hemophilia A; VH gene.  
XX  
OS Homo sapiens.  
XX  
PN WO958680-A2.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-NL00285.  
XX  
PR 08-MAY-1998; 98EP-0201543.  
XX  
PA (SANO-) STICHTING SANQUIN BLOEDVOORZINNING.  
XX  
PI Voorberg JJ, Van Den Brink EN, Turenhout EM;  
XX  
DR WPI; 2000-053102/04.  
XX  
PT New polynucleotide, polypeptide and antibody useful for diagnosing the  
PT presence of neutralizing antibodies against factor VIII and for  
PT treatment of hemophilia A patients with these antibodies -  
XX  
PS Example 4; Fig 4B; 61pp; English.  
XX  
CC This invention describes a novel polynucleotide (I) (and complements and  
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence  
CC coding for a human antibody with factor VIII specificity which has  
CC hemostatic activity. (I) is useful a primer or probe for detecting the  
CC presence of inhibitory antibodies directed against factor VIII. The  
CC polypeptides of the invention and the antibodies generated from them  
CC are useful in compositions for neutralizing factor VIII inhibiting  
CC anti-factor VIII antibody clone DP-14 protein which is used in the method  
CC of the invention.  
XX  
SQ Sequence 98 AA;  
XX  
Query Match 87.5%; Score 456; DB 21; Length 98;  
Best Local Similarity 87.8%; Pred. No. 2e-39;  
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 1 QVOLLQSATVKKPKGASMKVSCMASGYPTSTSYDISWVRQAPQGLQEMWGMISAVNGNTY 60  
DB 1 QVOLLQSAEAEVKKPKGASVSVCKASGYTTSTSYDISWVRQAPQGLQEMWGMISAVNGNTY 60

OY 61 AOKFQGRVTMTTDSRRTAYMELRSLSRSDDTAVYYCAR 98  
DB 61 AOKLQGRVTMTTDTISTATYMELSRLSRSDDTAVYYCAR 98

RESULT 10  
ABG91862  
ID ABG91862 standard; Protein; 98 AA.  
XX  
AC ABG91862;  
XX  
DT 04-DEC-2002 (first entry)



AC ABP45549;  
 XX  
 DT 19-AUG-2002 (first entry)  
 DE Human Blys binding scFv SEQ ID 1560.  
 XX  
 XX Blys: B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
 OS Homo sapiens.  
 XX  
 XX MO200202641-A1.  
 PN 10-JAN-2002.  
 PD 15-JUN-2001; 2001WO-US19110.  
 XX  
 XX 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX WPI; 2002-114799/15.  
 DR  
 XX  
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 XX  
 XX Claim 1; Page 2264-2265; 3148pp; English.  
 XX  
 XX This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX  
 SQ Sequence 250 AA;  
 Query Match 88.9%; Score 463; DB 23; Length 250;  
 Best Local Similarity 89.8%; Pred. No. 1,1e-39;  
 Matches 88; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 QVOLLQSATVEVKKPGASMKVSCMASGYPTFTSYDISWVROAPGQGLEWVGMSIAYNGNTHY 60  
 DB 1 QVOLLQSAEAEVKKPGASVKVSCKASGYTFTSYGISWVROAPGQGLEWVGMSIAYNGNTHY 60  
 QY 61 AOKFOGRTVMTTDTSTRTAYMELRSLSDDTAYYYCAR 98  
 DB 61 AOKLQGRVTMTTDTSTRTAYMELRSLSDDTAYYYCAR 98  
 RESULT 7

ABP45727  
 ID ABP45727 standard; Protein; 251 AA.  
 XX  
 AC ABP45727;  
 XX  
 DT 19-AUG-2002 (first entry)  
 DE Human Blys binding scFv SEQ ID 1738.  
 XX  
 XX Blys: B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
 OS Homo sapiens.  
 XX  
 XX MO200202641-A1.  
 PN 10-JAN-2002.  
 PD 15-JUN-2001; 2001WO-US19110.  
 XX  
 XX 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX WPI; 2002-114799/15.  
 DR  
 XX  
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 XX  
 XX Claim 1; Page 2476-2477; 3148pp; English.  
 XX  
 XX This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX  
 SQ Sequence 251 AA;  
 Query Match 88.9%; Score 463; DB 23; Length 251;  
 Best Local Similarity 88.8%; Pred. No. 1,1e-39;  
 Matches 87; Conservative 3; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 QVOLLQSATVEVKKPGASMKVSCMASGYPTFTSYDISWVROAPGQGLEWVGMSIAYNGNTHY 60  
 DB 1 QVOLLQSAEAEVKKPGASVKVSCKASGYTFTSYGISWVROAPGQGLEWVGMSIAYNGNTHY 60  
 QY 61 AOKFOGRTVMTTDTSTRTAYMELRSLSDDTAYYYCAR 98  
 DB 61 AOKLQGRVTMTTDTSTRTAYMELRSLSDDTAYYYCAR 98

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OY      61 AOKFOGRVTMTTDSRTAYMELSLRSDPTAVYYCAR 98
      |||
      61 AOKFOGRVTMTTDSRTAYMELSLRSDPTAVYYCAR 98
DB
RESULT 4
AA50955
ID      AA50955 standard; Protein; 98 AA.
XX
AC      AA50955;
XX
DT      23-MAR-2000 (first entry)
XX
DE      Human anti-factor VIII antibody VH protein VH EL-25.
XX
KM      Human; heavy chain; antibody; factor VIII; hemostatic;
KM      hemophilia A; VH protein.
XX
OS      Homo sapiens.
XX
PN      MO958680-A2.
XX
PD      18-NOV-1999.
XX
PF      07-MAY-1999; 99MO-NL00285.
XX
PR      08-MAY-1998; 98EP-0201543.
PA      (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
PI      Voorberg JJ, Van Den Brink EN, Turenhout EM;
DR      WPI; 2000-053102/04.
XX
PT      New polynucleotide, polypeptide and antibody useful for diagnosing the
PT      presence of neutralizing antibodies against factor VIII and for
PT      treatment of hemophilia A patients with these antibodies -
XX
PS      Example 4; Fig 4B; 61pp; English.
XX
CC      This invention describes a novel polynucleotide (I) (and complements and
CC      hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC      coding for a human antibody with factor VIII specificity which has
CC      hemostatic activity. (I) is useful a primer or probe for detecting the
CC      presence of inhibitory antibodies directed against factor VIII. The
CC      polypeptides of the invention and the antibodies generated from them
CC      are useful in compositions for neutralizing factor VIII inhibiting
CC      antibodies in hemophilia A patients. This sequence represents the human
CC      anti-factor VIII antibody VH EL-25 protein which is used in the method
CC      of the invention.
XX
SQ      Sequence 98 AA;
XX
Query Match      90.0%; Score 469; DB 21; Length 98;
Best Local Similarity 89.8%; Pred. No. 9,4e-41;
Matches 88; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
OY      1 QVOLLQSATBVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWVGISAYNGNTNY 60
      |||
      1 QVOLLQSAAEVRKPGASVSKVSCKASGYPTFSYDISWVRQAPGQGLEWVGISAYNGNTDY 60
DB
OY      61 AOKFOGRVTMTTDSRTAYMELSLRSDPTAVYYCAR 98
      |||
      61 AOKFOGRVTMTTDSRTAYMELSLRSDPTAVYYCAR 98
DB
RESULT 5
ABP45105
ID      ABP45105 standard; Protein; 247 AA.
XX
AC      ABP45105;
XX
DT      19-AUG-2002 (first entry)

```

```

XX      XX
DE      Human Blys binding scFv SEQ ID 1116.
XX
KM      Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM      tumour necrosis factor; B cell proliferation; B cell differentiation;
KM      immunosuppressive; immunostimulant; immunomodulator; antirheumatic;
KM      antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM      systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM      common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS      Homo sapiens.
XX
PN      WO200202641-A1.
XX
PD      10-JAN-2002.
XX
PF      15-JUN-2001; 2001MO-US19110.
XX
PR      16-JUN-2000; 2000US-212210P.
PR      17-OCT-2000; 2000US-240816P.
PR      16-MAR-2001; 2001US-276248P.
PR      21-MAR-2001; 2001US-277379P.
PR      25-MAY-2001; 2001US-293499P.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
PA      (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI      Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
DR      WPI; 2002-114799/15.
XX
PT      Antibodies against B lymphocyte stimulating polypeptides, useful for
PT      the diagnosis and treatment of cancers and immune disorders -
XX
PS      Claim 1; Page 1734-1735; 3148pp; English.
XX
CC      This invention describes novel antibodies that immunospecifically bind to
CC      B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC      tumour necrosis factor (TNF) super family and induces B cell
CC      proliferation and differentiation. The antibodies of the invention have
CC      cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC      antirheumatic and antiAIDS activity and can be used in vaccines to
CC      inhibit the expression and activity of Blys. The antibodies bind to Blys
CC      and so may be used to detect and quantitate the presence of Blys in
CC      biological samples and may be used in this way to diagnose disease
CC      associated with aberrant expression of Blys. They may also be
CC      administered to treat diseases associated with aberrant Blys expression
CC      and activity such as cancer, immune, and autoimmune disorders and
CC      diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC      immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC      acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC      the antibodies and fragments of the antibodies described in the method
CC      of the invention.
XX
SQ      Sequence 247 AA;
XX
Query Match      88.9%; Score 463; DB 23; Length 247;
Best Local Similarity 89.8%; Pred. No. 1.1e-39;
Matches 88; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
OY      1 QVOLLQSATBVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWVGISAYNGNTNY 60
      |||
      1 QVOLLQSAAEVRKPGASVSKVSCKASGYTTTSGISWVRQAPGQGLEWVGISAYNGNTNY 60
DB
OY      61 AOKFOGRVTMTTDSRTAYMELSLRSDPTAVYYCAR 98
      |||
      61 AOKFOGRVTMTTDSRTAYMELSLRSDPTAVYYCAR 98
DB
RESULT 6
ABP45549
ID      ABP45549 standard; Protein; 250 AA.
XX

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XX Example 4; Fig 4B; 61pp; English.
XX
CC This invention describes a novel polynucleotide (I) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (I) is useful a primer or probe for detecting the
CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents the human
CC anti-factor VIII antibody VH E1-5 protein which is used in the method
CC of the invention.
XX
SQ Sequence 98 AA;

Query Match          98.1%; Score 511; DB 21; Length 98;
Best Local Similarity 98.0%; Pred. No. 4.5e-45;
Matches 96; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVRQAPQGLEWVGWISAYNGNTHY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 QVQLVLSATEVKKPGASMKVSCMASGYPTSYDISWVRQAPQGLEWVGWISAYNGNTHY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 AOKFGGRVTMTTDSRRTAYMELRSLRSDPTAVYYCAR 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 AOKFGGRVTMTTDSRRTAYMELRSLRSDPTAVYYCAR 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
AAVS0953
ID AAVS0953 standard; Protein; 132 AA.
XX
AC AAVS0953;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human anti-factor VIII antibody VH protein VH IT-2.
XX
KW Human; heavy chain; antibody; factor VIII; hemostatic;
KM hemophilia A; VH protein.
XX
OS Homo sapiens.
XX
PN WO958680-A2.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-NL00285.
XX
PR 08-MAY-1998; 98EP-0201543.
XX
PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
XX
PI Voorberg JJ, Van Den Brink EN, Turenhout EM;
XX
DR WPI; 2000-053102/04.
XX
PT New polynucleotide, polypeptide and antibody useful for diagnosing the
PT presence of neutralizing antibodies against factor VIII and for
PT treatment of hemophilia A patients with these antibodies -
XX
XX Example 4; Fig 4B; 61pp; English.
XX
CC This invention describes a novel polynucleotide (I) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (I) is useful a primer or probe for detecting the
CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents the human
CC anti-factor VIII antibody VH IT-2 protein which is used in the method

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CC of the invention.
XX
SQ Sequence 132 AA;

Query Match          95.8%; Score 499; DB 21; Length 132;
Best Local Similarity 95.9%; Pred. No. 1.1e-43;
Matches 94; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 QVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVRQAPQGLEWVGWISAYNGNTHY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 QVQLVLSATEVKKPGASMKVSCMASGYPTSYDISWVRQAPQGLEWVGWISAYNGNTHY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 AOKFGGRVTMTTDSRRTAYMELRSLRSDPTAVYYCAR 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 AOKFGGRVTMTTDSRRTAYMELRSLRSDPTAVYYCAR 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
AAVS0950
ID AAVS0950 standard; Protein; 132 AA.
XX
AC AAVS0950;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human anti-factor VIII antibody VH clone IT-2 encoded protein.
XX
KW Human; heavy chain; antibody; factor VIII; hemostatic;
KM hemophilia A; VH gene.
XX
OS Homo sapiens.
XX
PN WO958680-A2.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-NL00285.
XX
PR 08-MAY-1998; 98EP-0201543.
XX
PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
XX
PI Voorberg JJ, Van Den Brink EN, Turenhout EM;
XX
DR WPI; 2000-053102/04.
XX
PT New polynucleotide, polypeptide and antibody useful for diagnosing the
PT presence of neutralizing antibodies against factor VIII and for
PT treatment of hemophilia A patients with these antibodies -
XX
XX Example 4; Fig 4A; 61pp; English.
XX
CC This invention describes a novel polynucleotide (I) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (I) is useful a primer or probe for detecting the
CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents the human
CC anti-factor VIII antibody clone IT-2 protein which is used in the method
CC of the invention.
XX
SQ Sequence 132 AA;

Query Match          94.0%; Score 490; DB 21; Length 132;
Best Local Similarity 94.9%; Pred. No. 9e-43;
Matches 93; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 QVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVRQAPQGLEWVGWISAYNGNTHY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 QVQLVLSATEVKKPGASMKVSCMASGYPTSYDISWVRQAPQGLEWVGWISAYNGNTHY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 61 AOKLOGRVMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

## RESULT 2

US-09-880-748-1560  
; Sequence 1560, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 1560  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1560

Query Match 88.9%; Score 463; DB 11; Length 250;  
Best Local Similarity 89.8%; Pred. No. 7e-40;  
Matches 88; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 OVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVRQAPGQGLEWGMISAYNGNTHY 60  
Db 1 OVQLQSAEYKKGASVSKASGYFTSYGISWVRQAPGQGLEWGMISAYNGNTHY 60

QY 61 AOKFOGRVMTTDTSTRRTAYMELRSLRSDDTAVYYCAR 98  
Db 61 AOKLOGRVMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

## RESULT 3

US-09-880-748-1738  
; Sequence 1738, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 1738  
; LENGTH: 251  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1738

Query Match 88.9%; Score 463; DB 11; Length 251;

Best Local Similarity 88.8%; Pred. No. 7e-40;  
Matches 87; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 OVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVRQAPGQGLEWGMISAYNGNTHY 60

Db 1 OVQLQSAEYKKGASVSKASGYFTSYGISWVRQAPGQGLEWGMISAYNGNTHY 60

QY 61 AOKFOGRVMTTDTSTRRTAYMELRSLRSDDTAVYYCAR 98  
Db 61 AOKLOGRVMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

## RESULT 4

US-09-880-748-1595  
; Sequence 1595, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 1595  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1595

Query Match 88.3%; Score 460; DB 11; Length 250;  
Best Local Similarity 88.8%; Pred. No. 1.4e-39;  
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 OVQLQSATEVKKPGASMKVSCMASGYPTSYDISWVRQAPGQGLEWGMISAYNGNTHY 60

Db 1 OVQLQSAEYKKGASVSKASGYFTSYGISWVRQAPGQGLEWGMISAYNGNTHY 60

QY 61 AOKFOGRVMTTDTSTRRTAYMELRSLRSDDTAVYYCAR 98  
Db 61 AOKLOGRVMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

## RESULT 5

US-10-041-860-2  
; Sequence 2, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao-Dong  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gad  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezabeh, Binyam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES  
; FILE REFERENCE: ABGENIX-051A  
; CURRENT APPLICATION NUMBER: US/10/041,860  
; CURRENT FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2  
LENGTH: 98  
TYPE: PRT  
ORGANISM: homo sapiens  
US-10-041-860-2

Query Match 87.5%; Score 456; DB 12; Length 98;  
Best Local Similarity 87.8%; Pred. No. 1.3e-39;  
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLLQATVEVKKPGASMKVSCMASGYPTFSYDISWVROAPGQGLEWVGWISAYNGNTNY 60  
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVROAPGQGLEWVGWISAYNGNTNY 60  
QY 61 AOKFGQRTMTTDTSRRTAYMELRSLSRSDDTAVYYCAR 98  
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 98

## RESULT 6

US-10-041-860-324  
Sequence 324, Application US/10041860  
Publication No. US20030157109A1  
GENERAL INFORMATION:  
APPLICANT: Corvalan, Jose R.F.  
APPLICANT: Jia, Xiao-Chi  
APPLICANT: Peng, Xiao  
APPLICANT: Yang, Xiao-Dong  
APPLICANT: Chen, Francine  
APPLICANT: Gazit, Gadl  
APPLICANT: Weber, Richard  
APPLICANT: Bezabeh, Binyam  
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
FILE REFERENCE: AGENIX.051A  
CURRENT FILING DATE: 2002-01-07  
NUMBER OF SEQ ID NOS: 377  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 324  
LENGTH: 98  
TYPE: PRT  
ORGANISM: homo sapiens  
US-10-041-860-324

Query Match 87.5%; Score 456; DB 12; Length 98;  
Best Local Similarity 87.8%; Pred. No. 1.3e-39;  
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLLQATVEVKKPGASMKVSCMASGYPTFSYDISWVROAPGQGLEWVGWISAYNGNTNY 60  
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVROAPGQGLEWVGWISAYNGNTNY 60  
QY 61 AOKFGQRTMTTDTSRRTAYMELRSLSRSDDTAVYYCAR 98  
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 98

## RESULT 7

US-10-041-860-326  
Sequence 326, Application US/10041860  
Publication No. US20030157109A1  
GENERAL INFORMATION:  
APPLICANT: Corvalan, Jose R.F.  
APPLICANT: Jia, Xiao-Chi  
APPLICANT: Peng, Xiao  
APPLICANT: Yang, Xiao-Dong  
APPLICANT: Chen, Francine  
APPLICANT: Gazit, Gadl  
APPLICANT: Weber, Richard  
APPLICANT: Bezabeh, Binyam  
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
FILE REFERENCE: AGENIX.051A  
CURRENT FILING DATE: 2002-01-07  
NUMBER OF SEQ ID NOS: 377  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 324  
LENGTH: 98  
TYPE: PRT  
ORGANISM: homo sapiens  
US-10-041-860-326

FILE REFERENCE: AGENIX.051A  
CURRENT APPLICATION NUMBER: US/10/041,860  
CURRENT FILING DATE: 2002-01-07  
NUMBER OF SEQ ID NOS: 377  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 326  
LENGTH: 98  
TYPE: PRT  
ORGANISM: homo sapiens  
US-10-041-860-326

Query Match 87.5%; Score 456; DB 12; Length 98;  
Best Local Similarity 87.8%; Pred. No. 1.3e-39;  
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLLQATVEVKKPGASMKVSCMASGYPTFSYDISWVROAPGQGLEWVGWISAYNGNTNY 60  
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVROAPGQGLEWVGWISAYNGNTNY 60  
QY 61 AOKFGQRTMTTDTSRRTAYMELRSLSRSDDTAVYYCAR 98  
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 98

## RESULT 8

US-10-041-860-355  
Sequence 355, Application US/10041860  
Publication No. US20030157109A1  
GENERAL INFORMATION:  
APPLICANT: Corvalan, Jose R.F.  
APPLICANT: Jia, Xiao-Chi  
APPLICANT: Peng, Xiao  
APPLICANT: Yang, Xiao-Dong  
APPLICANT: Chen, Francine  
APPLICANT: Gazit, Gadl  
APPLICANT: Weber, Richard  
APPLICANT: Bezabeh, Binyam  
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
FILE REFERENCE: AGENIX.051A  
CURRENT FILING DATE: 2002-01-07  
NUMBER OF SEQ ID NOS: 377  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 355  
LENGTH: 98  
TYPE: PRT  
ORGANISM: homo sapiens  
US-10-041-860-355

Query Match 87.5%; Score 456; DB 12; Length 98;  
Best Local Similarity 87.8%; Pred. No. 1.3e-39;  
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLLQATVEVKKPGASMKVSCMASGYPTFSYDISWVROAPGQGLEWVGWISAYNGNTNY 60  
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVROAPGQGLEWVGWISAYNGNTNY 60  
QY 61 AOKFGQRTMTTDTSRRTAYMELRSLSRSDDTAVYYCAR 98  
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 98

## RESULT 9

US-10-041-860-356  
Sequence 356, Application US/10041860  
Publication No. US20030157109A1  
GENERAL INFORMATION:  
APPLICANT: Corvalan, Jose R.F.  
APPLICANT: Jia, Xiao-Chi  
APPLICANT: Peng, Xiao  
APPLICANT: Yang, Xiao-Dong  
APPLICANT: Chen, Francine

```

; APPLICANT: Gazit, Gad
; APPLICANT: Weber, Richard
; APPLICANT: Bezaheh, Binayam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ARGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 356
; LENGTH: 98
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-356

Query Match
Best Local Similarity 87.5%; Score 456; DB 12; Length 98;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWROAPQGLEWGMISAYNGNTY 60
DB 1 QVOLLVSGAEVKKPGASVSKVSCASGYFTSYGISWROAPQGLEWGMISAYNGNTY 60

QY 61 AOKFGQRYVTMTDTSRTATYMLRLSLRSDDTAVYYCAR 98
DB 61 AOKLQGRVTMTDTSRTATYMLRLSLRSDDTAVYYCAR 98

RESULT 10
US-10-308-817-44
; Sequence 44, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rochet, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-44

Query Match
Best Local Similarity 87.8%; Score 456; DB 12; Length 98;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWROAPQGLEWGMISAYNGNTY 60
DB 1 QVOLLVSGAEVKKPGASVSKVSCASGYFTSYGISWROAPQGLEWGMISAYNGNTY 60

QY 61 AOKFGQRYVTMTDTSRTATYMLRLSLRSDDTAVYYCAR 98
DB 61 AOKLQGRVTMTDTSRTATYMLRLSLRSDDTAVYYCAR 98

RESULT 11
US-10-194-975-4
; Sequence 4, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
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; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-4

Query Match
Best Local Similarity 87.8%; Score 456; DB 15; Length 98;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWROAPQGLEWGMISAYNGNTY 60
DB 1 QVOLLVSGAEVKKPGASVSKVSCASGYFTSYGISWROAPQGLEWGMISAYNGNTY 60

QY 61 AOKFGQRYVTMTDTSRTATYMLRLSLRSDDTAVYYCAR 98
DB 61 AOKLQGRVTMTDTSRTATYMLRLSLRSDDTAVYYCAR 98

RESULT 12
US-09-864-761-47285
; Sequence 47285, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
```



```
; SEQ ID NO 47285
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019440.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.42
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.8
; OTHER INFORMATION: SWISSPROT HIT: P21083, EVALU 2.00e-39
; OTHER INFORMATION: EST_HUMAN HIT: AM403728.1, EVALU 4.00e-45
US-09-864-761-47285
```

```
Query Match      87.5%; Score 456; DB 9; Length 104;
Best Local Similarity 87.8%; Pred. No. 1.4e-39;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
```

```
OY 1 OVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVROAPQGLEWGMISAYNGNTH 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 OVQLVQSGAEVKKPKGASVSKASGYFTSYGISWVROAPQGLEWGMISAYNGNTH 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 AOKFGRVMTTDTSRRTAYMELRSLSRSDDTAVYYCAR 98
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Db 64 AOKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCAR 101
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RESULT 13
US-10-041-860-206
; Sequence 206, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 117
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-206
```

```
Query Match      87.5%; Score 456; DB 12; Length 117;
Best Local Similarity 87.8%; Pred. No. 1.6e-39;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
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OY 1 OVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVROAPQGLEWGMISAYNGNTH 60
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Db 1 OVQLVQSGAEVKKPKGASVSKASGYFTSYGISWVROAPQGLEWGMISAYNGNTH 60
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RESULT 14
US-10-041-860-42
; Sequence 42, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
```

```
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-42
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Query Match      87.5%; Score 456; DB 12; Length 125;
Best Local Similarity 87.8%; Pred. No. 1.7e-39;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
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OY 1 OVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVROAPQGLEWGMISAYNGNTH 60
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Db 1 OVQLVQSGAEVKKPKGASVSKASGYFTSYGISWVROAPQGLEWGMISAYNGNTH 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 AOKFGRVMTTDTSRRTAYMELRSLSRSDDTAVYYCAR 98
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RESULT 15
US-10-041-860-207
; Sequence 207, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-207
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Query Match      87.5%; Score 456; DB 12; Length 125;
Best Local Similarity 87.8%; Pred. No. 1.7e-39;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
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OY 1 OVQLQSATEVKKPKGASMKVSCMASGYPTSYDISWVROAPQGLEWGMISAYNGNTH 60
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Db 1 OVQLVQSGAEVKKPKGASVSKASGYFTSYGISWVROAPQGLEWGMISAYNGNTH 60
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Search completed: December 30, 2003, 11:45:22  
Job time : 21.0171 secs



Db 20 QVVLVSGAEVKKPGASVKASCASGYFTSYGISWVRQAPGQGLEWMGMSAINGNTNY 79  
QY 61 AAKFGQRYVTMTDTSRTAYMELRSLSDDTAAYYCAR 98  
Db 80 AAKFGQRYVTMTDTSRTAYMELRSLSDDTAAYYCAR 117

RESULT 2  
US-08-264-093-3  
Sequence 3, Application US/08264093  
Patent No. 5639863  
GENERAL INFORMATION:  
APPLICANT: Michael D. Dan  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO  
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE  
TITLE OF INVENTION: ANTIGEN  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ridout & Maybee  
STREET: 2300 Richmond-Adelaide Centre  
STREET: 101 Richmond Street West  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5H 2J7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS-DOS 6.00  
SOFTWARE: ASCII Editor  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/264,093  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA: No. 5639863 applicable  
ATTORNEY/AGENT INFORMATION:  
NAME: Lake, James R.  
REGISTRATION NUMBER: 31081  
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 868-1482  
TELEFAX: (416) 362-0823  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
STRANDEDNESS: not applicable  
TOPOLOGY: linear  
US-08-264-093-3

Query Match 83.7%; Score 436; DB 1; Length 121;  
Best Local Similarity 82.7%; Pred. No. 6,6e-40;  
Matches 81; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVVLVSGATEVKKPGASVKSCMASGYFTSYDSWVRQAPGQGLEWMGMSAINGNTNY 60  
Db 1 QVVLVSGAEVKKPGASVKASCASGYFTTFTYGISWVRQAPGQGLEWMGMSAINGNTNS 60  
QY 61 AAKFGQRYVTMTDTSRTAYMELRSLSDDTAAYYCAR 98  
Db 61 AAKFGQRYVTMTDTSRTAYMELRSLSDDTAAYYCAR 98

RESULT 3  
US-08-202-047-22  
Sequence 22, Application US/08202047  
Patent No. 5800815  
GENERAL INFORMATION:  
APPLICANT: CHESNUT, Robert W.  
APPLICANT: POLLEY, Margaret J.  
APPLICANT: PAULSON, James C.  
APPLICANT: JONES, S. Tarran  
APPLICANT: SALDANHA, Jose W.

APPLICANT: BENDIG, Mary M.  
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,047  
FILING DATE: 25-FEB-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14137-77  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..128  
OTHER INFORMATION: /label= HUMAN\_1  
US-08-202-047-22

Query Match 80.3%; Score 418.5; DB 1; Length 128;  
Best Local Similarity 80.8%; Pred. No. 5,4e-38;  
Matches 80; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVVLVSGATEVKKPGASVKSCMASGYFTSYDSWVRQAPGQGLEWMGMSAINGNTNY 59  
Db 1 QVVLVSGAEVKKPGASVKASCASGYFTTFTSYAISWVRQAPGQGLEWMGMSAINGNDIN 60  
QY 60 YAAKFGQRYVTMTDTSRTAYMELRSLSDDTAAYYCAR 98  
Db 61 YAAKFGQRYVTMTDTSRTAYMELRSLSDDTAAYYCAR 99

RESULT 4  
US-08-964-690-22  
Sequence 22, Application US/08964690  
Patent No. 6033667  
GENERAL INFORMATION:  
APPLICANT: CHESNUT, Robert W.  
APPLICANT: POLLEY, Margaret J.  
APPLICANT: PAULSON, James C.  
APPLICANT: JONES, S. Tarran  
APPLICANT: SALDANHA, Jose W.  
APPLICANT: BENDIG, Mary M.  
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,690
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,047
; FILING DATE: 25-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..128
; OTHER INFORMATION: /label= HUMAN_1
;
US-08-964-690-22

Query Match      80.3%; Score 418.5; DB 3; Length 128;
Best Local Similarity 80.8%; Pred. No. 5.4e-38;
Matches 80; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVOLLQSTAEVKKPKGASMKVSCMASGYPTSYDISWVRQAPGQGLEWGWISAY-NGNTH 59
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Db 1 QVOLLQSGAEVKKPKGASVSKASGYFTSYAISWVRQAPGQGLEWGWINPYNGDPTN 60
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QY 60 YAAKFGKRVTTMTDTSRTTAYMELRSLSRSDPTAVYYCAR 98
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Db 61 YAAKFGKRVTTTADTSTSTAYMELSLRSEDTAVYYCAR 99
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
US-08-561-521-45
; Sequence 45, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Legier, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-561-521-45

Query Match      80.3%; Score 418.5; DB 2; Length 129;
Best Local Similarity 80.8%; Pred. No. 5.5e-38;
Matches 80; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVOLLQSTAEVKKPKGASMKVSCMASGYPTSYDISWVRQAPGQGLEWGWISAY-NGNTH 59
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Db 1 QVOLLQSGAEVKKPKGASVSKASGYFTSYAISWVRQAPGQGLEWGWINPYNGDPTN 60
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QY 60 YAAKFGKRVTTMTDTSRTTAYMELRSLSRSDPTAVYYCAR 98
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Db 61 YAAKFGKRVTTTADTSTSTAYMELSLRSEDTAVYYCAR 99
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RESULT 6
US-08-525-539A-77
; Sequence 77, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J. R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: M33 ANTI-B446 ANTIBODY, METHODS OF USE THEREOF, AND
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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Query Match      78.1%; Score 407; DB 3; Length 117;
Best Local Similarity 78.6%; Pred. No. 8.5e-37;
Matches 77; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

OY 1 QVOLLQSATEVKKFGKASMKVSCMASGYFTSYDISMVRQAPQGGLEWYGMISA YGNTHY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVLLVQSGAEVKKFGKASVKSCKASGYFTSYDINWVRQATGGGLEWGMGNPNISGNTGY 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 AAKFGQRTVMTDTSRRATYAMELSLRDDPTAVYYCAR 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AAKFGQRTVMTDTSRRATYAMELSLRDDPTAVYYCAR 117
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-08-561-521-10
: Sequence 10, Application US/08561521
: Patent No. 5840299
: GENERAL INFORMATION:
: APPLICANT: Bendig, Mary M.
: APPLICANT: Leger, Olivier J.
: APPLICANT: Saldaña, Jose
: APPLICANT: Jones, S. Tarran
: TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
: TITLE OF INVENTION: Adhesion Molecule VLA-4
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: One Market Plaza, Steuart Tower, Suite 2000
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424

```

```

: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/186,269A
: FILING DATE: 25-JAN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William L.
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 15270-14
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-543-9600
: TELEFAX: 415-543-5043
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 119 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-561-521-10

```

[illegible]

```
/ Sequence 10, Application PC/TUS9501219
/ GENERAL INFORMATION:
/ APPLICANT: Bendig, Mary M.
/ APPLICANT: Leger, Olivier J.
/ APPLICANT: Saldanha, Jose
/ APPLICANT: Jones, S. Tarran
/ TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
/ TITLE OF INVENTION: Adhesion Molecule VLA-4
/ NUMBER OF SEQUENCES: 45
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Kourie and Crew
/ STREET: One Market Plaza, Stewart Tower, Suite 2000
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94105
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/01219
/ FILING DATE: 25-JAN-1995
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/186,269
/ FILING DATE: 25-JAN-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Smith, William L.
/ REGISTRATION NUMBER: 30,223
/ REFERENCE/DOCKET NUMBER: 15270-14
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-543-9600
/ TELEFAX: 415-543-5043
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 119 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ PCT-US95-01219-10

Query Match 78.1%; Score 407; DB 5; Length 119;
Best Local Similarity 78.6%; Pred. No. 8.7e-37;
Matches 77; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

OY 1 QVQLQSATEVKKPKGASKVSCMASGYPFTSYDISVWRQAPGQGLEWVGWISAYNGNTHY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGAEVKKPKGASVSKVSCASGYFTSYAMHWVRQAPGQRLIEWMGWIMAGNGNTKY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 AOKFGQGVTTMTDTSRRRAYMELRSLSRSDDTAVYYCAR 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SQKFGQGVTTTRDTISASTAYMELSSLSRSEDTAVYYCAR 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-09-025-769B-36
/ Sequence 36, Application US/09025769B
/ Patent No. 6300064
/ GENERAL INFORMATION:
/ APPLICANT: Knappik, Achim
/ APPLICANT: Pack, Peter
/ APPLICANT: Ilag, Vic
/ APPLICANT: Ge, Liming
/ APPLICANT: Moroney, Simon
/ APPLICANT: Pluckethun, Andreas
/ TITLE OF INVENTION: Protein/(Poly)peptide libraries
/ NUMBER OF SEQUENCES: 373
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
/ STREET: 1251 Avenue of the Americas
```

```

/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10021
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/025,769B
/ FILING DATE: 18-FEB-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 95 11 3021.0
/ FILING DATE: 18-AUG-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: James F. Haley, Jr., Esq.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: MORPHO/5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)596-9000
/ TELEFAX: (212)596-9090
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 120 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-025-769B-36

Query Match 77.9%; Score 406; DB 4; Length 120;
Best Local Similarity 78.6%; Pred. No. 1.1e-36;
Matches 77; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

OY 1 QVQLQSATEVKKPKGASKVSCMASGYPFTSYDISVWRQAPGQGLEWVGWISAYNGNTHY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGAEVKKPKGASVSKVSCASGYFTSYAMHWVRQAPGQRLIEWMGWIMAGNGNTKY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 AOKFGQGVTTMTDTSRRRAYMELRSLSRSDDTAVYYCAR 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKFGQGVTTTRDTISASTAYMELSSLSRSEDTAVYYCAR 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
US-09-025-769B-59
/ Sequence 59, Application US/09025769B
/ Patent No. 6300064
/ GENERAL INFORMATION:
/ APPLICANT: Knappik, Achim
/ APPLICANT: Pack, Peter
/ APPLICANT: Ilag, Vic
/ APPLICANT: Ge, Liming
/ APPLICANT: Moroney, Simon
/ APPLICANT: Pluckethun, Andreas
/ TITLE OF INVENTION: Protein/(Poly)peptide libraries
/ NUMBER OF SEQUENCES: 373
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
/ STREET: 1251 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10021
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/025,769B
/ FILING DATE: 18-FEB-1998
/ PRIOR APPLICATION DATA:
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APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-59

Query Match 77.9%; Score 406; DB 4; Length 120;  
Best Local Similarity 78.6%; Pred. No. 1.1e-36;  
Matches 77; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Qy 1 QVQLQSATEYVKKPGASKMKVSCMASGYPTSYDISWVRQAPQGLRWGWSAYNGNTHY 60  
Db 1 QVQLVQSGAEVKKPKQASVYKSCASGYFTSYMHVWROAPQGLEMMGWINPNSGNTY 60  
Qy 61 AOKFGRYVTMTTDSRRTAYMELRLSRSDDTAVYYCAR 98  
Db 61 AOKFGRYVTMTTDSRRTAYMELRLSRSDDTAVYYCAR 98

RESULT 15  
US-08-652-816A-19  
Sequence 19, Application US/08652816A  
Patent No. 5872215  
GENERAL INFORMATION:  
APPLICANT: Osbourn, JK  
APPLICANT: Allen, DJ  
TITLE OF INVENTION: Specific binding members, materials and  
TITLE OF INVENTION: methods.  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,816A  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.4  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.8  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9525004.9  
FILING DATE: 07-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02240  
FILING DATE: 02-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/244,597  
FILING DATE: 01-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33308  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-652-816A-19

Query Match 77.8%; Score 405.5; DB 2; Length 120;  
Best Local Similarity 80.4%; Pred. No. 1.3e-36;  
Matches 78; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

Qy 1 QVQLQSATEYVKKPGASKMKVSCMASGYPTSYDISWVRQAPQGLRWGWSAYNGNTHY 60  
Db 1 QVTLVQSGAEVKKPKQASVYKSCASGYFTSYMHVWROAPQGLEMMGWISAYSGNTKY 59  
Qy 61 AOKFGRYVTMTTDSRRTAYMELRLSRSDDTAVYYCA 97  
Db 61 AOKFGRYVTMTTDSRRTAYMELRLSRSDDTAVYYCA 96

Search completed: December 30, 2003, 11:05:32  
Job time: 11.0346 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 / Search time 9.39399 Seconds  
(without alignments)  
1003.251 Million cell updates/sec

Title: US-09-674-752-28

Sequence: 1 QVQLQSGAEVRRKPGASVKV.....AYMELRLSRSDDTAVYYCAR 98

Scoring table: BLASTUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	460	89.1	98	2	S26919 Ig heavy chain V r
2	457	88.6	129	2	S36260 Ig heavy chain V r
3	455	88.2	122	2	S36271 Ig heavy chain V r
4	454	88.0	124	2	S19665 Ig heavy chain V r
5	444	86.0	131	2	S21924 Ig heavy chain V r
6	443	85.9	160	2	PI0105 anti-PR2 erythrocy
7	424	82.2	111	2	S21925 Ig heavy chain V r
8	423	82.0	98	2	S26918 Ig heavy chain V r
9	420	81.4	136	2	S31600 Ig heavy chain V r
10	416	80.6	98	2	S26938 Ig heavy chain V r
11	416	80.6	117	2	S31680 Ig heavy chain V r
12	416	80.6	117	2	S18551 Ig heavy chain V r
13	415	80.6	135	2	S49530 anti-Sm antibody V
14	415	80.4	118	2	S36265 Ig heavy chain V r
15	413	80.0	127	2	S34014 Ig heavy chain V r
16	411	79.7	117	2	S18553 Ig heavy chain V r
17	408	79.1	98	2	S26912 Ig heavy chain V r
18	408	79.1	125	2	S68170 Ig heavy chain V r
19	408	79.1	129	2	S46393 Ig heavy chain V r
20	406	78.7	132	2	S31596 Ig heavy chain V r
21	403	78.1	104	2	S69899 Ig heavy chain V r
22	401	77.7	98	2	S26920 Ig heavy chain V r
23	401	77.7	123	2	D33548 Ig heavy chain V r
24	399	77.3	148	2	S29257 Ig heavy chain V r
25	396	76.7	117	1	HYTHUG Ig heavy chain pre
26	396	76.7	171	1	S23623 Ig heavy chain V r
27	395	76.6	98	2	PH0871 Ig heavy chain V r
28	395	76.6	117	2	S18552 Ig heavy chain V r
29	394	76.4	110	2	PH1670 Ig heavy chain V r

30	393	76.2	142	2	A32483 Ig heavy chain V r
31	392	76.0	117	1	HYTHUG3 Ig heavy chain pre
32	390	75.0	116	2	S31667 Ig heavy chain V r
33	387	75.0	126	2	I44151 Ig heavy chain V r
34	386	74.6	114	2	PH1667 Ig heavy chain V r
35	386	74.6	118	2	PH1666 Ig heavy chain V r
36	385	74.6	98	2	S24680 Ig heavy chain V1
37	383	74.7	117	2	PR0371 Ig gamma chain pre
38	381	73.8	109	2	PH1668 Ig heavy chain V r
39	381	73.6	119	2	JN0295 Ig heavy chain V-D
40	381	73.6	135	2	B32274 Ig heavy chain pre
41	380	73.6	98	2	S26915 Ig heavy chain V r
42	380	73.6	116	2	S31698 Ig heavy chain pre
43	380	73.6	119	2	PH0959 Ig heavy chain V r
44	380	73.6	119	2	PH0961 Ig heavy chain V r
45	380	73.6	120	2	PH0962 Ig heavy chain V r

## ALIGNMENTS

## RESULT 1

Ig heavy chain V regi  
C:Species: Homo sapie  
C:Date: 22-Nov-1993 #  
C:Accession: S26919  
R:Tomlinson, I.M.; We  
J. Mol. Biol. 227, 77  
A>Title: The repetoi  
A:Reference number: S  
A:Accession: S26919  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-98 <TOR  
A:Cross-References: E  
C:Superfamily: Immun  
C:Keywords: heterotet  
F,15-98/Domain: immun

Query Match  
Best Local Similari  
Matches 87; Cons

QY	1	QVQLQSG	89.1%	Score 460; DB 2; Length 98;
DB	1	QVQLVQS	88.8%	Pred. No. 1.5e-38;
QY	61	AQKPGGR	4; Mismatches 7; Indels 0; Gaps 0;	
DB	61	AQKLGGR		

## RESULT 2

Ig heavy chain V regi  
C:Species: Homo sapie  
C:Date: 03-Feb-1994 #  
C:Accession: S36260  
R:Griffiths, A.D.; Ma  
EMBO J. 12, 725-734,  
A>Title: Human anti-e  
A:Reference number: S  
A:Accession: S36260  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-129 <GR  
A:Cross-References: E  
C:Superfamily: immun  
C:Keywords: heterotet  
F,15-98/Domain: immun

wcletic acid sequence not shown

:218551; NID:933124; PIDN:CAA79303.1; PID:9939903

bulin V region; immunoglobulin homology  
C:Keywords: heterotet  
F,15-98/Domain: immun

Query Match 88.6%; Score 457; DB 2; Length 129;

Best Local Similarity 88.8%; Pred. No. 4e-38;  
Matches 87; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLLQSAEVRKPGASVKSCASGYPTFTSYDLSWVRQAPGQGLEWMGMSISYSGNTDY 60  
|||||  
EVRKPGASVSKSCASGYPTFTSYDLSWVRQAPGQGLEWMGMSISYSGNTDY 60

DB 1 QVOLLQSGAEVKKRPGASVKSCASGYTFTSYGISWVRQAPGQGLEWMGMSISYNGNTNY 60  
|||||  
EVRKPGASVSKSCASGYTFTSYGISWVRQAPGQGLEWMGMSISYNGNTNY 60

QY 61 AOKFOGRVTMTTDSRTAYMELRLSRSDDTAVYYCAR 98  
|||||  
MTTDSRTAYMELRLSRSDDTAVYYCAR 98

DB 61 AOKLQGRVTMTTDTSTSTAYMELRLSRSDDTAVYYCAR 98  
|||||  
MTTDTSTSTAYMELRLSRSDDTAVYYCAR 98

#### RESULT 3

S16271

Ig heavy chain V region (clone alpha-THY-29) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999

C/Accession: S36271

R/Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A/Title: Human anti-self antibodies with high specificity from phage display libraries.

A/Reference number: S36256; MUID:93178448; PMID:7679990

A/Status: preliminary; nucleic acid sequence not shown

A/Residues: 1-122 <CRI>

A/Cross-references: EMBL:Z18832; NID:g33115; PIDN:CAA79284.1; PID:g939895

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 455; DB 2; Length 122;  
Best Local Similarity 88.7%; Pred. No. 6e-38; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVOLLQSAEVRKPGASVKSCASGYPTFTSYDLSWVRQAPGQGLEWMGMSISYSGNTDY 60  
|||||  
EVRKPGASVSKSCASGYPTFTSYDLSWVRQAPGQGLEWMGMSISYSGNTDY 60

DB 1 QVOLLQSGAEVKKRPGASVKSCASGYTFTSYGISWVRQAPGQGLEWMGMSISYNGNTNY 60  
|||||  
EVRKPGASVSKSCASGYTFTSYGISWVRQAPGQGLEWMGMSISYNGNTNY 60

QY 61 AOKFOGRVTMTTDSRTAYMELRLSRSDDTAVYYCAR 97  
|||||  
MTTDSRTAYMELRLSRSDDTAVYYCAR 97

DB 61 AOKLQGRVTMTTDTSTSTAYMELRLSRSDDTAVYYCAR 97  
|||||  
MTTDTSTSTAYMELRLSRSDDTAVYYCAR 97

#### RESULT 4

S19665

Ig heavy chain V region (alpha-phox15) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 20-Jun-2000

C/Accession: S19665; S24442

R/Marks, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.

J. Mol. Biol. 222, 581-597, 1991

A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage

A/Reference number: S19663; MUID:92085276; PMID:1748994

A/Accession: S19665

A/Molecule type: mRNA

A/Residues: 1-124 <MAR>

A/Cross-references: EMBL:X61647

R/Jones, P.T.

Submitted to the EMBL Data Library, October 1991

A/Reference number: S24442

A/Accession: S24442

A/Molecule type: mRNA

A/Residues: 1-40; GLSGMPGSAITMTQTSLDK', 61-118, 'T', 120-124 <ON>

A/Cross-references: EMBL:X61647; NID:937667; PIDN:CAA43828.1; PID:g1335368

A/Note: the difference for residues 41-60 results from misplacement of 10 bases in the B

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 88.0%; Score 454; DB 2; Length 124;  
Best Local Similarity 87.8%; Pred. No. 7.6e-38;  
Matches 86; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVOLLQSAEVRKPGASVKSCASGYPTFTSYDLSWVRQAPGQGLEWMGMSISYSGNTDY 60  
|||||  
EVRKPGASVSKSCASGYPTFTSYDLSWVRQAPGQGLEWMGMSISYSGNTDY 60

DB 1 QVOLLQSGAEVKKRPGASVKSCASGYTFTSYGISWVRQAPGQGLEWMGMSISYNGNTNY 60  
|||||  
EVRKPGASVSKSCASGYTFTSYGISWVRQAPGQGLEWMGMSISYNGNTNY 60

QY 61 AOKFOGRVTMTTDSRTAYMELRLSRSDDTAVYYCAR 98  
|||||  
MTTDSRTAYMELRLSRSDDTAVYYCAR 98

DB 61 AOKLQGRVTMTTDTSTSTAYMELRLSRSDDTAVYYCAR 98  
|||||  
MTTDTSTSTAYMELRLSRSDDTAVYYCAR 98

#### RESULT 5

S21924

Ig heavy chain V region (man)

C/Species: Homo sapiens (man)

C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999

C/Accession: S21924

R/Friedman, D.F.

Submitted to the EMBL Data Library, July 1991

A/Reference number: S21924

A/Accession: S21924

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-131 <F>

A/Cross-references: C/Genetics: 16/1

A/Intons: 16/1

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/34-117/Domain: Immunoglobulin homology <IMM>

Query Match 86.0%; Score 444; DB 2; Length 131;  
Best Local Similarity 84.7%; Pred. No. 7.8e-37; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVOLLQSAEVRKPGASVKSCASGYPTFTSYDLSWVRQAPGQGLEWMGMSISYSGNTDY 60  
|||||  
EVRKPGASVSKSCASGYPTFTSYDLSWVRQAPGQGLEWMGMSISYSGNTDY 60

DB 20 QVOLLQSGAEVKKRPGASVKSCASGYTFTSYGISWVRQAPGQGLEWMGMSISYNGNTNY 79  
|||||  
EVRKPGASVSKSCASGYTFTSYGISWVRQAPGQGLEWMGMSISYNGNTNY 79

QY 61 AOKFOGRVTMTTDSRTAYMELRLSRSDDTAVYYCAR 98  
|||||  
MTTDSRTAYMELRLSRSDDTAVYYCAR 98

DB 80 AOKLQGRVTMTTDTSTSTAYMELRLSRSDDTAVYYCAR 117  
|||||  
MTTDTSTSTAYMELRLSRSDDTAVYYCAR 117

#### RESULT 6

PL0105

anti-PR2 erythrocyte

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 26-Apr-1996

C/Accession: PL0105

R/Silberstein, L.E.

J. Exp. Med. 169, 16

A/Title: Relationship between the codon GAC for residues 108 and 109 as Glu

A/Reference number: PL0105

A/Accession: PL0105

A/Molecule type: mRNA

A/Residues: 1-160 <S>

A/Note: the authors isolated the codon GAC for residues 108 and 109 as Glu

C/Comment: The antibody heavy chain precursor - human (fragment)

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: autocalytic; hemagglutinin

F/1-19/Domain: signal sequence; status predicted <SIG>

F/34-117/Domain: immunoglobulin homology <IMM>

F/69-84/Region: complementarity-determining 1

F/118-131/Domain: complementarity-determining 2

F/132-144/Domain: complementarity-determining 3

F/145-160/Domain: complementarity-determining 4

Query Match 85.9%; Score 443; DB 2; Length 160;  
Best Local Similarity 84.7%; Pred. No. 1.2e-36; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVOLLQSAEVRKPGASVKSCASGYPTFTSYDLSWVRQAPGQGLEWMGMSISYSGNTDY 60  
|||||  
EVRKPGASVSKSCASGYPTFTSYDLSWVRQAPGQGLEWMGMSISYSGNTDY 60

Db 20 QVQLVSAEYVKKASVYKSCSKASGYFTSYGISMWRQAPGQGLEWMGMSISVNGDTNY 79  
Oy 61 AOKFOGRVTMTTDSRRTAYMELSLRSDPTAVYYCAR 98  
Db 80 AONLQGRVTMTTDTSTSTAYMELSLRSDPTAVYYCAR 117

## RESULT 7

S21925

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999

C:Accession: S21925

R:Friedman, D.F.

submitted to the EMBL Data Library, July 1991

A:Reference number: S21923

A:Accession: S21925

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-111 &lt;FRI&gt;

A:Cross-references: EMBL:X60503; NID:g33626; PIDN:CAA43023.1; PID:g33627

C:Genetics:

A:Insertions: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 82.2%; Score 424; DB 2; Length 111;  
Best Local Similarity 88.0%; Pred. No. 6.2e-35;  
Matches 81; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Oy 1 QVQLVSAEYVKKASVYKSCSKASGYFTSYDISWVRQAPGQGLEWMGMSISVNGTNDY 60  
Db 20 QVQLVSGAEYVKKASVYKSCSKASGYFTSYGISWVRQAPGQGLEWMGMSISVNGTNY 79  
Oy 61 AOKFOGRVTMTTDSRRTAYMELSLRSDPTA 92  
Db 80 AOKLQGRVTMTTDTSTSTAYMELSLRSDPTA 111

## RESULT 8

S26918

Ig heavy chain V region (DP-15) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S26918

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26918

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 &lt;TOM&gt;

A:Cross-references: EMBL:Z1317; NID:g32857; PIDN:CAA78187.1; PID:g32858

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 82.0%; Score 423; DB 2; Length 98;  
Best Local Similarity 82.7%; Pred. No. 6.8e-35;  
Matches 81; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Oy 1 QVQLVSAEYVKKASVYKSCSKASGYFTSYDISWVRQAPGQGLEWMGMSISVNGTNDY 60  
Db 1 QVQLVSGAEYVKKASVYKSCSKASGYFTSYDINWVRQAPGQGLEWMGMSISVNGTNGY 60  
Oy 61 AOKFOGRVTMTTDSRRTAYMELSLRSDPTAVYYCAR 98  
Db 61 AOKFOGRVTMTTDTSTSTAYMELSLRSDPTAVYYCAR 98

## RESULT 9

S31600  
Ig heavy chain V region (DP-75) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993  
C:Accession: S31600  
R:Cuisinier, A.M.; G  
submitted to the EMB  
A:Description: Mecha  
A:Reference number: S  
A:Accession: S31600  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-136 <C  
A:Cross-references: S  
C:Superfamily: immun  
C:Keywords: heterote  
F:34-117/Domain: imm

Query Match 81.4%; Score 420; DB 2; Length 136;  
Best Local Similarity 81.6%; Pred. No. 1.9e-34;  
Matches 80; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Oy 1 QVQLVSAEYVKKASVYKSCSKASGYFTSYDISWVRQAPGQGLEWMGMSISVNGTNDY 60  
Db 20 QVQLVSGAEYVKKASVYKSCSKASGYFTSYDINWVRQAPGQGLEWMGMSISVNGTNGY 79  
Oy 61 AOKFOGRVTMTTDSRRTAYMELSLRSDPTAVYYCAR 98  
Db 80 AOKFOGRVTMTTDTSTSTAYMELSLRSDPTAVYYCAR 117

## RESULT 10

S26938

Ig heavy chain V region (DP-75) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993

C:Accession: S26938

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A:Reference number: S26938

A:Accession: S26938

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 &lt;TOM&gt;

A:Cross-references: S

A&gt;Note: The nucleotide sequence was submitted to the EMBL Data Library, July 1992

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 80.6%; Score 416; DB 2; Length 98;  
Best Local Similarity 81.6%; Pred. No. 3.3e-34;  
Matches 80; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Oy 1 QVQLVSAEYVKKASVYKSCSKASGYFTSYDISWVRQAPGQGLEWMGMSISVNGTNDY 60  
Db 1 QVQLVSGAEYVKKASVYKSCSKASGYFTSYDINWVRQAPGQGLEWMGMSISVNGTNGY 60  
Oy 61 AOKFOGRVTMTTDSRRTAYMELSLRSDPTAVYYCAR 98  
Db 61 AOKFOGRVTMTTDTSTSTAYMELSLRSDPTAVYYCAR 98

## RESULT 11

S31680

Ig heavy chain V region (DP-75) - human (man)

C:Species: Homo sapiens (man)

C:Date: 03-Mar-1994

C:Accession: S31680

R:Cuisinier, A.M.; G  
submitted to the EMBL

A:Description: Mechanism that generate human immunoglobulin diversity operate from th

- human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31680  
R:Cuisinier, A.M.; G  
submitted to the EMBL Data Library, June 1992  
A:Description: Mechanism that generate human immunoglobulin diversity operate from th

Query Match 81.4%; Score 420; DB 2; Length 136;  
Best Local Similarity 81.6%; Pred. No. 1.9e-34;  
Matches 80; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Oy 1 QVQLVSAEYVKKASVYKSCSKASGYFTSYDISWVRQAPGQGLEWMGMSISVNGTNDY 60  
Db 20 QVQLVSGAEYVKKASVYKSCSKASGYFTSYDINWVRQAPGQGLEWMGMSISVNGTNGY 79  
Oy 61 AOKFOGRVTMTTDSRRTAYMELSLRSDPTAVYYCAR 98  
Db 80 AOKFOGRVTMTTDTSTSTAYMELSLRSDPTAVYYCAR 117

RESULT 10  
S26938  
Ig heavy chain V region (DP-75) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993  
C:Accession: S26938  
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
A:Reference number: S26938  
A:Accession: S26938  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-98 <TOM>  
A:Cross-references: S  
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, July 1992  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 80.6%; Score 416; DB 2; Length 98;  
Best Local Similarity 81.6%; Pred. No. 3.3e-34;  
Matches 80; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Oy 1 QVQLVSAEYVKKASVYKSCSKASGYFTSYDISWVRQAPGQGLEWMGMSISVNGTNDY 60  
Db 1 QVQLVSGAEYVKKASVYKSCSKASGYFTSYDINWVRQAPGQGLEWMGMSISVNGTNGY 60  
Oy 61 AOKFOGRVTMTTDSRRTAYMELSLRSDPTAVYYCAR 98  
Db 61 AOKFOGRVTMTTDTSTSTAYMELSLRSDPTAVYYCAR 98

RESULT 11  
S31680  
Ig heavy chain V region (DP-75) - human (man)  
C:Species: Homo sapiens (man)  
C:Date: 03-Mar-1994  
C:Accession: S31680  
R:Cuisinier, A.M.; G  
submitted to the EMBL Data Library, June 1992  
A:Description: Mechanism that generate human immunoglobulin diversity operate from th

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A:Reference number: S31585
A:Accession: S31680
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <CUI>
A:Cross-references: EMBL:Z14213; NID:g37795; PIDN:CAA78582.1; PID:g37796
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      80.6%; Score 416; DB 2; Length 117;
Best Local Similarity 81.6%; Pred. No. 4e-34;
Matches 80; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

OY 1 OVOLLQSAAEVRKPKGASVKSCKASGYPTFSYDLSWVRQAQGCLLEMGWISYSGNTDY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 OVQLVQSAGAEVKRKPASVKSCKASGYFTFSYHWMWRQAQGCLLEMGWINPNSGCTNY 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 AOKFOGRVTMTTDSRTATAYMELRLSRSDDTAVYYCAR 98
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AOKFOGRVTMTTDSRTATAYMELRLSRSDDTAVYYCAR 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
S18551
Ig heavy chain V region precursor (VI-2) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C:Accession: S18551; S23625
R:Shin, B.K.; Matsuda, F.; Nagaoaka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Seede, E.; H
EMBO J. 10, 3641-3645, 1991
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A:Reference number: S18551; MUID:92037524; PMID:1935893
A:Accession: S18551
A:Molecule type: DNA
A:Residues: 1-117 <SH1>
A:Cross-references: EMBL:X62106; NID:g37831; PIDN:CAA44016.1; PID:g37832
J:ROlde, T.; Lu, E.W.; Huang, D.F.; Soto-Gill, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associated immunoglobulin G rheumatoid factors from t
A:Reference number: S23623; MUID:92156804; PMID:1740665
A:Accession: S23625
A:Molecule type: DNA
A:Residues: 1-117 <OLE>
A:Cross-references: EMBL:X59704; NID:g32552; PIDN:CAA42225.1; PID:g32553
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      80.6%; Score 416; DB 2; Length 117;
Best Local Similarity 81.6%; Pred. NO. 4e-34;
Matches 80; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

OY 1 OVOLLQSAAEVRKPKGASVKSCKASGYPTFSYDLSWVRQAQGCLLEMGWISYSGNTDY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 OVQLVQSAGAEVKRKPASVKSCKASGYFTFSYHWMWRQAQGCLLEMGWINPNSGCTNY 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 AOKFOGRVTMTTDSRTATAYMELRLSRSDDTAVYYCAR 98
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 AOKFOGRVTMTTDSRTATAYMELRLSRSDDTAVYYCAR 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C:Species: Homo sapiens (man)
C>Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999

```

C:Accession: S49530  
 R:Mahmoudi, M.; Edwa  
 submitted to the EMF  
 A:Description: Molec  
 A:Reference number:  
 A:Accession: S49530  
 A:Status: preliminary  
 A:Molecule type: mR  
 A:Residues: 1-135 <b  
 A:Cross-references:  
 C:Superfamily: Immun  
 F:34-117/Domain: imm

Query Match  
 Best Local Similar  
 Matches 80; Cor

QY 1 QVQLL  
 Db 20 QVQLV  
 QY 61 AOKFO  
 Db 80 AOKFO

RESULT 14  
 S36265  
 Ig heavy chain V re  
 C:Species: Homo sap  
 C:Date: 03-Feb-1994  
 C:Accession: S36265  
 R:Griffiths, A.D.; b  
 EMBO J. 12, 725-734  
 A:Title: Human anti-  
 A:Reference number:  
 A:Accession: S36265  
 A:Status: preliminary  
 A:Molecule type: mR  
 A:Residues: 1-118 <b  
 A:Cross-references:  
 C:Superfamily: Immun  
 C:Keywords: heteroc  
 F:15-98/Domain: imm

Query Match  
 Best Local Similar  
 Matches 79; Cor

QY 1 QVQLL  
 Db 1 QVQLV  
 QY 61 AOKFO  
 Db 61 AOKFO

RESULT 15  
 S34014  
 Ig heavy chain V re  
 C:Species: Homo sap  
 C:Date: 02-Dec-1993  
 C:Accession: S34014  
 R:Maricette, X.; Tsai  
 Eur J. Immunol. 23  
 A:Title: Nucleotid  
 A:Reference number:  
 A:Accession: S34014  
 A:Status: preliminary  
 A:Molecule type: mR  
 A:Residues: 1-127 <b  
 A:Cross-references

Query Match  
 Best Local Similar  
 Matches 79; Cor

QY 1 QVQLL  
 Db 1 QVQLV  
 QY 61 AOKFO  
 Db 61 AOKFO

RESULT 16  
 S34014  
 Ig heavy chain V re  
 C:Species: Homo sap  
 C:Date: 02-Dec-1993  
 C:Accession: S34014  
 R:Maricette, X.; Tsai  
 Eur J. Immunol. 23  
 A:Title: Nucleotid  
 A:Reference number:  
 A:Accession: S34014  
 A:Status: preliminary  
 A:Molecule type: mR  
 A:Residues: 1-127 <b  
 A:Cross-references

Query Match  
 Best Local Similar  
 Matches 79; Cor

QY 1 QVQLL  
 Db 1 QVQLV  
 QY 61 AOKFO  
 Db 61 AOKFO

RESULT 17  
 S34014  
 Ig heavy chain V re  
 C:Species: Homo sap  
 C:Date: 02-Dec-1993  
 C:Accession: S34014  
 R:Maricette, X.; Tsai  
 Eur J. Immunol. 23  
 A:Title: Nucleotid  
 A:Reference number:  
 A:Accession: S34014  
 A:Status: preliminary  
 A:Molecule type: mR  
 A:Residues: 1-127 <b  
 A:Cross-references

Query Match  
 Best Local Similar  
 Matches 79; Cor

QY 1 QVQLL  
 Db 1 QVQLV  
 QY 61 AOKFO  
 Db 61 AOKFO

RESULT 18  
 S34014  
 Ig heavy chain V re  
 C:Species: Homo sap  
 C:Date: 02-Dec-1993  
 C:Accession: S34014  
 R:Maricette, X.; Tsai  
 Eur J. Immunol. 23  
 A:Title: Nucleotid  
 A:Reference number:  
 A:Accession: S34014  
 A:Status: preliminary  
 A:Molecule type: mR  
 A:Residues: 1-127 <b  
 A:Cross-references

Query Match  
 Best Local Similar  
 Matches 79; Cor

QY 1 QVQLL  
 Db 1 QVQLV  
 QY 61 AOKFO  
 Db 61 AOKFO

RESULT 19  
 S34014  
 Ig heavy chain V re  
 C:Species: Homo sap  
 C:Date: 02-Dec-1993  
 C:Accession: S34014  
 R:Maricette, X.; Tsai  
 Eur J. Immunol. 23  
 A:Title: Nucleotid  
 A:Reference number:  
 A:Accession: S34014  
 A:Status: preliminary  
 A:Molecule type: mR  
 A:Residues: 1-127 <b  
 A:Cross-references

Query Match  
 Best Local Similar  
 Matches 79; Cor

QY 1 QVQLL  
 Db 1 QVQLV  
 QY 61 AOKFO  
 Db 61 AOKFO

RESULT 20  
 S34014  
 Ig heavy chain V re  
 C:Species: Homo sap  
 C:Date: 02-Dec-1993  
 C:Accession: S34014  
 R:Maricette, X.; Tsai  
 Eur J. Immunol. 23  
 A:Title: Nucleotid  
 A:Reference number:  
 A:Accession: S34014  
 A:Status: preliminary  
 A:Molecule type: mR  
 A:Residues: 1-127 <b  
 A:Cross-references

Query Match  
 Best Local Similar  
 Matches 79; Cor

QY 1 QVQLL  
 Db 1 QVQLV  
 QY 61 AOKFO  
 Db 61 AOKFO

RESULT 21  
 S34014  
 Ig heavy chain V re  
 C:Species: Homo sap  
 C:Date: 02-Dec-1993  
 C:Accession: S34014  
 R:Maricette, X.; Tsai  
 Eur J. Immunol. 23  
 A:Title: Nucleotid  
 A:Reference number:  
 A:Accession: S34014  
 A:Status: preliminary  
 A:Molecule type: mR  
 A:Residues: 1-127 <b  
 A:Cross-references

Query Match  
 Best Local Similar  
 Matches 79; Cor

QY 1 QVQLL  
 Db 1 QVQLV  
 QY 61 AOKFO  
 Db 61 AOKFO

RESULT 22  
 S34014  
 Ig heavy chain V re  
 C:Species: Homo sap  
 C:Date: 02-Dec-1993  
 C:Accession: S34014  
 R:Maricette, X.; Tsai  
 Eur J. Immunol. 23  
 A:Title: Nucleotid  
 A:Reference number:  
 A:Accession: S34014  
 A:Status: preliminary  
 A:Molecule type: mR  
 A:Residues: 1-127 <b  
 A:Cross-references

Query Match  
 Best Local Similar  
 Matches 79; Cor

QY 1 QVQLL  
 Db 1 QVQLV  
 QY 61 AOKFO  
 Db 61 AOKFO

RESULT 23  
 S34014  
 Ig heavy chain V re  
 C:Species: Homo sap  
 C:Date: 02-Dec-1993  
 C:Accession: S34014  
 R:Maricette, X.; Tsai  
 Eur J. Immunol. 23  
 A:Title: Nucleotid  
 A:Reference number:  
 A:Accession: S34014  
 A:Status: preliminary  
 A:Molecule type: mR  
 A:Residues: 1-127 <b  
 A:Cross-references

Query Match  
 Best Local Similar  
 Matches 79; Cor

QY 1 QVQLL  
 Db 1 QVQLV  
 QY 61 AOKFO  
 Db 61 AOKFO

RESULT 24  
 S34014  
 Ig heavy chain V re  
 C:Species: Homo sap  
 C:Date: 02-Dec-1993  
 C:Accession: S34014  
 R:Maricette, X.; Tsai  
 Eur J. Immunol. 23  
 A:Title: Nucleotid  
 A:Reference number:  
 A:Accession: S34014  
 A:Status: preliminary  
 A:Molecule type: mR  
 A:Residues: 1-127 <b  
 A:Cross-references

Query Match  
 Best Local Similar  
 Matches 79; Cor

QY 1 QVQLL  
 Db 1 QVQLV  
 QY 61 AOKFO  
 Db 61 AOKFO

RESULT 25  
 S34014  
 Ig heavy chain V re  
 C:Species: Homo sap  
 C:Date: 02-Dec-1993  
 C:Accession: S34014  
 R:Maricette, X.; Tsai  
 Eur J. Immunol. 23  
 A:Title: Nucleotid  
 A:Reference number:  
 A:Accession: S34014  
 A:Status: preliminary  
 A:Molecule type: mR  
 A:Residues: 1-127 <b  
 A:Cross-references

Query Match  
 Best Local Similar  
 Matches 79; Cor

QY 1 QVQLL  
 Db 1 QVQLV  
 QY 61 AOKFO  
 Db 61 AOKFO

RESULT 26  
 S34014  
 Ig heavy chain V re  
 C:Species: Homo sap  
 C:Date: 02-Dec-1993  
 C:Accession: S34014  
 R:Maricette, X.; Tsai  
 Eur J. Immunol. 23  
 A:Title: Nucleotid  
 A:Reference number:  
 A:Accession: S34014  
 A:Status: preliminary  
 A:Molecule type: mR  
 A:Residues: 1-127 <b  
 A:Cross-references

Query Match  
 Best Local Similar  
 Matches 79; Cor

QY 1 QVQLL  
 Db 1 QVQLV  
 QY 61 AOKFO  
 Db 61 AOKFO

RESULT 27  
 S34014  
 Ig heavy chain V re  
 C:Species: Homo sap  
 C:Date: 02-Dec-1993  
 C:Accession: S34014  
 R:Maricette, X.; Tsai  
 Eur J. Immunol. 23  
 A:Title: Nucleotid  
 A:Reference number:  
 A:Accession: S34014  
 A:Status: preliminary  
 A:Molecule type: mR  
 A:Residues: 1-127 <b  
 A:Cross-references

Query Match  
 Best Local Similar  
 Matches 79; Cor

QY 1 QVQLL  
 Db 1 QVQLV  
 QY 61 AOKFO  
 Db 61 AOKFO

RESULT 28  
 S34014  
 Ig heavy chain V re  
 C:Species: Homo sap  
 C:Date: 02-Dec-1993  
 C:Accession: S34014  
 R:Maricette

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 413; DB 2; Length 127;  
Best Local Similarity 79.6%; Pred. No. 8.6e-34;  
Matches 78; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

OY	1	OVOLLQSAAEVRRKPKGASVYKVSCKASGYPTSYDISMVRQAPQGGLEMMGMWISIVSGNTDY	60
Db	1	OVQWYQSGAEVYKPKGASVYKVSCKASGYPTSYDINMVRQATGQGLEMMGMWNPSSGNTGY	60
QY	61	AQKFGGRVTMTTDSRRRTAYMELRSLSRSDDTAVYYCAR	98
Db	61	AQKFGGRVTMTTRNTSISTAYMELSLRSSEDTAVYFCAR	98

Search completed: December 30, 2003, 11:03:14  
Job time : 9.39399 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 30, 2003, 10:43:09 ; Search time 5.25426 Seconds

(without alignments)  
877.119 Million cell updates/sec

Title: US-09-674-752-28

Sequence: 1 QVQLQSGAEVRKPGASVKV.....AYMELRSIRSDPTAVYCAR 98

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	396	76.7	117	1	HY1B_HUMAN
2	392	76.0	117	1	HY1G_HUMAN
3	373	72.3	147	1	HY1C_HUMAN
4	344	66.7	117	1	HY1A_HUMAN
5	343	66.5	117	1	HY52_MOUSE
6	339	65.7	114	1	HY00_MOUSE
7	330	64.0	117	1	HY09_MOUSE
8	329	63.8	120	1	HY03_MOUSE
9	327	63.4	140	1	HY02_MOUSE
10	326	63.2	117	1	HY14_MOUSE
11	321	62.2	117	1	HY06_MOUSE
12	319	61.8	117	1	HY04_MOUSE
13	318	61.6	139	1	HY07_MOUSE
14	315	61.0	118	1	HY51_MOUSE
15	313	60.7	117	1	HY12_MOUSE
16	313	60.7	117	1	HY13_MOUSE
17	311	60.3	117	1	HY05_MOUSE
18	308	59.7	117	1	HY10_MOUSE
19	308	59.7	117	1	HY49_MOUSE
20	308	59.7	120	1	HY50_MOUSE
21	307	59.5	137	1	HY11_MOUSE
22	301	58.3	136	1	HY15_MOUSE
23	301	58.3	138	1	HY48_MOUSE
24	300	58.1	125	1	HY1F_HUMAN
25	290	56.2	121	1	HY01_MOUSE
26	287.5	55.7	120	1	HY3C_HUMAN
27	286	55.4	117	1	HY3H_HUMAN
28	278	53.9	117	1	HY55_MOUSE
29	277	53.7	121	1	HY3J_HUMAN
30	271	52.5	119	1	HY3I_HUMAN
31	267	51.7	122	1	HY3H_HUMAN
32	267	51.7	124	1	HY1E_HUMAN
33	266	51.6	122	1	HY3G_HUMAN

34	264	51.2	117	1	HY03_CARAU	P19180 carassius a
35	262	50.8	114	1	HY3B_HUMAN	P01763 homo sapien
36	261	50.6	119	1	HY3P_HUMAN	P01777 homo sapien
37	261	50.6	124	1	HY1D_HUMAN	P01760 homo sapien
38	260.5	50.5	116	1	HY05_CARAU	P19181 carassius a
39	259	50.2	136	1	HY16_MOUSE	P01783 mus musculu
40	258.5	50.1	115	1	HY3F_HUMAN	P01767 homo sapien
41	258	50.0	119	1	HY3L_HUMAN	P01773 homo sapien
42	257	49.8	115	1	HY3D_HUMAN	P01765 homo sapien
43	257	49.8	117	1	HY01_CAIOR	P01813 catman croc
44	257	49.8	117	1	HY54_MOUSE	P18525 mus musculu
45	255	49.4	122	1	HY3A_HUMAN	P01762 homo sapien

## ALIGNMENTS

```

RESULT 1
HY1B_HUMAN          STANDARD;          PRT;          117 AA.
ID   HY1B_HUMAN
AC   P01743;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-I region Hg3 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83144028; PubMed=6298778;
RA   Reichart G., Ram D., Glazer L., Zakut R., Givol D.;
RT   "Evolutionary aspects of immunoglobulin heavy chain variable region
RT   (VH) gene subgroups.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC   -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   -----
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CC   or send an email to license@ebi.ac.uk).
CC   -----
DR   EMBL; J00240; AAA52988.1; -.
DR   PIR; A02024; HVHUG.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF0047; Ig; 1.
DR   SMART; SM00406; IgV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1
FT   CHAIN           19
FT   DOMAIN          20 .. 117
FT   NON_TER         117
FT   DOMAIN          117
FT   NON_TER         117
SQ   SEQUENCE      117 AA; 12946 MW; 2D3P92FC60CD1FE7 CRC64;
Query Match          76.7%; Score 396; DB 1; Length 117;
Best Local Similarity 76.6%; Pred. No. 1e-38;
Matches 77; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
QY   1 QVQLQSGAEVRKPGASVKASGYPFTSYDYSWVRQAPGQGLEWMGWSISYGNTRY 60
DB   20 QVQLQSGAEVRKPGASVKASGYSYTFNSYIMHWVRQAPGQGLEWMGIINPGSGSTSY 79

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QY 61 AOKFOGRVTMTDTSRTAYMEI.RSDDTAYVYCAR 98
DB 80 AOKFOGRVTMTDTSRTAYMEI.RSDDTAYVYCAR 117

RESULT 2
ID HV1G_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukushima S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus."
RL EMBO J. 7:1047-1051(1988).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL: X07448; NOT_ANNOTATED_CDS.
DR PIR; S00476; HYHUS3.
DR HSSP; P01772; 2PB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003066; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 1 17 IG HEAVY CHAIN V-I REGION V35.
FT DOMAIN 20 >117 IG-LIKE.
FT NON TER 117
SQ SEQUENCE 117 AA; 13009 MW; BE1CE63F8CE97BD CRC64;

Query Match 76.0%; Score 392; DB 1; Length 117;
Best Local Similarity 78.6%; Pred. No. 3e-38;
Matches 77; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVOLLQSAAEVRKPGASVYKSCASGYPTSYDISWYRQAPGQGLEMMGMISYSGNTDY 60
DB 20 QVOLLQSGAEVRKPGASVYKSCASGYPTSYDISWYRQAPGQGLEMMGMISYSGNTDY 79

RESULT 3
ID HV1C_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.U.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line."
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Benmich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; 1MCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003066; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal; Pyroglutamate carboxylic acid.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT DOMAIN 20 131 IG-LIKE.
FT MOD RES 20 20 PYROGLUTAMATE CARBOXYLIC ACID.
FT DISUFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON TER 147 147
SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 72.3%; Score 373; DB 1; Length 147;
Best Local Similarity 71.4%; Pred. No. 6e-36;
Matches 70; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVOLLQSAAEVRKPGASVYKSCASGYPTSYDISWYRQAPGQGLEMMGMISYSGNTDY 60
DB 20 QVOLLQSGAEVRKPGASVYKSCASGYPTSYDISWYRQAPGQGLEMMGMISYSGNTDY 79

RESULT 4
ID HV1A_HUMAN STANDARD; PRT; 117 AA.
AC P01742;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

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RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A.; Rutishauser U.; Gail W.E.; Gottlieb P.D.;
RA Maxdal M.J.; Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen Bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gail W.E.; Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS
CC MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90563; GIMHEU.
DR HSSP; P01772; 2PB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG LIKE; 1.
KM Immunoglobulin V region; Pyrolydione carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12472 MW; 99D60ADAEBD52818 CRC64;

Query Match 66.7%; Score 344; DB 1; Length 117;
Best Local Similarity 71.1%; Pred. No. 1e-32;
Matches 69; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 QVQLQSGAEVKKGASVKVSCKRSGYPFTSYDSWVRQAPGGGLEMMGWISITSGTDY 60
DB 1 QVQLVQSGAEVKKRQSSVKVSCKASGCTFSRAIHWROAPGGLEMMGWIVPMGEPNY 60
QY 61 AOKFGQVMTTDTSRRTAYMELSLRSDPTAVYYCA 97
DB 61 AOKFGQVMTTADSTRTAYMELSLRSDPTAVYYCA 97

RESULT 5
HV52_MOUSE STANDARD; PRT; 117 AA.
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578121;
RA Yancopoulos G.D.; Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
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CC -----
DR EMBL; M13787; AAA38499.1; -
DR PIR; A02029; HYMSA1.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DISULFID 86 117 FRAMEWORK-3.
FT NON_TER 41 115 BY SIMILARITY.
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138656DFC9D CRC64;

Query Match 66.5%; Score 343; DB 1; Length 117;
Best Local Similarity 64.3%; Pred. No. 1.3e-32;
Matches 63; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 1 QVQLQSGAEVKKRQSSVKVSCKASGYPFTSYDSWVRQAPGGGLEMMGWISITSGTDY 60
DB 20 QVQLVQSGAEVKKRQSSVKVSCKASGYPFTSYDSWVRQAPGGGLEMMGWIVPMGEPNY 79
QY 61 AOKFGQVMTTDTSRRTAYMELSLRSDPTAVYYCA 98
DB 80 NEKFGKATITADKSSRTAYMELSLRSDPTAVYYCA 117

RESULT 6
HV00_MOUSE STANDARD; PRT; 114 AA.
ID HV00_MOUSE STANDARD; PRT; 114 AA.
AC P01741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region (Anti-arsenate antibody).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=79195438; PubMed=109536;
RA Capra J.D.; Nisenzon A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
RT mice bearing a cross-reactive idiotype.";
RL J. Immunol. 123:279-284(1979).
CC -1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
CC THE IGH1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC REGION SEQUENCE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02022; GIMSA.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 106 IG-LIKE.
FT NON_TER 114 114

```



SQ SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A9F4BE CRC64;  
 Query Match 65.7%; Score 339; DB 1; Length 114;  
 Best Local Similarity 68.0%; Pred. No. 3.7e-32;  
 Matches 66; Conservative 14; Mismatches 17; Indels 0; Gaps 0;  
 QY 1 QVOLLQSAAEVRKPKASVYKSCASGYPTFSYDISWVRQAPGQGLMGMISISYSGNTDY 60  
 DB 1 EVOLLQSGAEIVKAGSVKMSCKATGYTFSYELTWVRQAPGQGLDGLGYISSSAYPRY 60  
 QY 61 AQFGQGVMTTDTSRRTAYMELRSLSRSDDTAYYYCA 97  
 DB 61 AQFGQGVMTTDESTNTAYMELSSLSRSDTAYYYCA 97  
 RESULT 7  
 HV09\_MOUSE STANDARD; PRT; 117 AA.  
 ID HV09\_MOUSE  
 AC P01753; P11271;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region 186-1 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6;  
 RX MEDLINE=81234548; PubMed=6788376;  
 RA Botwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NPB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
 RT Cell 24:625-637(1981).  
 CC -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY  
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NEW ANTIBODIES.  
 CC PIR; D90809; HVMS61.  
 DR HSSP; P01810; 2FBJ.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 1 19  
 FT DOMAIN 20 117 IG HEAVY CHAIN V REGION 186-1.  
 FT DOMAIN 20 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;  
 Query Match 64.0%; Score 330; DB 1; Length 117;  
 Best Local Similarity 64.3%; Pred. No. 4.1e-31;  
 Matches 63; Conservative 13; Mismatches 22; Indels 0; Gaps 0;  
 QY 1 QVOLLQSAAEVRKPKASVYKSCASGYPTFSYDISWVRQAPGQGLMGMISISYSGNTDY 60  
 DB 20 QVOLLQSGAEIVKAGSVKMSCKATGYTFSYELTWVRQAPGQGLDGLGYISSSAYPRY 79  
 QY 61 AQFGQGVMTTDTSRRTAYMELRSLSRSDDTAYYYCAR 98  
 DB 80 NEKFKSKATLTVDKSSSTAYMQLSLTSEDSAVYYCAR 117  
 RESULT 8  
 HV03\_MOUSE

ID HV03\_MOUSE STANDARD; PRT; 120 AA.  
 AC P01747;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region 36-65.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83131846; PubMed=6186498;  
 RA Siekevitz M., Gelfer M.L., Brodeur P., Riblet R.,  
 RA Marchak-Rothstein A.;  
 RT "The genetic basis of antibody production: the dominant anti-arsenate  
 RT idiotype response of the strain A mouse."  
 RL Eur. J. Immunol. 12:1023-1032(1982).  
 CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER  
 CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS  
 CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J  
 CC SEGMENT, JH2.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR HSSP; P01789; IMCP.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR Immunoglobulin V region; Hybridoma.  
 FT DOMAIN 1 111 IG-LIKE.  
 FT NON\_TER 120 120  
 SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;  
 Query Match 63.8%; Score 329; DB 1; Length 120;  
 Best Local Similarity 62.9%; Pred. No. 5.6e-31;  
 Matches 61; Conservative 18; Mismatches 18; Indels 0; Gaps 0;  
 QY 2 VOLLQSAAEVRKPKASVYKSCASGYPTFSYDISWVRQAPGQGLMGMISISYSGNTDYA 61  
 DB 1 VOLLQSGAEIVKAGSVKMSCKATGYTFSYELTWVRQAPGQGLDGLGYISSSAYPRY 60  
 QY 62 OKFGQGVMTTDTSRRTAYMELRSLSRSDDTAYYYCAR 98  
 DB 61 EKFKGKTTLTVDKSSSTAYMQLSLTSEDSAVYYCAR 97  
 RESULT 9  
 HV02\_MOUSE STANDARD; PRT; 140 AA.  
 ID HV02\_MOUSE  
 AC P01746;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region 93G7 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=A/J;  
 RX MEDLINE=82152818; PubMed=6801765;  
 RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,  
 RA Capra J.D.;  
 RT "Somatic mutation in genes for the variable portion of the  
 RT immunoglobulin heavy chain."  
 RL Science 216:309-311(1982).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL/J00493; AAA8128.1; -  
DR PIR; A94264; HVM5G7.  
DR HSSP; P01810; 2PBJ.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SMO0406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KM Immunoglobulin V region; Hybridoma; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.  
FT DOMAIN 20 139 IG-LIKE.  
FT NON TER 140 140  
SQ SEQUENCE 140 AA; 15514 MW; 25AACBBE31DA5C8 CRC64;

Query Match 63.4%; Score 327; DB 1; Length 140;  
Best Local Similarity 61.2%; Pred. No. 1.1e-30;  
Matches 60; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

OY 1 QVOLLQSAAEVRKPKASVYVSCSKASGYPTSDISWVRQAPGQGLWMGMWISYSGNTDY 60  
DB 20 EVQLQDSAEELVKKASVYVSCSKASGYFTSDYGNHVMVQSGKSLWIGIYIPVNGTGY 79

OY 61 AQKFGKVTMTDTSRRTAYMELRLSRDDPAVYYCAR 98  
DB 80 NEKFKGKTTLTVDNSSLTSSSTAYMELRLSRDSEDAVYYCAR 117

Db

RESULT 10  
HV14\_MOUSE  
ID HV14\_MOUSE STANDARD; PRT; 117 AA.  
AC P01758;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region 108A precursor.  
GN IGH-VJ558.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81245215; PubMed=6789211;  
RA Glivol D., Zakut R., Eitron K., Rechavi G., Ram D., Cohen J.B.;  
RT "Diversity of germ-line immunoglobulin VH genes."  
RL Nature 292:426-430(1981).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC  
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CC EMBL/J00488; AAA8519.1; -  
DR PIR; A02041; HVM58A.  
DR HSSP; P01810; 2PBJ.  
DR MGD; MGI:96486; Igh-VJ558.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IGV; 1.  
DR SMART; SMO0406; IGV; 1.  
DR SMART; SMO0406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.  
KM Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.  
FT DOMAIN 20 >117 IG-LIKE.  
FT NON TER 117 117  
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 63.2%; Score 326; DB 1; Length 117;  
Best Local Similarity 61.2%; Pred. No. 1.2e-30;  
Matches 60; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

OY 1 QVOLLQSAAEVRKPKASVYVSCSKASGYPTSDISWVRQAPGQGLWMGMWISYSGNTDY 60  
DB 20 EVQLQDSAEELVKKASVYVSCSKASGYFTSDYGNHVMVQSGKSLWIGIYIPVNGTGY 79

OY 61 AQKFGKVTMTDTSRRTAYMELRLSRDDPAVYYCAR 98  
DB 80 NQKFKSKATLTVDNSSLTSSSTAYMELRLSRDSEDAVYYCAR 117

Db

RESULT 11  
HV06\_MOUSE  
ID HV06\_MOUSE STANDARD; PRT; 117 AA.  
AC P01750;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region 102 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=81234548; PubMed=6788376;  
RA Botwell A.L.M., Paekind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NPB family of  
RT antibodies: somatic mutation evident in a gamma 2a variable region."  
RL Cell 24:625-637(1981).  
CC -1- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY  
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.  
CC  
CC PIR; A02032; HVM502.  
DR HSSP; P01810; 2PBJ.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IGV; 1.  
DR SMART; SMO0406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KM Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON TER 117 117  
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD51FCA8C CRC64;

Query Match 62.2%; Score 321; DB 1; Length 117;  
Best Local Similarity 64.6%; Pred. No. 4.5e-30;  
Matches 62; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

OY 2 VOLLQSAAEVRKPKASVYVSCSKASGYPTSDISWVRQAPGQGLWMGMWISYSGNTDYA 61  
DB 21 VQLQDSAEELVKKASVYVSCSKASGYFTSDYGNHVMVQSGKSLWIGIYIPVNGTGYN 80

OY 62 AQKFGKVTMTDTSRRTAYMELRLSRDDPAVYYCAR 97









DT 01-DEC-2001 (Tremblrel. 19, last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC009851; AAH09851.1; -  
DR InterPro; IPR000005; HTHARC.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig\_V.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00041; HTH\_ARC\_FAMILY\_1; 1.  
DR PROSITE; PS00835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 73.3%; Score 378; DB 4; Length 614;  
Best Local Similarity 72.4%; Pred. No. 2.3e-34;  
Matches 71; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

OY 1 QVOLLQSAEVRKPGASVSKASGYPTSYDISWVROAPGGLMMGMISISGNTDY 60  
DB 20 QVOLLQSGAEVRKPGASVSKASGYPTSYDISWVROAPGGLMMGMHITFNGNTY 79  
OY 61 AQKFGQRLTMTDTSRRRTAYMELRSLSRSDTAVYVCAR 98  
DB 80 AQKFGQRLTMTDTSRRRTAYMELRSLSRSDTAVYVCAR 117

RESULT 6  
Q8WY24 PRELIMINARY; PRT; 497 AA.  
AC Q8WY24;  
DT 01-MAR-2002 (Tremblrel. 20, Created)  
DT 01-MAR-2002 (Tremblrel. 20, last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)  
DE SNC66 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;  
RT "Identification and characterization of SNC66, a Ig-like gene which is  
RT down-regulated in colorectal cancer."  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF283666; AAL36987.1; -  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_V.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A63E5 CRC64;

Query Match 72.7%; Score 375; DB 4; Length 497;  
Best Local Similarity 70.4%; Pred. No. 3.9e-34;  
Matches 69; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

OY 1 QVOLLQSAEVRKPGASVSKASGYPTSYDISWVROAPGGLMMGMISISGNTDY 60  
DB 20 QVOLLQSGAEVRKPGASVSKASGYPTSYDISWVROAPGGLMMGMHITFNGNTY 79

OY 61 AQKFGQRLTMTDTSRRRTAYMELRSLSRSDTAVYVCAR 98  
DB 80 AQKFGQRLTMTDTSRRRTAYMELRSLSRSDTAVYVCAR 117

RESULT 7  
O96O50 PRELIMINARY; PRT; 159 AA.  
AC O96O50;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)  
DE Putative matrix cell adhesion molecule-3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tilson M.D.;  
RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3  
RT mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3)."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY039025; AAK82649.1; -  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_V.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 72.3%; Score 373; DB 4; Length 159;  
Best Local Similarity 72.4%; Pred. No. 1.6e-34;  
Matches 71; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

OY 1 QVOLLQSAEVRKPGASVSKASGYPTSYDISWVROAPGGLMMGMISISGNTDY 60  
DB 20 QVOLLQSGAEVRKPGASVSKASGYPTSYDISWVROAPGGLMMGMHITFNGNTY 79  
OY 61 AQKFGQRLTMTDTSRRRTAYMELRSLSRSDTAVYVCAR 98  
DB 80 AQKFGQRLTMTDTSRRRTAYMELRSLSRSDTAVYVCAR 117

RESULT 8  
O9GY22 PRELIMINARY; PRT; 119 AA.  
AC O9GY22;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, last annotation update)  
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region  
DE (Frigment).  
OS Schistosoma japonicum (Blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidae;  
OC Schistosomatidae; Schistosomatidae; Schistosoma.  
OX NCBI\_TaxID=6182;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Song X.T., Peng Z.Q., Guan X.H.;  
RT "Amplification, cloning and sequence analysis of the heavy chain  
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of  
RT Schistosoma japonicum."  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF282622; AAG01452.1; -  
DR HSP; P01772; 2F84.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_V.  
DR SMART; SM00406; IGV; 1.

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DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FDF5FA6AB CRC64;

Query Match 71.5%; Score 369; DB 5; Length 119;
Best Local Similarity 72.4%; Pred. No. 3,3e-34;
Matches 71; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 QVQLQSAAEVRKPGASVSKVSCKASGYPTSYDISWVRQAPGQGLWMGMWISYSGNTDY 60
DB 1 QVQLVESGAEVRKPGASVSKVSCKASGYPTGYVMWVRQADGHGLEGWIGYINPSRGYNY 60

QY 61 AOKFGQRYTMTDTSRRRTAYMELSLRSDPTAVYYCAR 98
DB 61 NQKFKRVRTMTTDSKFSSTAYMDLSLRSDASAVYYCAR 98

RESULT 9
QY 09UL89 PRELIMINARY; PRT; 116 AA.
AC 09UL89;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalie N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035025; AAD56261.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; 1g; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1 116
SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

Query Match 68.4%; Score 353; DB 4; Length 116;
Best Local Similarity 75.3%; Pred. No. 2,1e-32;
Matches 70; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 5 LOSAAEVRKPGASVSKVSCKASGYPTSYDISWVRQAPGQGLWMGMWISYSGNTDYAOKF 64
DB 1 VOSGAEEVRKPGSSVSKVSCKASGCTFSVAISWVRQAPGQGLWMGMRIIPILGIANVYAKKF 60

QY 65 QGRVMTTDTSTRRTAYMELSLRSDPTAVYYCA 97
DB 61 QGRVTTTADKSTSTAYMELSLRSEDPTAVYYCA 93

RESULT 10
QY 0925S3 PRELIMINARY; PRT; 147 AA.
AC 0925S3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE MRP3.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
   the repair of intestinal epithelium after irradiation in mice.";
RT world J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse gene related to repairing of intestinal epithelium
   of the irradiated mice by treatment with the intestinal RNA of mice of
   the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240166; AAK43731.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; 1g; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

Query Match 66.5%; Score 343; DB 11; Length 147;
Best Local Similarity 66.3%; Pred. No. 3,8e-31;
Matches 65; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 1 QVQLQSAAEVRKPGASVSKVSCKASGYPTSYDISWVRQAPGQGLWMGMWISYSGNTDY 60
DB 3 QVQLHOSGPEVRKPGASVSKVSCKASGYPTSYDIDWVRQPEQGLEWIGWIFPEGSTEX 62

QY 61 AOKFGQRYTMTDTSRRRTAYMELSLRSDPTAVYYCAR 98
DB 63 NEKFKRATLSVDSSTAYMELSLRSDASAVYYFCAR 100

RESULT 11
QY 09Y298 PRELIMINARY; PRT; 150 AA.
AC 09Y298;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE IGG VH protein precursor (Fragment).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96322155; PubMed=9657749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
   IgG4 monoclonal antibody derived from a hemophilia A patient with
   inhibitor.";
RT Blood 92:496-506(1998).
RL Blood 92:496-506(1998).
DR EMBL; AJ224083; CAA11829.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; 1g; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.

```



```

FT  NON TER      150      150
SQ  SEQUENCE      150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match
Best Local Similarity 66.3%; Score 342; DB 4; Length 150;
Best Local Similarity 69.1%; Pred. No. 5.1e-31;
Matches 67; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

OY  1 QVOLLQSAAEVKKPGASVVKVSCKASGYPTSDISWVQAPQGLQEMMGWISYSGNTDY 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  20 QVOLLQSGAEVKKPGASVVKVSCKASGYPTSLTPMHWGAPGKGLQEMVGSFDPESGESIT 79
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY  61 AOKFGQVYMTTDTSRRTAYMELSLRSDPTAVYYCA 97
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  80 AREFGSVTMTADTSTDIAVMELSLRSDPTAVYYCA 116
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 12
O8VCX7 PRELIMINARY; PRT; 613 AA.
O8VCX7
AC  O8VCX7;
DT  01-MAR-2002 (TREMBLrel. 20, Created)
DT  01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT  01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE  Hypothetical 67.9 kDa protein.
GN  IGH-6.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Salivary gland;
RA  Strausberg R.;
RL  Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC018315; AAH18315.1; -.
DR  MGD; MGI:96448; Igh-6.
DR  InterPro; IPR003006; Igh_MHC.
DR  InterPro; IPR003596; Igh_v.
DR  Pfam; PF00047; Igh_5.
DR  SMART; SM00406; Igv_1.
DR  PROSITE; PS50835; IGH_LIKE; 5.
DR  PROSITE; PS00290; IGH_MHC; 3.
SQ  Hypothetical protein.
KW  SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match
Best Local Similarity 65.7%; Score 339; DB 11; Length 613;
Matches 64; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

OY  1 QVOLLQSAAEVKKPGASVVKVSCKASGYPTSDISWVQAPQGLQEMMGWISYSGNTDY 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  20 QVOLLQSGAEVKKPGASVVKVSCKASGYPTSSWIEMVQKRPQHGELIPLGSGSTNY 79
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY  61 AOKFGQVYMTTDTSRRTAYMELSLRSDPTAVYYCA 98
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  80 NEKFKGKATFTADTSSNTAYMQLSLTSEDSAVYYCAR 117
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 13
O91WT1 PRELIMINARY; PRT; 481 AA.
O91WT1
AC  O91WT1;
DT  01-DEC-2001 (TREMBLrel. 19, Created)
DT  01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT  01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE  Hypothetical 52.1 kDa protein.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.

```

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RC  TISSUE=Colon;
RA  Strausberg R.;
RL  Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC013490; AAH13490.1; -.
DR  InterPro; IPR007110; Igh-Like.
DR  InterPro; IPR003006; Igh_MHC.
DR  InterPro; IPR003596; Igh_v.
DR  Pfam; PF00047; Igh_4.
DR  SMART; SM00406; Igv_1.
DR  PROSITE; PS50835; IGH_LIKE; 4.
DR  PROSITE; PS00290; IGH_MHC; 2.
KW  Hypothetical protein.
SQ  SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match
Best Local Similarity 65.5%; Score 338; DB 11; Length 481;
Matches 64; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

OY  1 QVOLLQSAAEVKKPGASVVKVSCKASGYPTSDISWVQAPQGLQEMMGWISYSGNTDY 60
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  20 QVOLLQSGPELVKPGASVVKVSCKASGYFTSYIHWVQKRPQGLQEMVGYGNTNY 79
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

OY  61 AOKFGQVYMTTDTSRRTAYMELSLRSDPTAVYYCA 98
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB  80 NEKFKGKATFTADKSSSTAYMFLSLTSEDSAVYFCTR 117
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 14
O9DBL4 PRELIMINARY; PRT; 473 AA.
O9DBL4
AC  O9DBL4;
DT  01-JUN-2001 (TREMBLrel. 17, Created)
DT  01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT  01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE  1810060099rik protein.
GN  IGH-1 OR 1810060009RIK.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J; TISSUE=Pancreas;
RX  MEDLINE=21085660; Pubmed=11217851;
RA  Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA  Atakawa T., Hara A., Fukumishi Y., Konno H., Adachi J., Fukuda S.,
RA  Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA  Saito T., Okazaki Y., Gotohori T., Bono H., Kaubakawa T., Saito R.,
RA  Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA  Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA  Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA  Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA  Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA  Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA  Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA  Guernicich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA  Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA  Nordone P., Ring B., Ringwald M., Rodriguez I., Sakanato N.,
RA  Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA  Suzuki H., Toyokawa K., Wang K.H., Weitz C., Wittlaker C., Wilming L.,
RA  Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA  Hayashizaki Y.;
RT  "Functional annotation of a full-length mouse cdna collection.";
RL  Nature 409:685-690(2001).
DR  EMBL; AK007918; BAB25349.1; -.
DR  HSSP; P01842; 7FAB.
DR  MGD; MGI:96443; Igh-1.
DR  InterPro; IPR007110; Igh-Like.
DR  InterPro; IPR003006; Igh_MHC.
DR  InterPro; IPR003596; Igh_v.
DR  Pfam; PF00047; Igh_4.
DR  SMART; SM00406; Igv_1.
DR  PROSITE; PS50835; IGH_LIKE; 4.

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 31.5256 Seconds  
(without alignments)  
493.415 Million cell updates/sec

Title: US-09-674-752-28  
Perfect score: 516  
Sequence: 1 QVQLQSGAEVRKRGASVKV.....AYWELRSLRSDTRAVYYCAR 98

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
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6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	504	97.7	98	21	AA50955 Human anti-factor
2	500	96.9	132	21	AA50953 Human anti-factor
3	491	95.2	132	21	AA50950 Human anti-factor
4	471	91.3	98	21	AA50954 Human anti-factor
5	467	90.5	247	23	ABP45105 Human Bly's binding
6	467	90.5	250	23	ABP45549 Human Bly's binding
7	464	89.9	250	23	ABP45584 Human Bly's binding
8	460	89.1	98	21	AA50952 Human anti-factor
9	460	89.1	98	23	ABG91862 Human antibody fra

10	460	89.1	98	23	ABG78171 Human Fv molecule
11	460	89.1	104	22	ABG55895 Human liver peptid
12	460	89.1	104	22	ABR40538 Peptide #8044 enco
13	460	89.1	117	16	ABR66311 Human immunoglobul
14	460	89.1	248	23	ABP45461 Human Bly's binding
15	460	89.1	251	23	ABP45551 Human Bly's binding
16	460	89.1	251	23	ABP45861 Human Bly's binding
17	460	89.1	251	23	ABP45910 Human Bly's binding
18	460	89.1	255	23	ABP45179 Human Bly's binding
19	460	89.1	259	23	ABP45345 Human Bly's binding
20	458	88.8	251	23	ABP45727 Human Bly's binding
21	457	88.6	247	23	ABP45862 Human Bly's binding
22	457	88.6	249	23	ABP45414 Human Bly's binding
23	457	88.6	250	23	ABP45550 Human Bly's binding
24	457	88.6	250	23	ABP45582 Human Bly's binding
25	457	88.6	251	23	ABP45867 Human Bly's binding
26	456	88.4	248	23	ABP45860 Human Bly's binding
27	456	88.4	251	23	ABP45575 Human Bly's binding
28	456	88.4	251	23	ABP45859 Human Bly's binding
29	455	88.2	248	23	ABP45767 Human Bly's binding
30	455	88.2	257	23	ABP45568 Human Bly's binding
31	454	88.0	251	23	ABP45544 Human Bly's binding
32	454	88.0	254	23	ABP45394 Human Bly's binding
33	453	87.8	253	23	ABP45953 Human Bly's binding
34	452	87.6	248	23	ABP45866 Human Bly's binding
35	451.5	87.5	246	23	ABP45181 Human Bly's binding
36	451	87.4	98	21	AA50951 Human anti-factor
37	451	87.4	247	23	ABP45715 Human Bly's binding
38	451	87.4	257	23	ABP45599 Human Bly's binding
39	451	87.4	259	23	ABP44962 Human Bly's binding
40	450	87.2	251	23	ABP44919 Human Bly's binding
41	450	87.2	251	23	ABP45725 Human Bly's binding
42	450	87.2	251	23	ABP45858 Human Bly's binding
43	449	87.0	121	22	AAU02549 Anti-adipocyte mon
44	449	87.0	253	23	ABP45625 Human Bly's binding
45	449	87.0	259	23	ABP45441 Human Bly's binding

## ALIGNMENTS

RESULT 1  
ID AA50955 standard; Protein: 98 AA.  
AC AA50955;  
XX 23-MAR-2000 (first entry)  
XX Human anti-factor VIII antibody VH protein VH EL-25.  
XX Human, heavy chain; antibody; factor VIII; hemostatic;  
XX hemophilia A; VH protein.  
XX Homo sapiens.  
XX W09958680-A2.  
XX 18-NOV-1999.  
XX 07-MAY-1999; 99WO-NL0285.  
XX 08-MAY-1998; 98EP-0201543.  
XX (SAND-) STICHTING SANDUIN BLOEDVOORZIENING.  
XX Voorberg JJ, Van Den Brink EN, Turenhout EAM;  
XX WPI: 2000-053102/04.  
XX New polynucleotide, polypeptide and antibody useful for diagnosing the  
XX presence of neutralizing antibodies against factor VIII and for  
XX treatment of hemophilia A patients with these antibodies -  
XX

XX Example 4; Fig 4B; 61pp; English.

XX This invention describes a novel polynucleotide (1) (and complements and

CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence

CC coding for a human antibody with factor VIII specificity which has

CC hemostatic activity. (1) is useful as a primer or probe for detecting the

CC presence of inhibitory antibodies directed against factor VIII. The

CC polypeptides of the invention and the antibodies generated from them

CC are useful in compositions for neutralizing factor VIII inhibiting

CC antibodies in hemophilia A patients. This sequence represents the human

CC anti-factor VIII antibody VH EL-25 protein which is used in the method

CC of the invention.

XX Sequence 98 AA;

SQ

Query Match 97.7%; Score 504; DB 21; Length 98;

Best Local Similarity 98.0%; Pred. No. 8,6e-43;

Matches 96; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLQSAAEVRKPGASVKVSCASGYPTSYDLSWVRQAPGQGLEWMGMSISGNTDY 60

DB 1 QVQLQSAAEVRKPGASVKVSCASGYPTSYDLSWVRQAPGQGLEWMGMSISGNTDY 60

OY 61 AQRFGQRYVTMTTDSRTTAYMELRSLSRSDPTAVYYCAR 98

DB 61 AQRFGQRYVTMTTDSRTTAYMELRSLSRSDPTAVYYCAR 98

RESULT 2

AA50953

ID AA50953 standard; Protein; 132 AA.

XX

AC AA50953;

XX

DT 23-MAR-2000 (first entry)

XX

DE Human anti-factor VIII antibody VH protein VH IT-2.

XX

KM Human; heavy chain; antibody; factor VIII; hemostatic;

XX

OS Homo sapiens.

XX

PN MO958680-A2.

XX

PD 18-NOV-1999.

XX

PF 07-MAY-1999; 99MO-NL00285.

XX

PR 08-MAY-1998; 98EP-0201543.

XX

PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.

XX

PI Voorberg JJ, Van Den Brink EN, Turenhout EAM;

XX

DR WPI; 2000-053102/04.

XX

PT New polynucleotide, polypeptide and antibody useful for diagnosing the

PT presence of neutralizing antibodies against factor VIII and for

PT treatment of hemophilia A patients with these antibodies -

XX

PS Example 4; Fig 4B; 61pp; English.

XX

CC This invention describes a novel polynucleotide (1) (and complements and

CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence

CC coding for a human antibody with factor VIII specificity which has

CC hemostatic activity. (1) is useful as a primer or probe for detecting the

CC presence of inhibitory antibodies directed against factor VIII. The

CC polypeptides of the invention and the antibodies generated from them

CC are useful in compositions for neutralizing factor VIII inhibiting

CC antibodies in hemophilia A patients. This sequence represents the human

CC anti-factor VIII antibody VH IT-2 protein which is used in the method

CC of the invention.

XX

SQ Sequence 132 AA;

Query Match 96.9%; Score 500; DB 21; Length 132;

Best Local Similarity 95.9%; Pred. No. 3e-42;

Matches 94; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLQSAAEVRKPGASVKVSCASGYPTSYDLSWVRQAPGQGLEWMGMSISGNTDY 60

DB 1 QVQLQSAAEVRKPGASVKVSCASGYPTSYDLSWVRQAPGQGLEWMGMSISGNTDY 60

OY 61 AQRFGQRYVTMTTDSRTTAYMELRSLSRSDPTAVYYCAR 98

DB 61 AQRFGQRYVTMTTDSRTTAYMELRSLSRSDPTAVYYCAR 98

RESULT 3

AA50950

ID AA50950 standard; Protein; 132 AA.

XX

AC AA50950;

XX

DT 23-MAR-2000 (first entry)

XX

DE Human anti-factor VIII antibody VH clone IT-2 encoded protein.

XX

KM Human; heavy chain; antibody; factor VIII; hemostatic;

XX

KM hemophilia A; VH gene.

XX

OS Homo sapiens.

XX

PN MO958680-A2.

XX

PD 18-NOV-1999.

XX

PF 07-MAY-1999; 99MO-NL00285.

XX

PR 08-MAY-1998; 98EP-0201543.

XX

PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.

XX

PI Voorberg JJ, Van Den Brink EN, Turenhout EAM;

XX

DR WPI; 2000-053102/04.

XX

PT New polynucleotide, polypeptide and antibody useful for diagnosing the

PT presence of neutralizing antibodies against factor VIII and for

PT treatment of hemophilia A patients with these antibodies -

XX

PS Example 4; Fig 4A; 61pp; English.

XX

CC This invention describes a novel polynucleotide (1) (and complements and

CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence

CC coding for a human antibody with factor VIII specificity which has

CC hemostatic activity. (1) is useful as a primer or probe for detecting the

CC presence of inhibitory antibodies directed against factor VIII. The

CC polypeptides of the invention and the antibodies generated from them

CC are useful in compositions for neutralizing factor VIII inhibiting

CC antibodies in hemophilia A patients. This sequence represents the human

CC anti-factor VIII antibody clone IT-2 protein which is used in the method

CC of the invention.

XX

SQ Sequence 132 AA;

Query Match 95.2%; Score 491; DB 21; Length 132;

Best Local Similarity 94.9%; Pred. No. 2,3e-41;

Matches 93; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLQSAAEVRKPGASVKVSCASGYPTSYDLSWVRQAPGQGLEWMGMSISGNTDY 60

DB 1 QVQLQSAAEVRKPGASVKVSCASGYPTSYDLSWVRQAPGQGLEWMGMSISGNTDY 60

```

QY 61 AAKFGGRVTMTTDSRRTAYMELSLRSDDTAAYYCAR 98
   |||||||
DB 61 AAKFGGRVTMTTDSRRTAYMELSLRSDDTAAYYCAR 98

RESULT 4
AAY50954
XX AAY50954 standard; Protein, 98 AA.
AC AAY50954;
XX
XX 23-MAR-2000 (first entry)
XX
XX Human anti-factor VIII antibody VH protein VH EL-5.
DE
XX
XX Human, heavy chain; antibody; factor VIII; hemostatic;
KM hemophilia A; VH protein.
XX
XX Homo sapiens.
OS
XX MO9958680-A2.
PN
XX 18-NOV-1999.
PD
XX
XX 07-MAY-1999; 99WO-NL00285.
PF
XX
XX 08-MAY-1998; 98EP-0201543.
PR
XX
XX (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING.
PA
XX
XX Voorberg JF, Van Den Brink EN, Turenhout EAM;
PI
XX WPI; 2000-053102/04.
DR
XX
XX New polynucleotide, polypeptide and antibody useful for diagnosing the
PT presence of neutralizing antibodies against factor VIII and for
PT treatment of hemophilia A patients with these antibodies -
PS
XX Example 4; Fig 4B; 61pp; English.
XX
XX This invention describes a novel polynucleotide (I) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (I) is useful a primer or probe for detecting the
CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents the human
CC anti-factor VIII antibody VH EL-5 protein which is used in the method
CC of the invention.
XX
XX Sequence 98 AA;
SQ

Query Match 91.3%; Score 471; DB 21; Length 98;
Best Local Similarity 89.8%; Pred. No. 1.7e-39;
Matches 88; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

```

```

XX
XX Human Blys binding scFv seq ID 116.
DE
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antineutritic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
OS
XX MO200202641-A1.
PN
XX
XX 10-JAN-2002.
PD
XX
XX 15-JUN-2001; 2001WO-US19110.
PR
XX
XX 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
PA
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI
XX WPI; 2002-114799/15.
DR
XX
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
PS
XX Claim 1; Page 1734-1735; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineutritic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
XX Sequence 247 AA;
SQ

Query Match 90.5%; Score 467; DB 23; Length 247;
Best Local Similarity 90.8%; Pred. No. 1.1e-38;
Matches 89; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

```

AC ABP45549;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 1560.  
XX  
KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KM tumor necrosis factor; B cell proliferation; B cell differentiation;  
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US19110.  
XX  
PR 16-JUN-2000; 2000US-212210P.  
XX  
PR 17-OCT-2000; 2000US-240816P.  
XX  
PR 16-MAR-2001; 2001US-276248P.  
XX  
PR 21-MAR-2001; 2001US-277379P.  
XX  
PR 25-MAY-2001; 2001US-293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX  
DR WPI; 2002-114799/15.  
XX  
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for  
XX the diagnosis and treatment of cancers and immune disorders -  
XX  
PS Claim 1; Page 2264-2265; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
CC tumor necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method  
CC of the invention.  
XX  
SQ Sequence 250 AA;  
XX  
Query Match 90.5%; Score 467; DB 23; Length 250;  
Best Local Similarity 90.8%; Pred. No. 1,1e-38;  
Matches 89; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
QY 1 OVOLLQSAAEVRKPGASVKSCAKSGYPFTSYDISWVRQAPGGGLEMGWISISGNTDY 60  
DB 1 OVOLLQSAAEVRKPGASVKSCAKSGYFTSYDISWVRQAPGGGLEMGWISISGNTNY 60  
QY 61 AOKFGQGVTTTDSRTAYMELRSLRSDPTAVYYCAR 98  
DB 61 AOKLQGRVTMTTDTSTAYMELRSLRSDPTAVYYCAR 98  
RESULT 7

ABP45584  
ID ABP45584 standard; Protein; 250 AA.  
XX  
AC ABP45584;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 1595.  
XX  
KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KM tumor necrosis factor; B cell proliferation; B cell differentiation;  
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US19110.  
XX  
PR 16-JUN-2000; 2000US-212210P.  
XX  
PR 17-OCT-2000; 2000US-240816P.  
XX  
PR 16-MAR-2001; 2001US-276248P.  
XX  
PR 21-MAR-2001; 2001US-277379P.  
XX  
PR 25-MAY-2001; 2001US-293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
XX  
DR WPI; 2002-114799/15.  
XX  
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for  
XX the diagnosis and treatment of cancers and immune disorders -  
XX  
PS Claim 1; Page 2306-2307; 3148pp; English.  
XX  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
CC tumor necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method  
CC of the invention.  
XX  
SQ Sequence 250 AA;  
XX  
Query Match 89.9%; Score 464; DB 23; Length 250;  
Best Local Similarity 89.8%; Pred. No. 2.2e-38;  
Matches 88; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 1 OVOLLQSAAEVRKPGASVKSCAKSGYPFTSYDISWVRQAPGGGLEMGWISISGNTDY 60  
DB 1 OVOLLQSAAEVRKPGASVKSCAKSGYFTSYDISWVRQAPGGGLEMGWISISGNTNY 60  
QY 61 AOKFGQGVTTTDSRTAYMELRSLRSDPTAVYYCAR 98  
DB 61 AOKLQGRVTMTTDTSTAYMELRSLRSDPTAVYYCAR 98

RESULT 8	
AAV50952	
ID	AAV50952 standard; Protein; 98 AA.
AC	
XX	AAV50952;
XX	
DT	23-MAR-2000 (first entry)
XX	
DE	Human anti-factor VIII antibody VH clone DP-14 protein #2.
XX	
KW	Human; heavy chain; antibody; factor VIII; hemostatic;
XX	hemophilia A; VH gene.
XX	
OS	Homo sapiens.
XX	
PN	W09358680-A2.
PD	18-NOV-1999.
XX	
PF	07-MAY-1999; 99WO-NL00285.
XX	
PR	08-MAY-1998; 98EP-0201543.
XX	
PA	(SANQ-) STICHTING SANQUIN BLOEDVOORZIENING.
XX	
PI	Voorberg JJ, Van Den Brink EN, Turenhout EM;
XX	
DR	WPI: 2000-053102/04.
XX	
PT	New polynucleotide, polypeptide and antibody useful for diagnosing the
PT	presence of neutralizing antibodies against factor VIII and for
PT	treatment of hemophilia A patients with these antibodies -
XX	
PS	Example 4; Fig 4B: 61pp; English.
XX	
CC	This invention describes a novel polynucleotide (I) (and complements and
CC	hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC	coding for a human antibody with factor VIII specificity which has
CC	hemostatic activity. (I) is useful a primer or probe for detecting the
CC	presence of inhibitory antibodies directed against factor VIII. The
CC	polypeptides of the invention and the antibodies generated from them
CC	are useful in compositions for neutralizing factor VIII inhibiting
CC	antibodies in hemophilia A patients. This sequence represents the human
CC	anti-factor VIII antibody clone DP-14 protein which is used in the method
CC	of the invention.
XX	
XX	
SO	Sequence 98 AA;
XX	
Query Match	89.1%; Score 460; DB 21; Length 98;
Best Local Similarity	88.8%; Pred. No. 2.1e-38;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0.	
OY	1 OVOLLQSAAEYRRKPPASVYKSCAGGYFTSDISMVQAPCGLEMMGWISYSGNTDY 60
DB	1 OVQLVQSGAEYRRKPPASVYKSCAGGYFTSDISMVQAPCGLEMMGWISYSGNTDY 60
OY	61 AOKFQGRVTMTTDSRRATYMLRLSRDPTAVYYCAR 98
DB	61 AOKLQGRVTMTTDSSTAYMYELRLSRDPTAVYYCAR 98
XX	
RESULT 9	
ABG91862	
XX	ABG91862 standard; Protein; 98 AA.
XX	
AC	ABG91862;
XX	
DT	04-DEC-2002 (first entry)
XX	
DE	Human antibody fragment #46.
XX	

XX	Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KM	metastasis; hypervariable region; autoimmune disease; thrombosis;
KM	restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KM	myocardial infarction; retinopathic disease; abnormal platelet function;
XX	sulphated tyrosine-dependent protein-protein interaction.
OS	
XX	Homo sapiens.
XX	
XX	WO200253700-A2.
XX	
XX	11-JUL-2002.
XX	
XX	31-DEC-2001; 2001WO-US49442.
XX	
XX	29-DEC-2000; 2000US-258948P.
XX	
XX	29-DEC-2000; 2000US-0751181.
XX	
XX	(BIOT-) BIO-TECHNOLOGY GEN CORP.
XX	
XX	Lazarovits J, Hagat Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;
XX	Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX	WPI, 2002-674776/72.
XX	
XX	Novel isolated epitope present on cancer cells and important in
XX	physiological phenomena such as cell rolling, metastasis and
XX	inflammation, for treating autoimmune, inflammatory or cardiovascular
XX	diseases, and cancer -
XX	
XX	Disclosure; Page 246-247; 310pp; English.
XX	
XX	The invention relates to an isolated epitope present on cancer cells and
XX	important in physiological phenomena such as cell rolling, metastasis and
XX	inflammation, where the epitope is capable of being bound by an antibody,
XX	its antigen-binding fragment or its complex comprising at least one
XX	antibody or its binding fragment having a first hypervariable region. The
XX	epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
XX	disease, thrombosis, restenosis, metastasis, growth and/or replication of
XX	tumour or leukaemia cells, increase in number of tumour or leukaemia
XX	cells in a patient, cell-cell, cell-matrix, platelet-matrix,
XX	platelet-platelet and/or cell-platelet adhesion or aggregation, for
XX	increasing mortality of tumour or leukaemia cells, for increasing the
XX	susceptibility of diseased cells to damage by anti-disease, anti-cancer
XX	or anti-leukaemia agents, or for decreasing the number of tumour or
XX	leukaemia cells in a patient, or in the manufacture of a medicament for
XX	the above mentioned purposes. The epitopes are useful for diagnosing and
XX	treating diseases such as cancer, leukaemia, autoimmune diseases,
XX	inflammatory diseases, cardiovascular diseases such as myocardial
XX	infarction, retinopathic diseases and other diseases mediated by abnormal
XX	platelet function and diseases caused by sulphated tyrosine-dependent
XX	protein-protein interactions. This sequence represents a human antibody
XX	fragment of the invention.
XX	
XX	
XX	Sequence 98 AA:
XX	
XX	Query Match 89.1%; Score 460; DB 23; Length 98;
XX	Best Local Similarity 88.8%; Pred. No. 2,1e-38;
XX	Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
XX	
XX	1 QVOLLQSAAEVRKKGASVYVSCAKSGYGFSTSYDISWRQAPGQGLNMGWISISGNTDY 60
XX	
XX	1 QVQLVQSGAEVKKPKQASVYVSCAKSGYGFSTSYDISWRQAPGQGLNMGWISAVNGNTNY 60
XX	
XX	61 AOKFGQGRVTMTTDSRKRAVYVELSLSSDDPAVYYCAK 98
XX	
XX	61 AOKLQGRVTMTTDSSTAYVVELSLSSDDPAVYYCAK 98
XX	
XX	
XX	RESULT 10
XX	ABG78171
XX	ID ABG78171 standard; Protein; 98 AA.
XX	
XX	ABG78171;

```
XX DT 15-NOV-2002 (first entry)
XX XX
DE Human Fv molecule hypervariable region related peptide #46.
XX XX
KM Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
XX KM disulfide Fv; dsFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
XX KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX OS Homo sapiens.
XX PN WO200259264-A2.
XX PD 01-AUG-2002.
XX PF 31-DEC-2001; 2001WO-US49440.
XX PR 29-DEC-2000; 2000US-0751181.
XX XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX XX
PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;
PI Plaksin D, Peretz T;
XX XX
DR WPI; 2002-619166/66.
XX XX
PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favour of other
PT cells -
XX XX
PS Claim 13; Page 169; 232pp; English.
XX XX
CC The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention.
XX XX
SQ Sequence 98 AA;
XX XX
Query Match 89.1%; Score 460; DB 23; Length 98;
Best Local Similarity 88.8%; Pred. No. 2.1e-38;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
XX XX
QY 1 QVQLTQSAAEVRKRGASVSKASGYPTFTSYDTSWVRQAPGQGLEWMGMSISYSGTDY 60
XX |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 1 QVQLVQSGAEVKKPKGASVSKASGYTFTSYGISWVRQAPGQGLEWMGMISAYNGTNY 60
XX |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 AOKFGKRVMTTDTSTRTAYMELRSRSDPTAVYYCAR 98
XX |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 61 AOKLQGRVMTTDTSTRTAYMELRSRSDPTAVYYCAR 98
XX |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
XX XX
RESULT 11
ID ABB55895
XX ABB55895 standard; Peptide; 104 AA.
XX AC ABB55895;
XX XX
DT 25-FEB-2003 (first entry)
XX XX
DE Human liver peptide, SEQ ID No 34543.
XX XX
```

```
XX KM Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX KM hypercholesterolaemia; coronary heart disease.
XX XX
OS Homo sapiens.
XX PN WO200157273-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00664.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX
DR WPI; 2001-488898/53.
XX XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analysing gene expression in human adult liver -
XX XX
PS Claim 27; SEQ ID No 34543; 658pp; English.
XX XX
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult
CC liver. (I) may be used for predicting, measuring and displaying gene
CC expression in samples derived from human adult liver. The genes
CC identified may be involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
CC is associated with coronary heart disease. ABB47348-ABB5930 represent
CC human liver single exon encoded peptides of the invention.
CC Note: The sequence information for this patent does not appear in the
CC printed specification but was obtained in electronic format directly
CC from WIPO at ffp.wipo.int/pub/published_pct_sequences.
XX XX
SQ Sequence 104 AA;
XX XX
Query Match 89.1%; Score 460; DB 22; Length 104;
Best Local Similarity 88.8%; Pred. No. 2.2e-38;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
XX XX
QY 1 QVQLTQSAAEVRKRGASVSKASGYPTFTSYDTSWVRQAPGQGLEWMGMSISYSGTDY 60
XX |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 4 QVQLVQSGAEVKKPKGASVSKASGYTFTSYGISWVRQAPGQGLEWMGMISAYNGTNY 63
XX |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 AOKFGKRVMTTDTSTRTAYMELRSRSDPTAVYYCAR 98
XX |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 64 AOKLQGRVMTTDTSTRTAYMELRSRSDPTAVYYCAR 101
XX |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
XX XX
RESULT 12
ID ABB40538
XX ABB40538 standard; Peptide; 104 AA.
XX AC ABB40538;
XX XX
DT 04-FEB-2002 (first entry)
XX XX
DE Peptide #8044 encoded by human foetal liver single exon probe.
XX KM Human; foetal liver; gene expression; single exon nucleic acid probe.
XX XX
```



OS Homo sapiens.  
 XX  
 XX MO200157277-A2.  
 PN  
 XX  
 XX 09-AUG-2001.  
 PD  
 XX  
 XX 30-JAN-2001; 2001WO-US00669.  
 PF  
 XX  
 XX 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 P1  
 XX WPI; 2001-483447/52.  
 DR  
 XX  
 XX Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human fetal liver -  
 PT  
 XX  
 XX Claim 27; SEQ ID NO 33173; 639pp + sequence listing; English.  
 PS  
 XX The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal  
 CC liver. The single exon nucleic acid probes may be used for predicting,  
 CC measuring and displaying gene expression in samples derived from human  
 CC fetal liver. The present sequence is a peptide encoded by a single exon  
 CC nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SO Sequence 104 AA;  
 Query Match 89.1%; Score 460; DB 22; Length 104;  
 Best Local Similarity 88.8%; Pred. No. 2.2e-38;  
 Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 OVOLLGSAAEVRKPGASVKVSKASGYPTFSYDISWVRAPGGGLEWVGWISAYNGNTDY 60  
 DB 4 OVOLLGSAAEVRKPGASVKVSKASGYPTFSYDISWVRAPGGGLEWVGWISAYNGNTNY 63  
 QY 61 AOKFQGRVTMTTDTSRRTAYMELSLRSDDTAAYYCAR 98  
 DB 64 AOKLQGRVTMTTDTSRRTAYMELSLRSDDTAAYYCAR 101  
 QY  
 DB  
 DE Human immunoglobulin variable heavy chain #17.  
 XX  
 XX  
 XX Primer: PCR; amplify; human; immunoglobulin; variable; heavy chain;  
 KM cosmid; placenta; vector; pJB81; E.coli; mammalian.  
 OS  
 XX Homo sapiens.  
 OS  
 XX WO9426895-A1.  
 PN  
 XX 24-NOV-1994.  
 PD  
 XX 10-MAY-1993; 93MO-JP00603.  
 PF

XX  
 PR 10-MAY-1993; 93MO-JP00603.  
 XX  
 XX (NISR ) JAPAN TOBACCO INC.  
 PA  
 XX  
 XX Honjo T, Matsuda F;  
 P1  
 XX WPI; 1995-006791/01.  
 DR N-PSDB; AAQ78956.  
 DR  
 XX  
 XX DNA fragment comprising human immunoglobulin Vh genes - for the  
 PT production of human immunoglobulin in mammalian hosts  
 PT  
 XX  
 XX Claim 27; Page 54-55; 130pp; Japanese.  
 PS  
 XX Protein sequences (AA66295-51) are novel human immunoglobulin heavy  
 CC chain sequences encoded by novel isolated genes. The genes  
 CC (AAQ78939-79002) were isolated and cloned from a series of cosmid  
 CC constructs: Y202; Y103; Y21; Y6; Y24; 3-31; M84; M18 and M31, by PCR  
 CC amplification using primers AAQ78917-38. The genes are subdivided into 5  
 CC families of Vh genes. The fragments cover a region of 800 kb. The DNA  
 CC fragments were isolated from high molecular weight DNA from human  
 CC placenta. The DNA was partially digested with Taqi restriction enzyme.  
 CC The fragments were separated by gel electrophoresis and 35-45 kb fractions  
 CC were collected. The fragments were ligated with ClaI-digested cosmid  
 CC vector pJB81. The ligation products were in vitro packed and infected  
 CC into E.coli 490A. The fragments were then subcloned by colony  
 CC hybridisation. The Vh genes and the DNA fragments encoding them are  
 CC useful in producing human immunoglobulin in mammalian hosts.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX  
 SO Sequence 117 AA;  
 Query Match 89.1%; Score 460; DB 16; Length 117;  
 Best Local Similarity 88.8%; Pred. No. 2.5e-38;  
 Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 OVOLLGSAAEVRKPGASVKVSKASGYPTFSYDISWVRAPGGGLEWVGWISAYNGNTDY 60  
 DB 20 OVOLLGSAAEVRKPGASVKVSKASGYPTFSYDISWVRAPGGGLEWVGWISAYNGNTNY 79  
 QY 61 AOKFQGRVTMTTDTSRRTAYMELSLRSDDTAAYYCAR 98  
 DB 80 AOKLQGRVTMTTDTSRRTAYMELSLRSDDTAAYYCAR 117  
 QY  
 DB  
 DE Human Bly's binding scFv SEQ ID 1472.  
 XX  
 XX  
 XX 19-AUG-2002 (first entry)  
 DT  
 XX  
 XX  
 XX Bly's; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KM immunosuppressive; immunostimulant; immunomodulatory; antithumatic;  
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200202641-A1.  
 PN  
 XX  
 XX 10-JAN-2002.  
 PD  
 XX  
 XX 15-JUN-2001; 2001WO-US19110.  
 PF  
 XX  
 XX 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR

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PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 2159-2160; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 248 AA;
XX
Query Match 89.1%; Score 460; DB 23; Length 248;
Best Local Similarity 88.8%; Pred. No. 5,5e-38;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
XX
QY 1 QVOLLGSAAEVKKPGASVSVKSCASGYPTTSYDISWVRQAPGGGLEMMGMISYSGNTDY 60
DB 1 QVOLLVSGAEVKKPGASVSVKSCASGYPTTSYDISWVRQAPGGGLEMMGMISYNGNTNY 60
XX
QY 61 AOKFGGRVTMTTDSRTAYMELRLSRSDDTAVYYCAR 98
DB 61 AOKLQGRVTMTTDSRTAYMELRLSRSDDTAVYYCAR 98
XX
RESULT 15
ABP4551
ID ABP4551 standard; Protein; 251 AA.
XX
AC ABP4551;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1562.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.

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XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 2267-2268; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 251 AA;
XX
Query Match 89.1%; Score 460; DB 23; Length 251;
Best Local Similarity 88.8%; Pred. No. 5,6e-38;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
XX
QY 1 QVOLLGSAAEVKKPGASVSVKSCASGYPTTSYDISWVRQAPGGGLEMMGMISYSGNTDY 60
DB 1 QVOLLVSGAEVKKPGASVSVKSCASGYPTTSYDISWVRQAPGGGLEMMGMISYNGNTNY 60
XX
QY 61 AOKFGGRVTMTTDSRTAYMELRLSRSDDTAVYYCAR 98
DB 61 AOKLQGRVTMTTDSRTAYMELRLSRSDDTAVYYCAR 98
XX
Search completed: December 30, 2003, 10:54:31
Job time : 31.6089 secs

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Db 61 AOKLQGRVTMTDTSTSTAYMELRSLSRSDDTAVYYCAR 98

## RESULT 2

US-09-880-748-1560  
; Sequence 1560, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1560  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1560

Query Match 90.5%; Score 467; DB 11; Length 250;

Best Local Similarity 90.8%; Pred. No. 1,9e-40;

Matches 89; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 QVOLLQSAAEVRRKPGASVSKVSCASGYPTFTSYDISWVRQAPQGGLMMGMISAYNGNTDY 60

Db 1 QVOLLQSAAEVRRKPGASVSKVSCASGYPTFTSYDISWVRQAPQGGLMMGMISAYNGNTDY 60

QY 61 AOKFQGRVTMTDTSTSTAYMELRSLSRSDDTAVYYCAR 98

Db 61 AOKLQGRVTMTDTSTSTAYMELRSLSRSDDTAVYYCAR 98

## RESULT 3

US-09-880-748-1595  
; Sequence 1595, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1595  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1595

Query Match 89.9%; Score 464; DB 11; Length 250;

Best Local Similarity 89.8%; Pred. No. 3.8e-40;

Matches 88; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 QVOLLQSAAEVRRKPGASVSKVSCASGYPTFTSYDISWVRQAPQGGLMMGMISAYNGNTDY 60

Db 1 QVOLLQSAAEVRRKPGASVSKVSCASGYPTFTSYDISWVRQAPQGGLMMGMISAYNGNTDY 60

QY 61 AOKFQGRVTMTDTSTSTAYMELRSLSRSDDTAVYYCAR 98

Db 61 AOKLQGRVTMTDTSTSTAYMELRSLSRSDDTAVYYCAR 98

## RESULT 4

US-10-041-860-2  
; Sequence 2, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gad  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezabeh, Binyam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES  
; FILE REFERENCE: ABGENIX.051A  
; CURRENT APPLICATION NUMBER: US/10/041,860  
; CURRENT FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-041-860-2

Query Match 89.1%; Score 460; DB 12; Length 98;

Best Local Similarity 88.8%; Pred. No. 3.6e-40;

Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVOLLQSAAEVRRKPGASVSKVSCASGYPTFTSYDISWVRQAPQGGLMMGMISAYNGNTDY 60

Db 1 QVOLLQSAAEVRRKPGASVSKVSCASGYPTFTSYDISWVRQAPQGGLMMGMISAYNGNTDY 60

QY 61 AOKFQGRVTMTDTSTSTAYMELRSLSRSDDTAVYYCAR 98

Db 61 AOKLQGRVTMTDTSTSTAYMELRSLSRSDDTAVYYCAR 98

## RESULT 5

US-10-041-860-324  
; Sequence 324, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Feng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gad  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezabeh, Binyam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES  
; FILE REFERENCE: ABGENIX.051A  
; CURRENT APPLICATION NUMBER: US/10/041,860  
; CURRENT FILING DATE: 2002-01-07  
; NUMBER OF SEQ ID NOS: 377  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 324  
; LENGTH: 98

TYPE: PRT  
ORGANISM: homo sapiens  
US-10-041-860-324

Query Match 89.1%; Score 460; DB 12; Length 98;  
Best Local Similarity 88.8%; Pred. No. 3.6e-40;  
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLTQSAEVRKPGASVSKVSCKASGYPTSYDISWVRQAPGQGLEWMGMISISGNTDY 60  
Db 1 QVQLVSGAEVKKRPGASVSKVSCKASGYTFTSYGISWVRQAPGQGLEWMGMISAYNGNTNY 60

Qy 61 AOKFGKRVMTTDTTSRTAYMELRLSRSDDTAVYYCAR 98  
Db 61 AOKLQGRVTMTTDTSTSTAYMELRLSRSDDTAVYYCAR 98

RESULT 6  
US-10-041-860-326

Sequence 326, Application US/10041860  
Publication No. US20030157109A1

GENERAL INFORMATION:  
APPLICANT: Corvalan, Jose R.F.

APPLICANT: Jia, Xiao-Chi

APPLICANT: Feng, Xiao

APPLICANT: Yang, Xiao-Dong

APPLICANT: Chen, Francine

APPLICANT: Gazit, Gadi

APPLICANT: Weber, Richard

APPLICANT: Bezabeh, Binyam

TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES

FILE REFERENCE: ABGENIX.051A

CURRENT APPLICATION NUMBER: US/10/041,860

CURRENT FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

SOFTWARE: FaestSeq for Windows Version 4.0

SEQ ID NO 326

LENGTH: 98

TYPE: PRT

ORGANISM: homo sapiens

US-10-041-860-326

Query Match 89.1%; Score 460; DB 12; Length 98;  
Best Local Similarity 88.8%; Pred. No. 3.6e-40;  
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLTQSAEVRKPGASVSKVSCKASGYPTSYDISWVRQAPGQGLEWMGMISISGNTDY 60  
Db 1 QVQLVSGAEVKKRPGASVSKVSCKASGYTFTSYGISWVRQAPGQGLEWMGMISAYNGNTNY 60

Qy 61 AOKFGKRVMTTDTTSRTAYMELRLSRSDDTAVYYCAR 98  
Db 61 AOKLQGRVTMTTDTSTSTAYMELRLSRSDDTAVYYCAR 98

RESULT 7  
US-10-041-860-355

Sequence 355, Application US/10041860  
Publication No. US20030157109A1

GENERAL INFORMATION:  
APPLICANT: Corvalan, Jose R.F.

APPLICANT: Jia, Xiao-Chi

APPLICANT: Feng, Xiao

APPLICANT: Yang, Xiao-Dong

APPLICANT: Chen, Francine

APPLICANT: Gazit, Gadi

APPLICANT: Weber, Richard

APPLICANT: Bezabeh, Binyam

TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES

FILE REFERENCE: ABGENIX.051A

CURRENT APPLICATION NUMBER: US/10/041,860

CURRENT FILING DATE: 2002-01-07  
NUMBER OF SEQ ID NOS: 377  
SOFTWARE: FaestSeq for Windows Version 4.0  
SEQ ID NO 355  
LENGTH: 98  
TYPE: PRT  
ORGANISM: homo sapiens  
US-10-041-860-355

Query Match 89.1%; Score 460; DB 12; Length 98;  
Best Local Similarity 88.8%; Pred. No. 3.6e-40;  
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLTQSAEVRKPGASVSKVSCKASGYPTSYDISWVRQAPGQGLEWMGMISISGNTDY 60  
Db 1 QVQLVSGAEVKKRPGASVSKVSCKASGYTFTSYGISWVRQAPGQGLEWMGMISAYNGNTNY 60

Qy 61 AOKFGKRVMTTDTTSRTAYMELRLSRSDDTAVYYCAR 98  
Db 61 AOKLQGRVTMTTDTSTSTAYMELRLSRSDDTAVYYCAR 98

RESULT 8  
US-10-041-860-356

Sequence 356, Application US/10041860  
Publication No. US20030157109A1

GENERAL INFORMATION:  
APPLICANT: Corvalan, Jose R.F.

APPLICANT: Jia, Xiao-Chi

APPLICANT: Feng, Xiao

APPLICANT: Yang, Xiao-Dong

APPLICANT: Chen, Francine

APPLICANT: Gazit, Gadi

APPLICANT: Weber, Richard

APPLICANT: Bezabeh, Binyam

TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES

FILE REFERENCE: ABGENIX.051A

CURRENT APPLICATION NUMBER: US/10/041,860

CURRENT FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

SOFTWARE: FaestSeq for Windows Version 4.0

SEQ ID NO 356

LENGTH: 98

TYPE: PRT

ORGANISM: homo sapiens

US-10-041-860-356

Query Match 89.1%; Score 460; DB 12; Length 98;  
Best Local Similarity 88.8%; Pred. No. 3.6e-40;  
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLTQSAEVRKPGASVSKVSCKASGYPTSYDISWVRQAPGQGLEWMGMISISGNTDY 60  
Db 1 QVQLVSGAEVKKRPGASVSKVSCKASGYTFTSYGISWVRQAPGQGLEWMGMISAYNGNTNY 60

Qy 61 AOKFGKRVMTTDTTSRTAYMELRLSRSDDTAVYYCAR 98  
Db 61 AOKLQGRVTMTTDTSTSTAYMELRLSRSDDTAVYYCAR 98

RESULT 9  
US-10-308-817-44

Sequence 44, Application US/10308817  
Publication No. US20030219861A1

GENERAL INFORMATION:  
APPLICANT: Rocher, Russell

APPLICANT: Wu, Dayang

APPLICANT: Bezabeh, Binyam

TITLE OF INVENTION: HYBRID ANTIBODIES

FILE REFERENCE: 1087-37

CURRENT APPLICATION NUMBER: US/10/308,817

CURRENT FILING DATE: 2002-12-03

NUMBER OF SEQ ID NOS: 195

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; SOFTWARE: Patentin version 3.1
; SEQ ID NO 44
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-44

Query Match      89.1%; Score 460; DB 12; Length 98;
Best Local Similarity 88.8%; Pred. No. 3.6e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 OVQLQSAAEVRKPGASVYKSCASGYPTSYDISWVQAQPGQGLEMMGWSISYSGNTDY 60
DB 1 OVQLVQSAEVRKPGASVYKSCASGYPTSYDISWVQAQPGQGLEMMGWSISYNGNTNY 60

QY 61 AOKFGQRYVTMTTDTSTRRTAYMELRSLRSDDTAVYYCAR 98
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

RESULT 10
US-10-194-975-4
; Sequence 4, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-4

Query Match      89.1%; Score 460; DB 15; Length 98;
Best Local Similarity 88.8%; Pred. No. 3.6e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 OVQLQSAAEVRKPGASVYKSCASGYPTSYDISWVQAQPGQGLEMMGWSISYSGNTDY 60
DB 1 OVQLVQSAEVRKPGASVYKSCASGYPTSYDISWVQAQPGQGLEMMGWSISYNGNTNY 60

QY 61 AOKFGQRYVTMTTDTSTRRTAYMELRSLRSDDTAVYYCAR 98
DB 61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98

RESULT 11
US-09-864-761-47285
; Sequence 47285, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
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; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47285
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB019440.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.42
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.8
; OTHER INFORMATION: SWISSPROT HIT: P23083, EVALU8 2.00e-39
; OTHER INFORMATION: EST_HUMAN HIT: AW403728.1, EVALU8 4.00e-45
US-09-864-761-47285

Query Match      89.1%; Score 460; DB 9; Length 104;
Best Local Similarity 88.8%; Pred. No. 3.8e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 OVQLQSAAEVRKPGASVYKSCASGYPTSYDISWVQAQPGQGLEMMGWSISYSGNTDY 60
DB 4 OVQLVQSAEVRKPGASVYKSCASGYPTSYDISWVQAQPGQGLEMMGWSISYNGNTNY 63

QY 61 AOKFGQRYVTMTTDTSTRRTAYMELRSLRSDDTAVYYCAR 98
DB 64 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 101

RESULT 12
US-10-041-860-206
; Sequence 206, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvajan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezbien, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USBS
; FILE REFERENCE: ABGENIX.051A
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; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 117
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-206

Query Match      89.1%; Score 460; DB 12; Length 117;
Best Local Similarity 88.8%; Pred. No. 4.7e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Oy 1 OVOLLQSAAEVRKPGASVYVSCKASGYPTSYDISWVRQAPGQGLEMMGWMISYSGNTDY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 OVOLLQSAAEVRKPGASVYVSCKASGYPTSYDISWVRQAPGQGLEMMGWMISAYNGNTNY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Oy 61 AOKFGQRYVTMTTDSRRTAYMELRSLRSDDTAVYYCAR 98
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98
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RESULT 13
US-10-041-860-42
; Sequence 42, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USBS
; FILE REFERENCE: ABGENTX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-42

Query Match      89.1%; Score 460; DB 12; Length 125;
Best Local Similarity 88.8%; Pred. No. 4.7e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Oy 1 OVOLLQSAAEVRKPGASVYVSCKASGYPTSYDISWVRQAPGQGLEMMGWMISYSGNTDY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 OVOLLQSAAEVRKPGASVYVSCKASGYPTSYDISWVRQAPGQGLEMMGWMISAYNGNTNY 60
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Oy 61 AOKFGQRYVTMTTDSRRTAYMELRSLRSDDTAVYYCAR 98
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Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98
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RESULT 14
US-10-041-860-207
; Sequence 207, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
```

```

; APPLICANT: Weber, Richa
; APPLICANT: Bezabeh, Bin
; TITLE OF INVENTION: ANTI
; TITLE OF INVENTION: THE
; FILE REFERENCE: ABGENTX.
; CURRENT APPLICATION NUMB
; CURRENT FILING DATE: 20
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Wi
; SEQ ID NO 207
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-207

Query Match      89.1%; Score 460; DB 12; Length 125;
Best Local Similarity 88.8%; Pred. No. 4.7e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Oy 1 OVOLLQSAAEVRKPGASVYVSCKASGYPTSYDISWVRQAPGQGLEMMGWMISYSGNTDY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 OVOLLQSAAEVRKPGASVYVSCKASGYPTSYDISWVRQAPGQGLEMMGWMISAYNGNTNY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Oy 61 AOKFGQRYVTMTTDSRRTAYMELRSLRSDDTAVYYCAR 98
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Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98
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RESULT 15
US-10-269-805-45
; Sequence 45, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLIVER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPEPTIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-45

Query Match      89.1%; Score 460; DB 15; Length 125;
Best Local Similarity 88.8%; Pred. No. 4.7e-40;
Matches 87; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Oy 1 OVOLLQSAAEVRKPGASVYVSCKASGYPTSYDISWVRQAPGQGLEMMGWMISYSGNTDY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 OVOLLQSAAEVRKPGASVYVSCKASGYPTSYDISWVRQAPGQGLEMMGWMISAYNGNTNY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Oy 61 AOKFGQRYVTMTTDSRRTAYMELRSLRSDDTAVYYCAR 98
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Db 61 AOKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR 98
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: December 30, 2003, 11:45:23
Job time : 22.0171 secs
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D<sub>b</sub> 20 QVQVGSGAEVKKRGASVXSKCASGYTTFISYGISWVRQAQGEGLEMGMISAYNONTNY 79  
Q<sub>y</sub> 61 AQKEGGRVTMTDTDSRRATAMELRSLRSDDTAVYYCAR 98  
D<sub>b</sub> 80 AQLKGSRVTMTDTDTSTSTAYMELRSLRSDDTAVYYCAR 117

RESULT 2  
US-08-264-093-3  
Continued on next page

```

1  APPLICANT: Michael D. Dan
2  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
3  TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
4  TITLE OF INVENTION: ANTIGEN
5  NUMBER OF SEQUENCES: 26
6  CORRESPONDENCE ADDRESS:

```

ADDRESSSEE: Ridout & Maybee  
STREET: 2300 Richmond-Adelaide Centre  
STREET: 101 Richmond Street West  
STREET: Main Street

```

1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Disquette - 3.5 inch, 1.4 Mb storage
3  COMPUTER: IBM PC Compatible
4  OPERATING SYSTEM: MS-DOS 6.00
5  SOFTWARE: ASCII Editor
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/08/564,.093

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CLASSIFICATION: 536  
PRIOR APPLICATION DATA: No. 5639863 applicable  
ATTORNEY/AGENT INFORMATION:

NAME: Lake, James R.  
REGISTRATION NUMBER: 31081  
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 868-1482  
TELEFAX: (416) 362-0823  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

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; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
US-08-264-093-3

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Query Match	85.3%;	Score 440;	DB 1;	Length 121;
Best Local Similarity	83.7%;	Pred. No. 1.7e-39;		
Matches	82;	Conservative	9;	Mismatches 7;
				Indels

Qy 1 QVQLTSLAEVKKPKGASVYVSCASGYPPTSYDLSWVRQAPGGGLGEMMGWISISYGNITDY 600

Db 1 QVQLVSGAEVKKPKGASVYVSCASGYTPTTYGSLWVRQAPGGGLGEMMGWISAHNGNTNS 600

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QY      61 AAKFQGRVTMTTDSRRATAYMELRSLRSDDTAVYYCAR 98
      |||||:||||| |||||:||||| |||||
DB      61 AAKFQGRVSMTTDTSTSTAYMEVRLSRSDDTAVYYCAR 98
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RESULT 3  
US-09-025-769B-22  
; Sequence 22, Application US/09025769B

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; GENERAL INFORMATION:
;
; APPLICANT: Knappik, Achim
;
; APPLICANT: Pack, Peter
;
; APPLICANT: Ilag, Vic
;
; APPLICANT: Ge, Liming
;
; APPLICANT: Moroney, Simon

```

APPLICANT: Plueckthun, Andreas  
 TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10021

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APPLICATION NUMBER: BE 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James P. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000

```

; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids

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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-025-769B-22

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Query Match	83.5%	Score 431	DB 4	Length 117
Best Local Similarity	84.7%	Pred. No. 1.5e-38		
Matches 83; Conservative	5	Mismatches 10	Indels 0	Gaps 0

**Oy**

1 QVOLLQSAAEYRKPFGASVKVSKASKGTPFTSIDISWTRQAPGGQJEMMGKISTISGNTDY 600  
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**Dd**

1 QVQLVDSGAETKKPGASVKVSKASKGTFPTSYTHMWRQAPGGQJEMMGKINPNSGNTNY 600

Qy 61 A Q K F G R V T M T D T S R K T A Y M E L R S L R S D D T A V Y Y C A R 98  
| | | | | | | | | | | | | | | | | | | | | |  
Db 61 A Q K F G R V T M T R D T S I S T A Y M E L S L R S D D T A V Y Y C A R 98

RESULT 4  
US-08-202-047-22  
; Sequence 22, Application US/08202047  
; Patent No. 5800815

?  
? APPLICANT: CHESNUT, Robert W.  
? APPLICANT: POLEY, Margaret J.  
? APPLICANT: PAULSON, James C.  
? APPLICANT: JONES, S. Tarran  
? APPLICANT: SALDANHA, Jose W.  
? APPLICANT: BENDIG, Mary M.  
? TITLE OF INVENTION: Antibodies to p-Selectin and Their Uses  
? NUMBER OF SEQUENCES: 45

ADDRESS: Townsend and Townsend Khourie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA

```

;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:      IBM PC compatible
;

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      OPERATING SYSTEM:  PC-DOS/MS-DOS
      SOFTWARE:  PatentIn Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER:  US/08/202,047
      FILING DATE:  25-FEB-1994
      CLASSIFICATION:  424
      ATTORNEY/AGENT INFORMATION:
      NAME:  Smith, William M.
      REGISTRATION NUMBER:  30,223
      REFERENCE/DOCKET NUMBER:  14137-77
      TELECOMMUNICATION INFORMATION:
      TELEPHONE:  415-326-2400
      TELEFAX:  415-326-2422
      INFORMATION FOR SEQ ID NO:  22:
      SEQUENCE CHARACTERISTICS:
      LENGTH:  128 amino acids
      TYPE:  amino acid
      STRANDEDNESS:  single
      TOPOLOGY:  linear
      MOLECULE TYPE:  protein
      FEATURE:
      NAME/KEY:  Protein
      LOCATION:  1..128
      OTHER INFORMATION:  /label= HUMAN_I
US-08-202-047-22

```

```

?      REGISTRATION NUMBER: 30,223
?      REFERENCE/DOCKET NUMBER: 14137-77
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: 415-326-2400
?      TELEFAX: 415-326-2422
?      INFORMATION FOR SEQ ID NO: 22:
?      SEQUENCE CHARACTERISTICS:
?          LENGTH: 128 amino acids
?          TYPE: amino acid
?          STRANDEDNESS: single
?          TOPOLOGY: linear
?      MOLECULE TYPE: protein
?      FEATURE:
?      NAME/KEY: Protein
?      LOCATION: 1..128
?      OTHER INFORMATION: /label= HUMAN_1
US-08-964-690-22

Query Match      82.5%; Score 425.5; DB 3; Length 128;
Best Local Similarity 82.8%; Pred. No. 6.2e-38;
Matches 82; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY      1 QVOLLGSAAEVRKKGASVKVSKASKAGVPFTSYSDISMYRQAPGGGLLEMMGMWISLY-SGNTD 59
|::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
DB      1 QVOLLVGSGAELKKKGGASVKVSKASKAGTTFITSTYALSMWRQAPGGGLLEMMGMINPYGNQDTN 60
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```

Query Match Similarity      82.5%; Score 425.5; DB 1; Length 128;
Best Local Similarity      82.8%; Pred No. 6,2e-38;
Matches      82; Conservative      8; Mismatches      8; Indels      1; Gaps      1
Dy      1 0VOLL0SAAEYKPKGASVYKSCAKSGYPTFSYDISWVR0APQGL0EMMGWISY-SGNTD 59
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Dy      1 0V0LV0SGAEYKPKASVYKSCKASGYFTFSYAI5MWVR0APQGL0EMMGWIMNPYNGDYN 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Dy      60 YAKQFGGRVMTTDSRRTAYMELRSLSSDDTAYYCAR 98
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      61 YAKQFGGRVTTADTSTSTAYMELSLRSDPTAYYCAR 99
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
US-08-964-690-22
; Sequence 22, Application US/08964690
; Patent No. 6033667
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: FOLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
; APPLICANT: BENDIG, Mary M.
; TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,690
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,047
; FILING DATE: 25-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.

```

```

01      60 YAAKFGKRVMTTDTSTRTATAMELRSLRSDDTAVYCAR 98
02      |||||: ||| ||||| ||||| |||||
03      61 YAAKFGKRVTTADTSTSTATAMELSLRSEDTAVYCAR 99
04
05 RESULT 6
06      US-08-561-521-45
07      ; Sequence 45, Application US/08561521
08      ; Patent No. 5840299
09      ; GENERAL INFORMATION:
10      ; APPLICANT: Bendig, Mary M.
11      ; APPLICANT: Leger, Olivier J.
12      ; APPLICANT: Saldanha, Jose
13      ; APPLICANT: Jones, S. Tarran
14      ; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
15      ; TITLE OF INVENTION: Adhesion Molecule VLA-4
16      ; NUMBER OF SEQUENCES: 45
17      ; CORRESPONDENCE ADDRESS:
18      ; ADDRESS: Townsend and Townsend Kourie and Crew
19      ; STREET: One Market Plaza, Steuart Tower, Suite 2000
20      ; CITY: San Francisco
21      ; STATE: California
22      ; COUNTRY: USA
23      ; ZIP: 94105
24
25      ; COMPUTER READABLE FORM:
26      ; MEDIUM TYPE: Floppy disk
27      ; COMPUTER: IBM PC compatible
28      ; OPERATING SYSTEM: PC-DOS/MS-DOS
29      ; SOFTWARE: Patent In Release #1.0, Version #1.25
30      ; CURRENT APPLICATION DATA:
31      ; APPLICATION NUMBER: US/08/561,521
32      ; FILING DATE:
33      ; CLASSIFICATION: 424
34      ; PRIOR APPLICATION DATA:
35      ; APPLICATION NUMBER: US/08/186,269A
36      ; FILING DATE: 25-JAN-1994
37      ; ATTORNEY/AGENT INFORMATION:
38      ; NAME: Smith, William L.
39      ; REGISTRATION NUMBER: 30,223
40      ; REFERENCE/DOCKET NUMBER: 15270-14
41      ; TELECOMMUNICATION INFORMATION:
42      ; TELEPHONE: 415-543-9600
43      ; TELEFAX: 415-543-5043
44      ; INFORMATION FOR SEQ ID NO: 45:
45      ; SEQUENCE CHARACTERISTICS:
46      ; LENGTH: 129 amino acids
47      ; TYPE: amino acid
48      ;

```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-45

Query Match      82.5%; Score 425.5; DB 2; Length 129;
Best Local Similarity 82.8%; Pred. No. 6.2e-38;
Matches 82; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVOLLGSAAEVRKFGASVYKSCASGYPTFSYDISWVRQAPGGGLEMMGMISY-SGNTD 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLLGSAAEVRKFGASVYKSCASGYPTFSYDISWVRQAPGGGLEMMGMINYGNDTN 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 YAAKFGQRYVTMTDTSRRTAYMELRSLRSDDTAVYYCAR 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YAAKFGQRYVTMTDTSRRTAYMELRSLRSDDTAVYYCAR 99
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
US-08-525-539A-77
; Sequence 77, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-525-539A-77

Query Match      82.5%; Score 425.5; DB 4; Length 129;
Best Local Similarity 82.8%; Pred. No. 6.2e-38;
Matches 82; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVOLLGSAAEVRKFGASVYKSCASGYPTFSYDISWVRQAPGGGLEMMGMISY-SGNTD 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLLGSAAEVRKFGASVYKSCASGYPTFSYDISWVRQAPGGGLEMMGMINYGNDTN 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 YAAKFGQRYVTMTDTSRRTAYMELRSLRSDDTAVYYCAR 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YAAKFGQRYVTMTDTSRRTAYMELRSLRSDDTAVYYCAR 99
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 8
PCT-US95-01219-45
; Sequence 45, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/186,269
; APPLICATION NUMBER: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-45

Query Match      82.5%; Score 425.5; DB 5; Length 129;
Best Local Similarity 82.8%; Pred. No. 6.2e-38;
Matches 82; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVOLLGSAAEVRKFGASVYKSCASGYPTFSYDISWVRQAPGGGLEMMGMISY-SGNTD 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVOLLGSAAEVRKFGASVYKSCASGYPTFSYDISWVRQAPGGGLEMMGMINYGNDTN 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 YAAKFGQRYVTMTDTSRRTAYMELRSLRSDDTAVYYCAR 98
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YAAKFGQRYVTMTDTSRRTAYMELRSLRSDDTAVYYCAR 99
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
US-08-545-809A-96
; Sequence 96, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Taseku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
```

STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/545,809A  
FILING DATE: 27-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/00603  
FILING DATE: 10-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 06501/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 96:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-545-809A-96

Query Match 82.0%; Score 423; DB 3; Length 117;  
Best Local Similarity 82.7%; Pred. No. 1e-37;  
Matches 81; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLQSAAEVRKPGASVKVSKASGYPTSYDISWVRQAPGQGLEWMGNIISYSGNTDY 60  
DB 20 QVQLVSGAEVKKRPGASVKVSKASGYPTSYDISWVRQAPGQGLEWMGNIISYSGNTGY 79

QY 61 AOKFQGRVTMTTDSRTTAYMEILSLRSDPTAVYYCAR 98  
DB 80 AOKFQGRVTMTTDSRTTAYMEILSLRSDPTAVYYCAR 117

RESULT 10  
US-09-025-769B-36  
Sequence 36, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckhuhn, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EFO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-36

Query Match 81.6%; Score 421; DB 4; Length 120;  
Best Local Similarity 82.7%; Pred. No. 1.7e-37;  
Matches 81; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVQLQSAAEVRKPGASVKVSKASGYPTSYDISWVRQAPGQGLEWMGNIISYSGNTDY 60  
DB 1 QVQLVSGAEVKKRPGASVKVSKASGYPTSYDISWVRQAPGQGLEWMGNIISYSGNTGY 60

QY 61 AOKFQGRVTMTTDSRTTAYMEILSLRSDPTAVYYCAR 98  
DB 61 AOKFQGRVTMTTDSRTTAYMEILSLRSDPTAVYYCAR 98

RESULT 11  
US-09-025-769B-59  
Sequence 59, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckhuhn, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EFO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids

1 MEDICAL LIFE. DISCOVER

```

, COMPUTER: IBM Compatible
, OPERATING SYSTEM: Windows95
, SOFTWARE: FastSeq for Windows Version 2.0
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/545, 809A
, FILING DATE: 27-MAR-1996
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: PCT/JP93/00603
, FILING DATE: 10-MAY-1993
, ATTORNEY/AGENT INFORMATION:
, NAME: Freeman, John W.
, REGISTRATION NUMBER: 29, 066
, REFERENCE/DOCKET NUMBER: 06501/004001
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 617-542-5070
, TELEFAX: 617-542-8906
, TELEX: 200154
, INFORMATION FOR SEQ ID NO: 90:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 117 amino acids
, TYPE: amino acid
, TOPOLOGY: linear
, MOLECULE TYPE: protein
,
, US-08-545-809A-90

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Query Match	80.6%;	Score 416;	DB 3;	Length 117;
Best Local Similarity	81.6%;	Pred. No. 5.7e-37;		
Matches 80; Conservative	5;	Mismatches 13;	Indels 0;	Gaps 0;

[illegible]

RESULT 15  
US-08-561

! Sequence 10, Application US/08561521  
! Patent No. 5840299

**GENERAL INFORMATION:**

APPLICANT: Bendig, Mary M.

APPLICANT: Saldanha, Jose

APPLICANT: Jones, S. Tarran

10 TITLE OF INVENTION: Humanized Antibodies Against Leukocytes

TITLE OF INVENTION: Adhesion molecule VLA-4

CORRESPONDENCE ADDRESSES: NUMBER OF SEQUENCES: 4

ADDRESS: Townsend and Townsend Khourie and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California  
COUNTRY: USA

COONIKI: USA  
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Police #1.0 Version #1.0c

```

```

;      SOFTWARE:  Patentlin Release #1.0,
:      CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/561,521

FILING DATE:

CLASSIFICATION: 424  
;  
; PRIOR ADDITION DATA

APPLI CATION NUMBER: IIS/09/186 269A

FILING DATE: 25-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William L.

REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15370-14

```

: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: 415-543-9600
: TELEFAX: 415-543-5043
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 119 amino acids
:   TYPE: amino acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
:   MOLECULE TYPE: protein
:
US-08-561-521-10

```

Query Match	79.7%;	Score 411;	DB 2;	Length 119;
Best Local Similarity	79.6%;	Pred. NO. 2e-36;		
Matches 78;	Conservative 8;	Mismatches 12;	Indels 0;	Gaps 0;

[illegible]

Search completed: December 30, 2003, 11:05:32  
Job time : 10.0346 secs

Job time : 10.0346 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 / Search time 2.013 Seconds

(Without alignments)  
1003.251 Million cell updates/sec

Title: US-09-674-752-29

Sequence: 1 QONGWYEGPLLEPRDLDI 21

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR.76:\*  
2: PIR3:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	43.3	1000	2 JE0110	mitotic control pr
2	51	42.5	435	2 A49171	translation elonga
3	50	41.7	164	2 T37174	protein-tyrosine-p
4	50	41.7	205	2 S26854	microfilarial sheat
5	50	41.7	403	2 H72634	proline-rich sheat
6	49	40.8	205	2 A40525	proline-rich sheat
7	49	40.8	363	2 AG0189	probable, denhydroge
8	49	40.8	435	2 S43507	translation elonga
9	49	40.8	435	2 H90162	hypothetical prote
10	48.5	40.4	75	2 G95891	hypothetical prote
11	48	40.0	354	2 T12741	hypothetical prote
12	48	40.0	435	1 EFUC1A	translation elonga
13	47	39.2	362	1 B64793	glycerol denhydroge
14	47	39.2	362	2 F90708	probable oxidoredu
15	47	39.2	362	2 B85559	probable oxidoredu
16	47	39.2	362	2 AD0576	hypothetical prote
17	46	38.3	366	2 P84247	hypothetical prote
18	46	38.3	423	2 A88339	sugar binding prote
19	46	38.3	423	2 A12943	hypothetical prote
20	46	38.3	524	2 S47143	A mating type prot
21	46	38.3	579	2 F83327	conserved hypotnet
22	46	38.3	647	2 T43952	hypothetical prote
23	46	38.3	759	2 T44142	DR1 protein (import
24	46	38.3	825	2 T23612	hypothetical prote
25	46	38.3	1062	2 T66444	hypothetical prote
26	45.5	37.9	1327	2 B90674	AIDA-1 adhesin-like
27	45.5	37.9	1349	2 B85524	surface beta-bar
28	45.5	37.9	2425	2 D69426	surface layer prot
29	45	37.5	213	2 B85066	hypothetical prote

30	45	37.5	255	2 A12578	conserved hypotnet
31	45	37.5	255	2 H97360	hypothetical prote
32	45	37.5	302	2 J01878	hypothetical 33.4K
33	45	37.5	376	2 G95949	probable oligopept
34	45	37.5	383	2 B87579	hypothetical prote
35	45	37.5	395	2 T43692	translation elonga
36	45	37.5	555	2 T45351	ferredoxin (import
37	45	37.5	1175	2 D85089	hypothetical prote
38	45	37.5	1472	2 A84470	hypothetical prote
39	45	37.5	1756	2 T02599	hypothetical prote
40	44.5	37.1	76	2 C71852	ribosomal protein
41	44.5	37.1	76	2 G64663	ribosomal protein
42	44.5	37.1	275	2 B49394	translation elonga
43	44.5	37.1	644	2 AD3471	adenyl-yl-sulfate k
44	44	36.7	147	2 H71016	hypothetical prote
45	44	36.7	239	2 T16159	hypothetical prote

#### ALIGNMENTS

RESULT 1  
JE0110  
mitotic control protein dis3 homolog - human  
C/Species: Homo sapiens (man)  
C/Date: 22-May-1998 #sequence\_revision 29-May-1998 #text\_change 02-Nov-2001  
C/Accession: JE0110; T12542  
R/Shiom, T.; Fukushima, K.; Suzuki, N.; Nakashima, N.; Noguchi, E.; Nishimoto, T.  
J. Biochem. 123, 883-890, 1998  
A/Title: Human Dis3, which binds to either GTP- or GDP-Ran, complements Saccharomyces  
A/Reference number: JE0110; MUID:98230695; PMID:9562621  
A/Accession: JE0110  
A/Molecule type: mRNA  
A/Residues: 1-1000 <SHI>  
R/Wambolt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, June 1999  
A/Reference number: Z17524  
A/Accession: T12542  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 369-593, 'K', 595-1000 <WAM>  
A/Cross-references: EMBL:AL080158  
A/Experimental source: adult testis; clone DKFZp434L194  
C/Comment: This protein enhances a temperature-sensitive mutant RCC1-stimulated nucleot  
C/Genetic:  
A/Note: DKFZp434L194.1  
C/Superfamily: mitotic control protein dis3

Query Match 43.3%; Score 52; DB 2; Length 1000;  
Best Local Similarity 69.2%; Pred. No. 11;  
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GQWYEGPLLEPRP 16  
Db 40 GQWYEGPLLEPRP 52

RESULT 2  
A49171  
translation elongation factor eEF-1 alpha chain - Tetrahymena pyriformis  
C/Species: Tetrahymena pyriformis  
C/Date: 21-Jan-1994 #sequence\_revision 15-Oct-1994 #text\_change 02-Feb-2001  
C/Accession: A49171; B49171  
R/Kuraawa, Y.; Numata, O.; Katoh, M.; Hirano, H.; Chiba, J.; Watanabe, Y.  
Exp. Cell Res. 203, 251-258, 1992  
A/Title: Identification of Tetrahymena 14-nm filament-associated protein as elongation  
A/Reference number: A49171; MUID:93049915; PMID:1385189  
A/Accession: A49171  
A/Molecule type: mRNA  
A/Residues: 1-435 <KUR>  
A/Cross-references: GB:D11083; NID:9217407; PIDN:BA01856.1; PID:9217408  
A/Note: sequence extracted from NCBI backbone (NCBI:117509, NCBI:P:117510)

A/Accession: B49171  
 A/Molecule type: protein  
 A/Residues: 2-21 <KU2>  
 C/Genetics:  
 A/Genetic code: SGCS  
 C/Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog  
 C/Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis  
 F/2-435/Product: translation elongation factor eEF-1 alpha chain #status experimental <E  
 F/9-157/Domains: translation elongation factor Tu homology <ETU>  
 F/15-22/Region: nucleotide-binding motif A (P-loop)  
 F/95-98/Region: GTP binding #status predicted  
 F/154-157/Region: GTP binding #status predicted

Query Match 42.5%; Score 51; DB 2; Length 435;  
 Best Local Similarity 50.0%; Pred. No. 6.1;  
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

DB 3 NGCWYEGPLLEPPDAL 20  
 208 NAWYKGPILVEALDALE 225

RESULT 3  
 T37174  
 protein-tyrosine-phosphatase, low molecular weight - Streptomyces coelicolor  
 C/Species: Streptomyces coelicolor  
 C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jan-2000  
 C/Accession: T37174  
 R/Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, July 1999  
 A/Reference number: 221598  
 A/Accession: T37174  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-164 <SEE>  
 A/Cross-references: EMBL:AL096823; PIDN:CA846955.1; GSPDB:GN00070; SCQDB:SCQ11.04c  
 A/Experimental source: strain A3(2)  
 C/Genetics:  
 A/Gene: ptpA; SCQDB:SCQ11.04c  
 C/Superfamily: protein-tyrosine-phosphatase, low molecular weight

Query Match 41.7%; Score 50; DB 2; Length 164;  
 Best Local Similarity 50.0%; Pred. No. 2.9;  
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

DB 4 GCMWYEGPLLEPPDAL 19  
 44 GCMWEGADPRPAV 59

RESULT 4  
 S26854  
 microfilament sheath protein, major component - nematode (Brugia pahangi)  
 C/Species: Brugia pahangi  
 C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Sep-1997  
 C/Accession: S26854  
 R/Selkirk, M.  
 submitted to the EMBL Data Library, February 1991  
 A/Reference number: S26854  
 A/Accession: S26854  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-205 <SEL>  
 A/Cross-references: EMBL:X58063; NID:G5951; PID:G5952  
 C/Genetics:  
 A/Introns: 123/2

Query Match 41.7%; Score 50; DB 2; Length 205;  
 Best Local Similarity 52.9%; Pred. No. 3.7;  
 Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

DB 2 QNGWYEGPLLEPPDA 18

DB 162 QTRGWTGPRLTPKPTA 178

RESULT 5  
 H72634  
 probable pyruvate formate lyase activating protein APE1535 - Aeropyrum pernix (strain  
 C/Species: Aeropyrum pernix  
 C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999  
 C/Accession: H72634  
 R/Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tak  
 awa, H.; Takamiya, M.; Maeda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;  
 DNA Res. 6, 83-101, 1999  
 A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerop  
 A/Reference number: A72450; MUID:99310339; PMID:10382966  
 A/Accession: H72634  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-403 <KAW>  
 A/Cross-references: DDBJ:AP000061; NID:G5104821; PIDN:BAAB0534.1; PID:dl044320; PID:G5  
 A/Experimental source: strain KI  
 C/Genetics:  
 A/Gene: APE1535

Query Match 41.7%; Score 50; DB 2; Length 403;  
 Best Local Similarity 40.0%; Pred. No. 7.9;  
 Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

DB 2 QNGWYEGPLLEPPDALDI 21  
 108 REGGYEGDIXDARPELMDV 127

RESULT 6  
 A40525  
 proline-rich sheath protein ME22 precursor - nematode (Brugia pahangi)  
 C/Species: Brugia pahangi  
 C/Date: 28-Feb-1992 #sequence\_revision 10-Apr-1992 #text\_change 27-Jan-1995  
 C/Accession: A40525; S18744  
 R/Selkirk, M.E.; Yazdankhah, M.; Freedman, D.; Blaxter, M.L.; Cookson, E.; Jenkins,  
 J. Biol. Chem. 266, 11002-11008, 1991  
 A/Title: A proline-rich structural protein of the surface sheath of larval Brugia flla  
 A/Reference number: A40525; MUID:91250404; PMID:1110216  
 A/Accession: A40525  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-205 <SEL>  
 A/Cross-references: GB:X58063  
 A/Note: the authors translated the codon GCA for residue 23 as Arg, CTG for residue 14

Query Match 40.8%; Score 49; DB 2; Length 205;  
 Best Local Similarity 52.9%; Pred. No. 5.2;  
 Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

DB 2 QNGWYEGPLLEPPDA 18  
 162 QTRGWTGPRLTPKPTA 178

RESULT 7  
 AG0189  
 probable dehydrogenase YPO1556 (imported) - Yersinia pestis (strain CO92)  
 C/Species: Yersinia pestis  
 C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Nov-2001  
 C/Accession: AG0189  
 R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlhalil, R.W.; Holden, M.T.G.; Prentice, M.  
 deno-Tarrega, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.  
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell  
 Nature 413, 523-527, 2001  
 A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A/Reference number: AB0001; MUID:21470413; PMID:11586360  
 A/Accession: AG0189  
 A/Status: preliminary  
 A/Molecule type: DNA



A:Residues: 1-363 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC90378.1; PID:G15979597; GSPDB:GN00175  
C:Genetics:  
A:Gene: YPO556  
C:Superfamily: glycerol dehydrogenase; lactaldehyde reductase homology

Query Match 40.8%; Score 49; DB 2; Length 363;  
Best Local Similarity 43.8%; Pred. No. 10;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 6 WYEGPLLEPPRLDLDI 21  
DB 178 WYEAVALSPQPERTSL 193

RESULT 8  
S43507  
translation elongation factor EF-1 alpha chain - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 02-Feb-2001  
C:Accession: S43507; S33719; S37631; T11747  
R:Arcari, P.; Gallo, M.; Iannicello, G.; Russo, A.D.; Bocchini, V.  
Biochim. Biophys. Acta 1217, 333-337, 1994  
A:Title: The nucleotide sequence of the gene coding for the elongation factor 1-alpha in Sulfolobus solfataricus.  
A:Reference number: S43507; MUID:94198299; PMID:8148382  
A:Accession: S43507  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-435 <ARC>  
A:Cross-references: EMBL:X70701; NID:G395380; PIDN:CAA50033.1; PID:G395381  
R:Arcari, P.; Gallo, M.; Iannicello, G.; dello Russo, A.; Bocchini, V.  
Nucleic Acids Res. 21, 1666, 1993  
A:Title: Primary structure of the elongation factor 1-alpha in Sulfolobus solfataricus.  
A:Reference number: S33719; MUID:93241951; PMID:8369039  
A:Accession: S33719  
A:Molecule type: DNA  
A:Residues: 1-113, 'Q', 15-435 <ARC1>  
A:Cross-references: EMBL:X70701  
A:Note: this sequence has been revised in reference S37631  
R:Arcari, P.; Gallo, M.; Iannicello, G.; dello Russo, A.; Bocchini, V.  
Nucleic Acids Res. 21, 3920, 1993  
A:Reference number: S37631  
A:Contents: erratum  
A:Accession: S37631  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 'H', 2-13, 'Q', 15-435 <ARC2>  
A:Note: this is a revision to the sequence from reference S33718  
R:Iannicello, G.; Gallo, M.; Arcari, P.; Bocchini, V.  
Biochem. Mol. Biol. Int. 33, 927-937, 1994  
A:Title: Organization of a Sulfolobus solfataricus gene cluster homologous to the Escherichia coli elongation factor Tu  
A:Accession: T11747  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-435 <IAN>  
A:Cross-references: EMBL:X76767; NID:G510206; PID:G510209  
A:Experimental source: ATCC 49255 / MT-4  
C:Genetics:  
A:Gene: EF-1a; aEF-1a1pha  
C:Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog  
C:Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis  
F:7-155/Domain: translation elongation factor Tu homology <ETU>  
F:113-20/Region: nucleotide-binding motif A (P-loop)  
F:155-155/Region: GTP-binding NKXD motif

Query Match 40.8%; Score 49; DB 2; Length 435;  
Best Local Similarity 45.0%; Pred. No. 12;  
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;  
QY 2 QNGGMYEGPLLEPPRLDLDI 21  
DB 205 ENMKMYNGPTLEEVLDQLEL 224

RESULT 9  
H90162  
hypothetical protein tuf-1 [imported] - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
C:Accession: H90162  
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyer, M.J.; Chararet, R.A.; Ragani, M.A.; Seneen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A:Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: H90162  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-435 <KUR>  
A:Cross-references: GB:AE006641; NID:G13813351; PIDN:AAK40559.1; GSPDB:GN00155  
C:Genetics:  
A:Gene: tuf-1

Query Match 40.8%; Score 49; DB 2; Length 435;  
Best Local Similarity 45.0%; Pred. No. 12;  
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;  
QY 2 QNGGMYEGPLLEPPRLDLDI 21  
DB 205 ENMKMYNGPTLEEVLDQLEL 224

RESULT 10  
G95891  
hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSym  
C:Species: Sinorhizobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
C:Accession: G95891  
R:Finan, T.M.; Weidner, S.; Wong, K.; Bhurmesster, J.; Chain, P.; Vorholter, F.J.; Herm  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A:Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing en  
A:Reference number: A95842; MUID:21396508; PMID:11481431  
A:Accession: G95891  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-75 <KUR>  
A:Cross-references: GB:AL591985; PIDN:CAC48799.1; PID:G15140272; GSPDB:GN00167  
A:Experimental source: strain 1021, megaplasmid pSymB  
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kias, E.; Komp, C.; LeLaur  
hebut, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Welle, D.H.; Wong, K.; Yeh, J  
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: Smb20413  
A:Genome: plasmid

Query Match 40.4%; Score 48.5; DB 2; Length 75;  
Best Local Similarity 61.1%; Pred. No. 2;  
Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;  
QY 2 QNGGMYEGPLLEPPRLDLDI 18  
DB 42 RSGGSRNGPILPLSPRDA 59

RESULT 11  
T12741  
hypothetical protein 25 - Methanobacterium phage psiM2  
C:Species: Methanobacterium phage psiM2

C/Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 05-May-2000  
 C/Accession: T12741  
 R/Pfister, P.; Wasserrfallen, A.; Stettler, R.; Leisinger, T.  
 submitted to the EMBL Data Library, May 1998  
 A/Description: Archaeophage PsiM2 complete genomic DNA.  
 A/Reference number: 217578  
 A/Accession: T12741  
 A/Status: translated from GB/EMBL/DBB  
 A/Molecule type: DNA  
 A/Residues: 1-354 <PFI>  
 A/Cross-references: EMBL:AF065411; NID:g1249585; PID:g1249610; PIDN:AAC27064.1  
 A/Experimental source: host Methanobacterium thermoautotrophicum strain Marburg  
 C/Superfamily: Methanobacterium phage psiM2 hypothetical protein 25

Query Match 40.0%; Score 48; DB 2; Length 354;  
 Best Local Similarity 50.0%; Pred. No. 14;  
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 QONGWYEPVLP 14  
 DB 8 QENRGWYVPDKP 21

RESULT 12  
 EFU01A  
 translation elongation factor aEF-1 alpha chain - Sulfolobus acidocaldarius  
 C/Species: Sulfolobus acidocaldarius  
 C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 19-Jan-2001  
 C/Accession: S12818  
 R/Auer, J.  
 submitted to the EMBL Data Library, March 1990  
 A/Reference number: S12817  
 A/Accession: S12818  
 A/Molecule type: DNA  
 A/Residues: 1-435 <AUE>  
 A/Cross-references: EMBL:X52382; NID:g46562; PIDN:CAA36608.1; PID:g46564  
 C/Genetics:  
 A/Gene: EF-1a  
 C/Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog  
 C/Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis  
 F;7-155/Domain: translation elongation factor Tu homology <ETU>  
 F;13-20/Region: nucleotide-binding motif A (P-loop)  
 F;152-155/Region: GTP-binding NKXD motif

Query Match 40.0%; Score 48; DB 1; Length 435;  
 Best Local Similarity 56.2%; Pred. No. 17;  
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 6 WYEGPLLEPRDALDI 21  
 DB 209 WYNGPLLEPLDQLEI 224

RESULT 13  
 E64793  
 glycerol dehydrogenase (EC 1.1.1.6) ybDh - Escherichia coli (strain K-12)  
 C/Species: Escherichia coli  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 01-Mar-2002  
 C/Accession: E64793  
 R/Baltner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
 A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A/Title: The complete genome sequence of Escherichia coli K-12.  
 A/Reference number: A64720; MUID:97426617; PMID:9278503  
 A/Accession: E64793  
 A/Status: nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-362 <BLAT>  
 A/Cross-references: GB:AE000165; GB:U00096; NID:g1786808; PIDN:AACT3700.1; PID:g1786815;  
 A/Experimental source: strain K-12, substrain MG1655  
 C/Genetics:  
 A/Gene: ybDh  
 C/Superfamily: glycerol dehydrogenase; lactaldehyde reductase homology

C/Keywords: oxidoreductase; transmembrane protein  
 F;9-354/Domain: lactaldehyde reductase homology <LAR>  
 F;109-125/Domain: transmembrane #status predicted <TM>

Query Match 39.2%; Score 47; DB 1; Length 362;  
 Best Local Similarity 43.8%; Pred. No. 20;  
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 6 WYEGPLLEPRDALDI 21  
 DB 178 WYEAVALAPQETPL 193

## RESULT 14

P90708  
 probable oxidoreductase EC0638 [imported] - Escherichia coli (strain O157:H7, substra  
 C/Species: Escherichia coli  
 C/Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001  
 C/Accession: P90708  
 R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.  
 gaewara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and ge  
 A/Reference number: A99629; MUID:21156231; PMID:11258796  
 A/Accession: P90708  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-362 <HAY>  
 A/Cross-references: GB:BA000007; PIDN:BAB34061.1; PID:g13360096; GSPDB:GN00154  
 A/Experimental source: strain O157:H7, substrain RIMD 0509952  
 C/Genetics:  
 A/Gene: EC0638  
 C/Superfamily: glycerol dehydrogenase; lactaldehyde reductase homology

Query Match 39.2%; Score 47; DB 2; Length 362;  
 Best Local Similarity 43.8%; Pred. No. 20;  
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 6 WYEGPLLEPRDALDI 21  
 DB 178 WYEAVALAPQETPL 193

## RESULT 15

B85559  
 probable oxidoreductase ybDh [imported] - Escherichia coli (strain O157:H7, substrain  
 C/Species: Escherichia coli  
 C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
 C/Accession: B85559  
 R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
 ller, V.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallante, E.; Potamousis, K.; Apodec  
 Nature 409, 529-533, 2001  
 A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A/Reference number: A85480; MUID:21074935; PMID:11206551  
 A/Accession: B85559  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-362 <STO>  
 A/Cross-references: GB:AE005174; NID:g12513492; PIDN:ANG54934.1; GSPDB:GN00145; UMGP:  
 A/Experimental source: strain O157:H7, substrain EDL933  
 C/Genetics:  
 A/Gene: ybDh  
 C/Superfamily: glycerol dehydrogenase; lactaldehyde reductase homology

Query Match 39.2%; Score 47; DB 2; Length 362;  
 Best Local Similarity 43.8%; Pred. No. 20;  
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 6 WYEGPLLEPRDALDI 21  
 DB 178 WYEAVALAPQETPL 193

Tue Dec 30 11:49:04 2003

us-09-674-752-29.rpr

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Search completed: December 30, 2003, 11:03:16  
Job time : 4.013 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 1.12391 Seconds  
(without alignments)  
877.119 Million cell updates/sec

Title: US-09-674-752-29

Perfect score: 120  
Sequence: 1 QQNGWYEGPLLEPRDALDI 21

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt 41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	43.3	928	1 RR44_HUMAN	Q9211 homo sapien
2	51	42.5	435	1 EF1A_TRYPY	Q04634 tetrahymena
3	50	41.7	164	1 PTFA_STRCO	P53433 streptomyces
4	50	41.7	348	1 DDL_ENTFA	Q47758 enterococcu
5	50	41.7	435	1 EF1A_SULTO	Q97651 sulfolobus
6	49	40.8	435	1 EF1A_SULTO	P35021 sulfolobus
7	48	40.0	435	1 EF1A_SULTO	P17196 sulfolobus
8	47	39.2	362	1 YBDH_ECOLI	P45579 escherichia
9	46	38.3	449	1 EF1C_PORPU	P50256 porphyra pu
10	45	37.5	555	1 FPRB_MYCLE	Q33064 mycobacteri
11	44.5	37.1	76	1 RS16_HELPU	Q9263 helicobacte
12	44.5	37.1	76	1 RS16_HELPU	P56023 helicobacte
13	44	36.7	128	1 Y14D_BPT4	P39507 bacteriopho
14	44	36.7	128	1 Y14D_BPT6	Q38169 bacteriopho
15	44	36.7	358	1 DDL_ENTHR	Q47827 enterococcu
16	44	36.7	414	1 YB8C_BACSU	P40407 bacillus su
17	44	36.7	476	1 CYSN_VIBPA	O878X9 vibrio para
18	44	36.2	208	1 NQ8R_HAEIN	P43558 haemophilus
19	43	35.8	74	1 COLE_ZOPAT	P80032 zophobas at
20	43	35.8	167	1 NUOE_RICCN	Q921d9 tickectesia
21	43	35.8	383	1 YJIM_ECOLI	P39384 escherichia
22	43	35.8	435	1 GALB_YEAST	P04387 saccharomyc
23	43	35.8	438	1 EF1A_DESMO	P41203 desulfuroco
24	43	35.8	862	1 SMAD_HUMAN	Q92854 homo sapien
25	42.5	35.4	396	1 EF1A_GIALA	Q08046 giardia lam
26	42.5	35.4	398	1 HEMT_ECOLI	P09128 escherichia
27	42.5	35.4	541	1 MYRO_ARATH	P37702 arabidopsis
28	42.5	35.4	1290	1 PIGI_RAT	P10686 rattus norv
29	42.5	35.4	88	1 YDHA_SCHPO	Q92349 schizosacch
30	42	35.0	88	1 ECLH_MANSE	P1919 manduca sex
31	42	35.0	172	1 BF1L_MOUSE	Q07440 mus musculu
32	42	35.0	246	1 NUKC_ORYSA	P12159 oryza sativ
33	42	35.0	324	1 B3G2_MOUSE	P59270 mus musculu

34	42	35.0	324	1 B3G2_RAT	Q92137 rattus norv
35	42	35.0	419	1 GLPB_ECOLI	P13033 escherichia
36	42	35.0	420	1 EF1A_HALMA	P16018 halocaula
37	42	35.0	457	1 GAL8_KULMA	Q06433 kluyveromyc
38	42	35.0	530	1 FUSA_BURCE	P24126 burkholderi
39	42	35.0	814	1 FADE_ECO57	O87122 escherichia
40	42	35.0	814	1 FADE_ECOLI	Q47146 escherichia
41	42	35.0	814	1 FADE_SALTI	Q82937 salmonella
42	42	35.0	814	1 FADE_SALTY	O82937 salmonella
43	42	35.0	824	1 JIP2_HUMAN	Q13387 homo sapien
44	42	35.0	888	1 YGB4_YEAST	P25339 saccharomyc
45	42	35.0	1550	1 GLTB_SYNY3	P55037 bynechochocyt

## ALIGNMENTS

RESULT 1  
RR44\_HUMAN STANDARD; PRT; 928 AA.  
ID RR44\_HUMAN  
AC Q9Y2L1; Q8WM12; Q9UC36;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Exosome complex exonuclease RRP44 (EC 3.1.13.-) (Ribosomal RNA processing protein 44) (D153 protein homolog).  
GN D153 OR RRP44 OR KIAA1008.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RX MEDLINE=98230695; PubMed=9562621;  
RA Shiomi T., Fukushima K., Suzuki N., Nakashima N., Noguchi E.,  
RT "Human dis3, which binds to either GTP- or GDP-Ran, complements  
RT Saccharomyces cerevisiae dis3.";  
RL J. Biochem. 123:883-890(1998).  
RN (2)  
RP ERRATUM.  
RA Shiomi T., Fukushima K., Suzuki N., Nakashima N., Noguchi E.,  
RT "Human dis3, which binds to either GTP- or GDP-Ran, complements  
RT Saccharomyces cerevisiae dis3.";  
RL J. Biochem. 123:883-890(1998).  
RN (3)  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=99246063; PubMed=10231032;  
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,  
RT Miyajima N., Tanaka A., Kohari H., Nomura N., Ohara O.,  
RT "Prediction of the coding sequences of unidentified human genes. XIII.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RL DNA Res. 6:63-70(1999).  
RN (4)  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain, and Peripheral blood leukocytes;  
RX MEDLINE=21932550; PubMed=11935316;  
RA Rozenblum E., Valteristo P., Sandberg T., Bergthorsson J.T.,  
RT Syrjakoski K., Weaver D., Haraldsson K., Johannsdottir H.K.,  
RA Vehneman P., Nigam S., Goldberg N., Robbins C., Pak E., Dutra A.,  
RA Gillander E., Stephan D.A., Bailey-Wilson J., Joo S.-H.H., Kalnu T.,  
RA Aarason A., Barkardottir R.B., Nevanlinna H., Borg A.,  
RA Kallioniemi O.-P.,  
RT "A genomic map of a 6-Mb region at 19q21-q22 implicated in cancer  
RT development: identification and characterization of candidate genes.";  
RL Hum. Genet. 110:111-121(2002).  
RN (5)  
RP SEQUENCE OF 297-928 FROM N.A.  
RC TISSUE=Testis;  
RA Wambutt R., Heubner D., Mewes H.-W., Gassenhuber J., Wiemann S.,  
RT Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.  
CC - FUNCTION: COMPONENT OF THE EXOSOME 3->5 EXORIBONUCLEASE COMPLEX.

```

RT "Complete genome sequence of an aerobic thermacidophilic
CC Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
CC -1- FUNCTION: This protein promotes the GTP-dependent binding of
CC antioacyl-tRNA to the A-site of ribosomes during protein
CC biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-TU/EF-1A SUBFAMILY.
CC -----
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CC -----
DR EMBL: AP000982; BAB65236.1; -
DR HAMAP: MF_00118; -, 1.
DR InterPro: IPR004539; EFT_alpha.
DR InterPro: IPR000795; EF_GTPbind.
DR InterPro: IPR004160; EFTU_Cterm.
DR InterPro: IPR004161; EFTU_D2.
DR Pfam: PF00009; GTP_EFTU; 1.
DR Pfam: PF03144; GTP_EFTU_D2; 1.
DR Pfam: PF03143; GTP_EFTU_D3; 1.
DR TIGRFAMs: TIGR00483; EF-1_alpha; 1.
DR PROSITE: PS00301; EFACITOR_GTP; 1.
KM Elongation factor: Protein biosynthesis; GTP-binding;
Complete proteome.
FT NP_BIND 13 20 GTP (BY SIMILARITY) .
FT NP_BIND 90 94 GTP (BY SIMILARITY) .
FT NP_BIND 152 155 GTP (BY SIMILARITY) .
SQ SEQUENCE 435 AA; 48331 MW; DA07188181D73D60 CRC64;

Query Match 41.7%; Score 50; DB 1; Length 435;
Best Local Similarity 50.0%; Pred. No. 4.5;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 QNGGMYEGPLLEPPDALDI 21
Db 205 ENMKMYTCPTLEEVYDQLEI 224

RESULT 6
EF1A_SULSO STANDARD: PRT; 435 AA.
AC P35021.
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Elongation factor 1-alpha (EF-1-alpha) (Elongation factor Tu) (EF-Tu).
DS TUF OR TEF1 OR SSO0216.
OS Sulfolobus solfataricus.
OC Archaeae; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49255 / DSM 5833 / MT-4;
RA MEDLINE=93241951; PubMed=8369039;
RA Arcati P., Gallo M., Ianniciello G., Dello Russo A., Bocchini V.;
RT "Primary structure of the elongation factor 1 alpha in Sulfolobus
RT solfataricus.";
RL Nucleic Acids Res. 21:1666-1666(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49255 / DSM 5833 / MT-4;
RA MEDLINE=94198299; PubMed=8148382;
RA Arcati P., Gallo M., Ianniciello G., Dello Russo A., Bocchini V.;
RT "The nucleotide sequence of the gene coding for the elongation factor
RT 1 alpha in Sulfolobus solfataricus. Homology of the product with

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RT related proteins.";  
RL Biochim. Biophys. Acta 1217:333-337(1994).  
[3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MT-3;  
RA Arcari P., Masullo M., Bocchini V.;  
RT "the nucleotide sequence of the gene encoding the elongation factor 1  
alpha from the archaeon Sulfolobus solfataricus isolate MT3";  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

[4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 35092 / DSM 1617 / P2;  
RX MEDLINE=21332296; PubMed=11427726;  
RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,  
R Aweyer M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,  
Ra Moore A., Eraso G., Fletcher C., Gordon P.M.K.,  
Ra Helkamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,  
Ra Thi-Ngoc H.P., Redder P., Schenk M.E., Thériault C., Tolstrup N.,  
Ra Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,  
Ra Garrett R.A., Ragun M.A., Sensen C.W., Van der Oost J.;  
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2,";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).  
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF  
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN  
BIOSYNTHESIS.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
CC EF-TU/EF-1A SUBFAMILY.

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DR EMBL; X70701; CAAS003.1; -;  
DR EMBL; X76767; CAAS4162.1; -;  
DR EMBL; AJ312397; CAC42886.1; -;  
DR EMBL; AE006658; AAK40559.1; -;  
DR PIR; H90162; H90162.  
DR PIR; S43507; S43507.  
DR PDB; 1JNY; 23-JAN-02.  
DR HAVAP; MF\_00118; -; 1.  
DR InterPro; IPRO04539; EF1\_alpha.  
DR InterPro; IPRO00795; EF\_Grpbind.  
DR InterPro; IPRO04160; EFTU\_Cterm.  
DR InterPro; IPRO04161; EFTU\_D2.  
DR Pfam; PF00009; GTP\_EFTU; 1.  
DR Pfam; PF03144; GTP\_EFTU\_D2; 1.  
DR Pfam; PF03143; GTP\_EFTU\_D3; 1.  
DR PRINTS; PR00315; ELONGACTNCT.  
DR TRGFAMS; TIGR00483; EF-1\_alpha; 1.  
DR PROSITE; PS00301; EFACOR\_GRP; 1.  
RW Elongation factor; Protein biosynthesis; GTP-binding;  
KW Complete proteome; 3D-structure.

FT NP BIND 13 GTP (BY SIMILARITY)  
FT NP BIND 90 GTP (BY SIMILARITY)  
FT NP BIND 152 GTP (BY SIMILARITY)  
FT VARIANT 196 A -> S (IN STRAINS MT-3 AND MT-4)  
FT VARIANT 203 R -> K (IN STRAINS MT-3 AND MT-4)  
FT VARIANT 347 I -> L (IN STRAINS MT-3 AND MT-4)  
FT CONFLICT 14 H -> Q (IN REF. 1)  
FT CONFLICT 240 V -> R (IN REF. 1 AND 2)  
SQ SEQUENCE 435 AA; 48489 MW; 222B540A31768A59 CRC64;

Query Match 40.8%; Score 49; DB 1; Length 435;  
Best Local Similarity 45.0%; Pred. No. 6.3;  
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

2 QNGGWYEGPLLEPPDALDI 21  
:| | | | | | | | :| :

Db 205 ENMKWNGPTLEBYLDQLEL 224

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RESULT 7
EF1A_SULAC STANDARD; PRT; 435 AA.
ID EF1A_SULAC
AC P17156;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor 1-alpha (EF-1-alpha) (Elongation factor Tu) (EF-Tu).
GN Sulfolobus acidocaldarius.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2285;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33909 / NCIB 11770 / DSM 639;
RA Auer J., Spicker G., Neyerhofer L., Puchler G., Boeck A.;
RT "Organisation and nucleotide sequence of a gene cluster comprising the
RT translation elongation factor 1-alpha from the extreme thermophilic
RT archaeobacterium Sulfolobus acidocaldarius: phylogenetic
RT implications";
RL Syste. Appl. Microbiol. 14:14-22(1991).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
CC AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
CC BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-TU/EF-1A SUBFAMILY.
CC -----
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CC -----
DR EMBL; X52382; CAA36608.1; -.
DR PIR; S12818; EFUC1A.
DR HSSP; P07157; IAP.
DR HAMAP; MF_00118; 1.
DR InterPro; IPR004539; EF1_alpha.
DR InterPro; IPR000795; EF_Grpbind.
DR InterPro; IPR004160; EFTU_Cterm.
DR InterPro; IPR004161; EFTU_D2.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR Pfam; PF03143; GTP_EFTU_D3; 1.
DR PRINTS; PRO0315; ELONGANTNCT.
DR TIGRFS; TIGR00483; EF-1_alpha; 1.
DR PROSITE; PS00301; EFATOR_GTP; 1.
DR Elongation factor; protein biosynthesis; GTP-binding.
FT NP_BIND 13 20 GTP (BY SIMILARITY).
FT NP_BIND 90 94 GTP (BY SIMILARITY).
FT NP_BIND 152 155 GTP (BY SIMILARITY).
SQ SEQUENCE 435 AA; 48200 MW; A012AF564624803F CRC64;
Query Match 40.0%; Score 48; DB 1; Length 435;
Best Local Similarity 56.2%; Pred. No. 8.9;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical oxidoreductase YbdH (EC 1.1.-.-).
GN YBDH OR B0599.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RA Federapfel N., Hyman R., Kaiman S., Komp C., Kurdi O., Lew H., Lin D.,
RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kasahimoto K.,
RA Kimura S., Kitagawa M., Makino K., Maeda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horinouchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [4]
RP SEQUENCE OF 282-362 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=91162636; PubMed=148300;
RA Schultz J.E., Martin A.;
RT "Molecular and functional characterization of a carbon starvation
RT gene of Escherichia coli.";
RL J. Mol. Biol. 218:129-140(1991).
RN [5]
RP IDENTIFICATION.
RX MEDLINE=96032851; PubMed=7567469;
RA Borodovsky M., McIninch J., Koonin E.V., Rudd K.E., Medigue C.,
RA Danchin A.;
RT "Detection of new genes in a bacterial genome using Markov models for
RT three gene classes.";
RL Nucleic Acids Res. 23:3554-3562(1995).
CC -1- SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL DEHYDROGENASE
CC FAMILY. STRONG, TO BACTERIAL GLYCEROL DEHYDROGENASE.
CC -----
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CC -----
DR EMBL; AB000165; AAC73700.1; -.
DR EMBL; U82598; AAB40800.1; -.
DR EMBL; D90701; BAA35229.1; -.
DR EMBL; X52904; -; NOT_ANNOTATED_CDS.
DR PIR; E64793; E64793.
DR EcoGene; EG12692; YbdH.
DR InterPro; IPR01670; Fe-ADH.

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DR Pfam: PF00465; Fe-ADH; 1.  
 DR PROSITE: PS00613; ADH\_IRON\_1; 1.  
 DR PROSITE: PS00060; ADH\_IRON\_2; FALSE\_NEG.  
 DR Hypothetical protein; Oxidoreductase; Complete proteome.  
 SQ SEQUENCE 362 AA; 39091 MW; C28BBB4F8F247AE2 CRC64;

Query Match 39.2%; Score 47; DB 1; Length 362;  
 Best Local Similarity 43.8%; Pred. No. 10;  
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 6 WYEGPLEPPDALDI 21  
 ||| : ||| :  
 Db 178 WYEAVALPQPETPL 193

RESULT 9  
 EFIC\_PORPU STANDARD; PRT; 449 AA.  
 AC P50256;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Elongation factor 1-alpha C (EF-1-alpha).  
 GN TEF-C.  
 OS Porphyra purpurea.  
 OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.  
 OX NCBI\_TaxID=2787;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Avonport;  
 RX MEDLINE=9630386; PubMed=8704161;  
 RA Liu Q.Y., Baidaut S.L., Reith M.E.;  
 RT "Elongation factor 1 alpha genes of the red alga Porphyra purpurea  
 include a novel, developmentally specialized variant.";  
 RL Plant Mol. Biol. 31:77-85(1996).  
 CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF  
 AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN  
 BIOSYNTHESIS.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN BOTH SPOROPHYTE AND GAMETOPHYTE  
 PHASES OF THE LIFE CYCLE.  
 CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
 CC EF-TU/EF-1A SUBFAMILY.  
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 -----  
 CC EMBL: U08844; AAA61793.1; -.  
 DR HSSP: P07157; IAP.  
 DR InterPro: IPR004539; EF\_alpha.  
 DR InterPro: IPR000795; EF\_GTPbind.  
 DR InterPro: IPR004160; EFPU\_Cterm.  
 DR InterPro: IPR004161; EFPU\_D2.  
 DR Pfam: PF00009; GTP\_EFTU; 1.  
 DR Pfam: PF03144; GTP\_EFTU\_D2; 1.  
 DR Pfam: PF03143; GTP\_EFTU\_D3; 1.  
 DR PRINTS: PR00315; ELONGATNFC1.  
 DR TIGRFAMs: TIGR00483; EF-1\_alpha; 1.  
 DR PROSITE: PS00301; EFACITOR\_GTP; 1.  
 DR Elongation factor; Protein bioynthesis; GTP-binding;  
 KW Multigene family.  
 FT NP\_BIND 14 21 GTP (BY SIMILARITY).  
 FT NP\_BIND 91 95 GTP (BY SIMILARITY).  
 FT NP\_BIND 153 156 GTP (BY SIMILARITY).  
 SQ SEQUENCE 449 AA; 49174 MW; 21C76036B1AB4DE CRC64;  
 Query Match 38.3%; Score 46; DB 1; Length 449;  
 Best Local Similarity 52.9%; Pred. No. 19;

Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
 Qy 4 GMYEGPLEPPDALD 20  
 ||| : ||| :  
 Db 212 GKMYKPCLEALDADC 228

RESULT 10  
 FPRB\_MYCLE STANDARD; PRT; 555 AA.  
 AC O33064;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Probable ferredoxin/ferredoxin--NADP reductase (EC 1.18.1.2) (FNR).  
 GN FPRB OR ML2134 OR MLCB57.39.  
 OS Mycobacterium leprae.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1769;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TN;  
 RX MEDLINE=21128732; PubMed=11234002;  
 RA Cole S.T., Eiglmeyer K., Parkhill J., James K.D., Thomson N.R.,  
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,  
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R.M., Devlin K., Duthoy S., Felwell T., Frazer A., Hamlin N.,  
 RA Holroyd S., Hornsby T., Jagers K., Lacroix C., Maclean J., Moule S.,  
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,  
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,  
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,  
 RA Batteil B.G.;  
 RT "Massive gene decay in the leprosy bacillus";  
 RL Nature 409:1007-1011(2001).  
 CC -1- CATALYTIC ACTIVITY: Reduced ferredoxin + NADP(+) = oxidized  
 ferredoxin + NADPH.  
 CC -1- COFACTOR: FAD; PROBABLY BINDS ONE OR TWO 4FE-4S CLUSTERS.  
 CC -1- SIMILARITY: IN THE N-TERMINAL, BELONGS TO THE BACTERIAL TYPE  
 FERREDOXIN FAMILY.  
 CC -1- SIMILARITY: IN THE C-TERMINAL, TO OTHER FERREDOXIN NADP  
 REDUCTASES.  
 -----  
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 -----  
 CC EMBL: Z99494; CAB16679.1; -.  
 DR EMBL: AL583924; CAC31089.1; -.  
 DR PIR: T45351; T45351.  
 DR HSSP: P55907; IXER.  
 DR Leprona: ML2134; -.  
 DR InterPro: IPR001450; 4Fe4S\_ferredoxin.  
 DR InterPro: IPR000813; 7Fe\_ferredoxin.  
 DR InterPro: IPR000759; Adnrxn\_reductase.  
 DR InterPro: IPR001327; FAD\_pyri\_redox.  
 DR Pfam: PF00037; fer4\_2.  
 DR PRINTS: PR00354; 7FE8FERDOXIN.  
 DR PRINTS: PR00419; ADKRDTRASE.  
 DR PRINTS: PR00368; FADPNR.  
 DR PROSITE: PS00198; 4FE4S\_FERREDOXIN; 1.  
 DR Oxidoreductase; Flavoprotein; NADP; FAD; Electron transport;  
 KW Iron-sulfur; 4Fe-4S; Complete proteome.  
 FT DOMAIN 1 83 FERREDOXIN.  
 FT DOMAIN 115 555 FERREDOXIN--NADP REDUCTASE.  
 FT METAL 9 9 IRON-SULFUR 1 (BY SIMILARITY).  
 FT METAL 15 15 IRON-SULFUR 1 (BY SIMILARITY).  
 FT METAL 19 19 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).  
 FT METAL 46 46 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).

FT METAL 49 49 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).  
 FT METAL 52 52 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).  
 FT METAL 56 56 IRON-SULFUR 1 (BY SIMILARITY).  
 SQ SEQUENCE 555 AA; 59712 MW; 43C7292E6A2DFD9 CRC64;

## Query Match

Best Local Similarity 37.1%; Score 45; DB 1; Length 555;  
 Matches 9; Conservative 3; Mismatches 6; Indels 10; Gaps 1;

QY 3 NGGWEYGPPLER-----RPDALD 20  
 DB 481 NAGWLTDPVAEPALAKLVHARQPTVD 508

## RESULT 11

RS16\_HELPY STANDARD; PRT; 76 AA.

AC 092K63;  
 DT 30-MAY-2000 (Rel. 39, Last Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 30S ribosomal protein S16.  
 GN RPS16 OR JHP1078.

OS Helicobacter pylori J99 (Campylobacter pylori J99).  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
 OC Helicobacteraceae; Helicobacter.  
 RN [1]\_TaxID=85963;

## SEQUENCE FROM N.A.

RA MEDLINE=99120557; PubMed=9923682;  
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,  
 RA Smith D.R., Noonan B., Guild B.C., deLonge B.L., Carmel G.,  
 RA Tummino P.J., Carno A., Uria-Nickelsen M., Mills D.M., Ives C.,  
 RA Gibson R., Werberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,  
 RA Trust T.V.;

RT "Genomic sequence comparison of two unrelated isolates of the human  
 RT gastric pathogen Helicobacter pylori";  
 RL Nature 397:176-180(1999).

CC -1- SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----

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DR EMBL; AE001535; AAD06658.1; -;  
 DR PIR; C71852; C71852.  
 DR HSSP; P80379; 1EMW.  
 DR HAMAP; MF\_00385; -; 1.  
 DR InterPro; IPR000307; Ribosomal\_S16.  
 DR Pfam; PF00886; Ribosomal\_S16; 1.  
 DR ProDom; PD003791; Ribosomal\_S16; 1.  
 DR TIGRFAMs; TIGR00002; S16; 1.  
 DR PROSITE; PS00732; RIBOSOMAL\_S16; 1.  
 KW Ribosomal protein; Complete proteome.

SQ SEQUENCE 76 AA; 8985 MW; FCF0FB21B58E230C8 CRC64;

Query Match 37.1%; Score 44.5; DB 1; Length 76;  
 Best Local Similarity 36.0%; Pred. No. 4.6;  
 Matches 9; Conservative 5; Mismatches 6; Indels 5; Gaps 1;

QY 1 QONGGM-----YEGPLERPPDALD 20  
 DB 27 RRDGMWISIGYVNPISPEKQVRID 51

## RESULT 12

RS16\_HELPY STANDARD; PRT; 76 AA.  
 AC P56023;

DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 30S ribosomal protein S16.  
 GN RPS16 OR HP1151.

OS Helicobacter pylori (Campylobacter pylori).

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
 OC Helicobacteraceae; Helicobacter.  
 RN [1]\_TaxID=210;

RP SEQUENCE FROM N.A.  
 RP STRAIN=26695 / ATCC 700392;  
 RX MEDLINE=97394467; PubMed=9252185;

RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,  
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,  
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,  
 RA Loftus B., Richardson D., Dodson R., Khairat H.G., Glodek A.,  
 RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,  
 RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,  
 RA Cotton M.D., Melman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,  
 RA Hayes W.S., Borodovsky M., Kar P.D., Smith H.O., Fraser C.M.,  
 RA Venter J.C.;

RT "The complete genome sequence of the gastric pathogen Helicobacter  
 RT pylori";  
 RL Nature 388:539-547(1997).

CC -1- SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----

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DR EMBL; AE000621; AAD08199.1; -;  
 DR PIR; G64663; G64663.  
 DR HSSP; P80379; 1EMW.  
 DR TIGR; HP1151; -;

DR HAMAP; MF\_00385; -; 1.  
 DR InterPro; IPR000307; Ribosomal\_S16.  
 DR Pfam; PF00886; Ribosomal\_S16; 1.  
 DR ProDom; PD003791; Ribosomal\_S16; 1.  
 DR TIGRFAMs; TIGR00002; S16; 1.  
 DR PROSITE; PS00732; RIBOSOMAL\_S16; 1.  
 KW Ribosomal protein; Complete proteome.

SQ SEQUENCE 76 AA; 8971 MW; FCF0FB203D79ADFC8 CRC64;

Query Match 37.1%; Score 44.5; DB 1; Length 76;  
 Best Local Similarity 36.0%; Pred. No. 4.6;  
 Matches 9; Conservative 5; Mismatches 6; Indels 5; Gaps 1;

QY 1 QONGGM-----YEGPLERPPDALD 20  
 DB 27 RRDGMWISIGYVNPISPEKQVRID 51

## RESULT 13

Y14D\_BP74 STANDARD; PRT; 128 AA.

AC P39507; Q9T0T2;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical 14.7 kDa protein in ftd-op32 intergenic region.  
 GN Y14D OR PRD.2.  
 OS Bacteriophage T4.

OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
 OC T4-like viruses.  
 RN [1]\_TaxID=10665;

RP SEQUENCE FROM N.A.  
 RA Poglaзов A.B., Meeyanzhinov V.V., Kutter E.M.;



```

RN Submitted (JAN-1995) to the EMBL/Genbank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G.,
RT Mesyanzhinov V., Ruger W., Stidham T., Thomas E.;
RL "Bacteriophage T4 genome analysis."
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
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CC -----
DR EMBL; U20859; AAA62284.1; ALT_INTT.
DR EMBL; AF158101; AAD42579.1; -.
DR InterPro; IPR004885; FRD2.
DR Pfam; PF03197; FRD2; 1.
DR Hypothetical protein.
SQ SEQUENCE 128 AA; 14741 MW; AE69390DBCFA6222 CRC64;

Query Match
Best Local Similarity 36.7%; Score 44; DB 1; Length 128;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 QONGGWYE 8
DB 32 QONGGWFE 39

RESULT 14
Y14D_BPT6 STANDARD; PRT; 128 AA.
ID Y14D_BPT6
AC Q38169;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 14.8 kDa protein in frd-gp32 intergenic region.
OS FRD.2 OR FRD2.
GN Bacteriophage T6.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_Taxid=10666;
RN (1)
RP SEQUENCE FROM N.A.
RA Foglazzov A.B., Porter D., Kutter E.M., Mesyanzhinov V.V.;
RT "DNA Sequences of the frd region in T4-related bacteriophages."
RL Submitted (AUG-1995) to the EMBL/Genbank/DBJ databases.
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CC -----
DR EMBL; L46846; AAA74669.1; -.
DR InterPro; IPR004885; FRD2.
DR Pfam; PF03197; FRD2; 1.
DR Hypothetical protein.
SQ SEQUENCE 128 AA; 14768 MW; 2CE311AF2D4372DC CRC64;

Query Match
Best Local Similarity 36.7%; Score 44; DB 1; Length 128;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 QONGGWYE 8
DB 32 QONGGWFE 39

```

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RESULT 15
DDL_ENTRR
ID DDL_ENTRR STANDARD; PRT; 358 AA.
AC Q47827;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE D-alanine--D-alanine ligase (EC 6.3.2.4) (D-alanylalanine synthetase)
DE (D-Ala-D-Ala ligase).
GN DDL.
OS Enterococcus hirae.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OC NCBI_Taxid=1354;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 8043;
RX MEDLINE=96270057; Pubmed=8662022;
RA Evers S., Casadewall B., Charles M., Dutka-Malen S., Galland M.,
RA Courvalin P.;
RT "Evolution of structure and substrate specificity in
RT D-alanine:D-alanine ligases and related enzymes."
RL J. Mol. Evol. 42:706-712(1996).
CC -1- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + 2 D-alanine = ADP + phosphate + D-
CC alanyl-D-alanine.
CC -1- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; second
CC step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the D-alanine--D-alanine ligase family.
CC -----
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CC -----
DR EMBL; U39788; AAB1904.1; -.
DR HSP; P07862; I10W.
DR HAMAP; MF_00047; -.
DR InterPro; IPR005905; D_ala_D_al.
DR Pfam; PF01820; Dala_dala_ligase; 1.
DR TIGRFAMs; TIGR01205; D_ala_D_alatig; 1.
DR PROSITE; PS00843; DALA_DALA_LIGASE_1; 1.
DR PROSITE; PS00844; DALA_DALA_LIGASE_2; 1.
DR KW Ligase; Cell wall; Peptidoglycan synthesis.
SQ SEQUENCE 358 AA; 40128 MW; 225CF988A0A979F1 CRC64;

Query Match
Best Local Similarity 46.7%; Score 29;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 QONGWYEGPLLEBP 16
DB 42 KEGOWKGPPLLEBP 56

```

Search completed: December 30, 2003, 10:55:51  
 Job time : 2.12591 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:46:19 ; Search time 5.11779 Seconds  
(without alignments)  
1058.876 Million cell updates/sec

Title: US-09-674-752-29  
Perfect score: 120  
Sequence: 1 QONGGWYEGPLPRPDALDI 21

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP\_RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_VIRUS:\*  
16: SP\_BACTERIAP:\*  
17: SP\_ARCHAEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	53	44.2	408	5	Q96979	Q96979 paranophrys
2	52	43.3	98	4	Q969F5	Q969F5 homo sapien
3	51	42.5	175	16	Q8KBC1	Q8KBC1 chlorobium
4	50	41.7	205	5	Q00032	Q00032 brugia paha
5	50	41.7	343	1	Q9HH38	Q9HH38 methanobact
6	50	41.7	358	2	Q47755	Q47755 enterococcu
7	50	41.7	358	2	Q9F0M3	Q9F0M3 enterococcu
8	50	41.7	403	17	Q9YBR4	Q9YBR4 aeropyrum p
9	49	40.8	322	4	Q9H685	Q9H685 homo sapien
10	49	40.8	363	16	Q8EFW9	Q8EFW9 yersinia pe
11	49	40.8	375	16	Q8D080	Q8D080 yersinia pe
12	48.5	40.4	75	16	Q9ZME1	Q9ZME1 rhizobium m
13	48	40.0	190	16	Q8EKCS	Q8EKCS shewanella
14	48	40.0	346	9	Q98700	Q98700 rhizobium 1
15	48	40.0	354	16	Q80215	Q80215 methanobact
16	48	40.0	1235	11	Q9JLS3	Q9JLS3 rattus norv

17	48	40.0	1576	10	Q9FGX4	Q9FGX4 arabidopsis
18	47	39.2	362	16	Q8ZR27	Q8ZR27 salmonella
19	47	39.2	362	16	Q8Z8K6	Q8Z8K6 salmonella
20	47	39.2	362	16	Q8XBU7	Q8XBU7 escherichia
21	47	39.2	362	16	Q8FK14	Q8FK14 escherichia
22	47	39.2	409	5	Q909P4	Q909P4 paramecium
23	47	39.2	437	5	Q909C6	Q909C6 paramecium
24	47	39.2	4150	2	Q9KIV4	Q9KIV4 streptomyce
25	47	39.2	9477	2	Q9LAX3	Q9LAX3 streptomyce
26	46	38.3	190	5	Q17171	Q17171 brugia mala
27	46	38.3	310	16	Q8PK92	Q8PK92 xanthomonas
28	46	38.3	366	17	Q9HR12	Q9HR12 halobacteri
29	46	38.3	423	16	Q8UB66	Q8UB66 agrobacteri
30	46	38.3	524	3	Q00354	Q00354 coprinus ci
31	46	38.3	579	16	Q910U1	Q910U1 pseudomonas
32	46	38.3	627	2	Q9JHS6	Q9JHS6 bradyrhizob
33	46	38.3	647	12	Q9W9C4	Q9W9C4 human hefte
34	46	38.3	717	5	Q8MXN3	Q8MXN3 dictyostell
35	46	38.3	759	12	Q9PMX1	Q9PMX1 human hefte
36	46	38.3	825	5	Q21430	Q21430 caenorhabdl
37	46	38.3	1062	4	Q9NSW2	Q9NSW2 homo sapien
38	46	38.3	1235	4	Q9UT54	Q9UT54 homo sapien
39	45.5	37.9	173	8	Q94SD1	Q94SD1 dactylopten
40	45.5	37.9	451	10	Q9ZSW2	Q9ZSW2 cyanophora
41	45.5	37.9	571	16	Q8KBC7	Q8KBC7 chlorobium
42	45.5	37.9	1349	16	Q8X6C1	Q8X6C1 escherichia
43	45.5	37.9	2380	16	Q8XYE8	Q8XYE8 ralatonia s
44	45.5	37.9	2425	17	Q28859	Q28859 archaeglob
45	45.5	37.5	99	2	Q9AK08	Q9AK08 rhizobium m

## ALIGNMENTS

RESULT 1  
ID 096979 PRELIMINARY; PRT; 408 AA.  
AC 096979;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Translation elongation factor 1-alpha (Fragment).  
GN TEFL.  
OS Paranophrys carnivora.  
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Scuticociliatia;  
OC Philasterida; Orchitophryidae; Paranophrys.  
OX NCBI\_Taxid=85900;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99152616; PubMed=10028290;  
RA Moreira D., Le Guyader H., Philippe H.;  
RT "Unusually high evolutionary rate of the elongation factor 1 alpha  
genes from the Ciliophora and its impact on the phylogeny of  
eukaryotes.";  
RL Mol. Biol. Evol. 16:234-245(1999).  
DR EMBL; AF056103; AAD03258.1; -.  
DR HSSP; P02990; 1FTU.  
DR InterPro; IPR004539; BPI\_alpha.  
DR InterPro; IPR004160; EFTU\_Cterm.  
DR InterPro; IPR004161; EFTU\_D2.  
DR InterPro; IPR000795; EF\_GTPbind.  
DR Pfam; PF00009; GTP\_EFTU\_1.  
DR Pfam; PF03144; GTP\_EFTU\_D2; 1.  
DR Pfam; PF03143; GTP\_EFTU\_D3; 1.  
DR PRINTS; PR00315; ELONGATNFCF.  
DR TIGRFAMs; TIGR00483; EF-1\_alpha; 1.  
DR PROSITE; PS00301; EFATOR\_GTP; 1.  
KW Elongation factor; GTP-binding; Protein biosynthesis.  
FT NON\_TER 1  
FT NON\_TER 408  
SQ SEQUENCE 408 AA; 45067 MW; 384973BB7F3F5FA1 CRC64;  
Query Match 44.2%; Score 53; DB 5; Length 408;

Best Local Similarity 55.6%; Pred. No. 8.5;  
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 NCGWYEGPLLEPRPDALD 20  
Db 192 NAWYKGPILCAALD 209

## RESULT 2

Q96SFS PRELIMINARY; PRT; 98 AA.  
AC Q96SFS;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE B555G22.1 (Hypothetical protein KIAA1008) (Fragment).  
GN B555G22.1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Blakey S.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL391384; CAC39623.1; -.  
KM Hypothetical protein.  
FT NON\_TER 98  
SQ SEQUENCE 98 AA; 10403 MW; DSFF25DD73ACF578 CRC64;

Query Match 43.3%; Score 52; DB 4; Length 98;  
Best Local Similarity 69.2%; Pred. No. 2.4;  
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GMYEGPLLEPRP 16  
Db 40 GGAHEGPALPEPP 52

## RESULT 3

Q8KBC1 PRELIMINARY; PRT; 175 AA.  
AC Q8KBC1;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Hypothetical protein C11868.  
GN C11868.  
OS Chlorobium tepidum.  
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;  
OC Chlorobium.  
OX NCBI\_TaxID=1097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TLS / ATCC 49652 / DSM 12025;  
RX MEDLINE=22103685; PubMed=12093901;  
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,  
RA Dodson R.J., Deboy K., Gwinn M.L., Nelson W.C., Haft D.H.,  
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,  
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,  
RA Niernan W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,  
RA Vamathevan J., Khouiri H., White O., Gruber T.M., Ketchum K.A.,  
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.,  
RT "The complete genome sequence of Chlorobium tepidum TLS, a  
RT photosynthetic, anaerobic, green-sulfur bacterium."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).  
DR EMBL; AE012938; AAM73087.1; -.  
DR TIGR; C11868; -.  
KM Hypothetical protein; Complete proteome.  
SQ SEQUENCE 175 AA; 19661 MW; 3C87FF6C5A7E930 CRC64;

Query Match 42.5%; Score 51; DB 16; Length 175;  
Best Local Similarity 47.1%; Pred. No. 6.6;

Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 QNGWYEGPLLEPRPD 18  
Db 138 ENGPWODGAVYVERPD 154

## RESULT 4

Q00032 PRELIMINARY; PRT; 205 AA.  
AC Q00032;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Major protein component of the microfilarial sheath.  
GN MF22.  
OS Brugia pahangi.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Brugia.  
OX NCBI\_TaxID=6280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91250404; PubMed=1710216;  
RA Seikirk M., Yazdankhsh M., Freedman D., Baxter M., Cookson E.,  
RA Jenkins R.E., Williams S.A.;  
RT "A proline-rich structural protein of the surface sheath of larval  
RT Brugia filarial nematode parasites."  
RL J. Biol. Chem. 266:11002-11008(1991).  
DR EMBL; X58063; CAA41094.1; -.  
SQ SEQUENCE 205 AA; 22199 MW; CAD79BDFC7225041 CRC64;

Query Match 41.7%; Score 50; DB 5; Length 205;  
Best Local Similarity 52.9%; Pred. No. 11;  
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 QNGWYEGPLLEPRPD 18  
Db 162 QTPGWTGPRLTPKPTA 178

## RESULT 5

Q9HH38 PRELIMINARY; PRT; 343 AA.  
AC Q9HH38;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical 38.6 kDa protein.  
OS Methanobacterium wolfei.  
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
OC Methanobacteriaceae; Methanothermobacter.  
OX NCBI\_TaxID=145261;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21429258; PubMed=11544247;  
RA Luo Y., Pfeister P., Leisinger T., Waserfallen A.;  
RT "The Genome of Archaeal Prophage PsiM100 Encodes the Lytic Enzyme  
RT Responsible for Autolysis of Methanothermobacter wolfeii."  
RL J. Bacteriol. 183:5788-5792(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Luo Y.;  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF01375; AAG39973.1; -.  
DR InterPro; IPR001993; Mitoch\_carrier.  
DR PROSITE; PS00215; MITOCH\_CARRIER; 1.  
KM Hypothetical protein.  
SQ SEQUENCE 343 AA; 38594 MW; 61D20A47A28905D3 CRC64;

Query Match 41.7%; Score 50; DB 1; Length 343;  
Best Local Similarity 40.0%; Pred. No. 20;  
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

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; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 127
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-325
```

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Query Match          73.8%; Score 524.5; DB 12; Length 127;
Best Local Similarity 78.9%; Pred. No. 1.4e-42;
Matches 105; Conservative 6; Mismatches 15; Indels 7; Gaps 3;
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Oy 1 OVQLQSLATEYKKPKASMKVSCMASGYPTSYDISWVQAPQGLMMGWSISYSGNTDY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 OVQLQSLATEYKKPKASMKVSCMASGYPTSYDISWVQAPQGLMMGWSISYSGNTNY 60
Oy 61 AOKFGRTVMTTDTSRRTAYMELRLSRDDTAIVVYCARDDGGGAYEDVWSGEY-PEYYAM 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKFGRTVMTTDTSRRTAYMELRLSRDDTAIVVYCARDDGGGAYEDVWSGEY-SSDYLYYYGL 114
Oy 120 DVWGQGTIVTVSS 132
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 DVWGQGTIVTVSS 127
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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```
RESULT 6
US-09-880-748-1674
; Sequence 1674, Application US/09880748
; Publication No. US2003005937A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1674
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1674
```

```
Query Match          73.7%; Score 524; DB 11; Length 252;
Best Local Similarity 78.0%; Pred. No. 3.2e-42;
Matches 103; Conservative 7; Mismatches 16; Indels 6; Gaps 2;
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```
Oy 1 OVQLQSLATEYKKPKASMKVSCMASGYPTSYDISWVQAPQGLMMGWSISYSGNTDY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 OVQLQSLATEYKKPKASMKVSCMASGYPTSYDISWVQAPQGLMMGWSISYSGNDNTNY 60
Oy 61 AOKFGRTVMTTDTSRRTAYMELRLSRDDTAIVVYCARDDGGGAYEDVWSGEYPEYYAM 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKFGRTVMTTDTSRRTAYMELRLSRDDTAIVVYCARDDGGGAYEDVWSGEY-YYGMD 114
Oy 121 VMGQGTIVTVSS 132
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 VMGQGTIVTVSS 126
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 7

```
US-09-880-748-1921
; Sequence 1921, Application US/09880748
; Publication No. US2003005937A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1921
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1921
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Query Match          73.6%; Score 523; DB 11; Length 251;
Best Local Similarity 74.6%; Pred. No. 4e-42;
Matches 103; Conservative 5; Mismatches 14; Indels 16; Gaps 2;
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Oy 1 OVQLQSLATEYKKPKASMKVSCMASGYPTSYDISWVQAPQGLMMGWSISYSGNTDY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 OVQLQSLATEYKKPKASMKVSCMASGYPTSYDISWVQAPQGLMMGWSISYSGNTNY 60
Oy 61 AOKFGRTVMTTDTSRRTAYMELRLSRDDTAIVVYCARDDGGGAYEDVWSGEY-PEYYAM 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AOKFGRTVMTTDTSRRTAYMELRLSRDDTAIVVYCARDDGGGAYEDVWSGEY-SSDYLYYYGL 111
Oy 115 EYVADVWGQGTIVTVSS 132
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 112 -YYGMDVWGQGTIVTVSS 128
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 8

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US-09-880-748-973
; Sequence 973, Application US/09880748
; Publication No. US2003005937A1
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; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 973
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-973
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```
Query Match          73.3%; Score 521.5; DB 11; Length 259;
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Best Local Similarity 74.5%; Pred. No. 5.8e-42;  
Matches 102; Conservative 8; Mismatches 18; Indels 9; Gaps 2

[illegible]

RESULT 9  
MS-09-88

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? Sequence 1777, Application US/09880748
? Publication No. US20030059937A1
? GENERAL INFORMATION:
? APPLICANT: Ruben et al.
? TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blyss
? FILE REFERENCE: PFS23
? CURRENT APPLICATION NUMBER: US/09/880,748
? PRIOR FILING DATE: 2001-06-15
? PRIOR APPLICATION NUMBER: 60/212,210
? PRIOR FILING DATE: 2000-06-15
? PRIOR APPLICATION NUMBER: 60/240,816
? PRIOR FILING DATE: 2000-10-17
? PRIOR APPLICATION NUMBER: 60/276,248
? PRIOR FILING DATE: 2001-03-16
? PRIOR APPLICATION NUMBER: 60/277,379
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/293,499
? PRIOR FILING DATE: 2001-05-25
? NUMBER OF SEQ ID NOS: 3239
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 1777
? LENGTH: 253
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-880-748-1777

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Query Match	73.1%	Score 520;	DB 11;	Length 253;
Best Local Similarity	75.8%	Pred. No. 7.8e-42;		
Matches 100;	Conservative 12;	Mismatches 18;	Indels 2;	Gaps 2

[illegible]

RESULT 10

US-09-880-748-1778  
Sequence 1778, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS  
FILE REFERENCE: P5523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIORITY APPLICATION NUMBER: 60/212,210  
PRIORITY FILING DATE: 2000-06-15

```

; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,459
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1778
; LENGTH: 248
; TYPE: PR1
; ORGANISM: Homo sapiens
US-03-880-748-1778

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Query Match	72.4%;	Score 514.5;	DB 11;	Length 240;
Best Local Similarity	75.8%;	Pred. No. 2.6e-41;		
Matches 100; Conservative	9;	Mismatches 16;	Indels 7;	Gaps 2;

Qy	1	QVOLLGSAFEVKKPKGSMKMS	CMAGGYEFTSDLSMWRQAGQGL	EMMGWTSISGNTDY	60
Db	1	QVQLDQSGAEVARKPGASIVYSC	KASGTYFTTSYGISWVRQAGHGL	EMMGWTSISAVNGTNY	60
Qy	61	AAKFGQRLMTDTDSRRRTATN	ELSLRLSDDTAVVYTCARDGGGAG	YEDVWGSEYPERYAMD	120
Db	61	AAQLQGRVMTDTDTSTATN	ELSLRLSDDTAVVYCAR----	SYDILTGYPP--FGMD	113
Qy	121	VWGQGTTVTVSS	132		
Db	114	VWGKGTMTVSS	125		

## RESULT 11

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US-09-880-748-1610
; Sequence 1610, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; FILE OF INVENTION: Antibodies that Immunospecifically Bind Blyss
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1610
; LENGTH: 257
; TYPE: PR1
; ORGANISM: Homo sapiens
; US-09-880-748-1610

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Query Match	72.4%	Score 514.5	DB 11	Length 257
Best Local Similarity	77.0%	Pred. No. 2.7e-41		
Matches 104; Conservative	6	Mismatches 18	Indels 7	Gaps 3

QY 1YVQLLOSLSTEVYKKPPASMKYS<sup>CMASG</sup>Y<sup>PF</sup>YSY<sup>DI</sup>SP<sup>MR</sup>QAPGCL<sup>EM</sup>MG<sup>NI</sup>SI<sup>Y</sup>SG<sup>NT</sup>DI 60

Db 1 QVQLQQSGAEYKKPPASV<sup>KVS</sup>CKASG<sup>CT</sup>FT<sup>YS</sup>IG<sup>IS</sup>SW<sup>MR</sup>QAPGCL<sup>EM</sup>MG<sup>NI</sup>SA<sup>NG</sup>NT<sup>KY</sup> 60

QY 61 AOKPGGR<sup>LT</sup>MT<sup>TD</sup>SR<sup>TR</sup>FA<sup>Y</sup>WE<sup>LS</sup>ASD<sup>DT</sup>AY<sup>Y</sup>CA<sup>RD</sup>GGC<sup>GA</sup>VED<sup>VS</sup>MG<sup>VE</sup>Y<sup>PE</sup>---YY 117

Db 61 AQLQLGRT<sup>TT</sup>TD<sup>TD</sup>SR<sup>TR</sup>FA<sup>Y</sup>WE<sup>LS</sup>ASD<sup>DT</sup>AY<sup>Y</sup>CA<sup>RD</sup>DL<sup>G</sup>---YD<sup>IL</sup>NG<sup>-</sup>Y<sup>PP</sup>PY<sup>Y</sup>Y 116





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OM protein - protein search, using SW model

Run on: December 30, 2003, 10:47:45 ; Search time 13.4037 Seconds

(without alignments)  
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Title: US-09-674-752-25

Sequence: 1 QVQLQSAIVEYKPGASMKV.....YPEYVMDVWGSGITTVTSS 132

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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
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4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	485	68.2	120	4	US-09-025-769B-36 Sequence 36, Appl
2	485	68.2	120	4	US-09-025-769B-59 Sequence 59, Appl
3	484.5	68.1	117	4	US-09-025-769B-22 Sequence 22, Appl
4	478.5	67.3	121	1	US-08-264-093-3 Sequence 3, Appl
5	476.5	67.0	129	2	US-08-561-521-45 Sequence 45, Appl
6	476.5	67.0	129	4	US-08-525-539A-77 Sequence 77, Appl
7	476.5	67.0	129	5	PCT-US95-01219-45 Sequence 45, Appl
8	476	66.9	128	1	US-08-202-047-22 Sequence 22, Appl
9	476	66.9	128	3	US-08-964-690-22 Sequence 22, Appl
10	471.5	66.3	125	3	US-09-199-149-3 Sequence 19, Appl
11	464	65.3	120	2	US-08-652-816A-19 Sequence 19, Appl
12	452.5	63.6	139	3	US-08-933-983-21 Sequence 21, Appl
13	450	63.3	117	3	US-08-545-809A-105 Sequence 105, Appl
14	448	63.0	139	2	US-08-253-877C-19 Sequence 19, Appl
15	448	63.0	139	2	US-08-452-164A-19 Sequence 19, Appl
16	448	63.0	139	2	US-08-603-024-16 Sequence 16, Appl
17	448	63.0	139	4	US-08-450-809-14 Sequence 14, Appl
18	447	62.9	123	3	US-09-049-672A-13 Sequence 13, Appl
19	444	62.4	120	4	US-09-025-769B-35 Sequence 35, Appl
20	444	62.4	120	4	US-09-025-769B-57 Sequence 57, Appl
21	443.5	62.4	119	2	US-08-561-521-10 Sequence 10, Appl
22	443.5	62.4	119	5	PCT-US95-01219-10 Sequence 10, Appl
23	440.5	62.0	146	1	US-08-276-852-155 Sequence 155, App
24	440.5	62.0	146	1	US-08-899-575-155 Sequence 155, App
25	440.5	62.0	146	1	US-08-899-575-155 Sequence 155, App
26	440.5	62.0	146	1	US-08-899-575-155 Sequence 155, App
27	440.5	62.0	146	5	PCT-US95-08743-155 Sequence 155, App

28	438	61.6	1	2	US-08-561-521-41 Sequence 41, Appl
29	438	61.6	1	5	PCT-US95-01219-41 Sequence 41, Appl
30	438	61.6	1	1	US-08-137-117D-102 Sequence 102, App
31	438	61.6	1	2	US-08-436-717-102 Sequence 102, App
32	436.5	61.4	1	1	US-08-300-386A-65 Sequence 65, Appl
33	436.5	61.4	1	3	US-08-931-645-65 Sequence 65, Appl
34	436.5	61.4	1	5	PCT-US95-11235-65 Sequence 65, Appl
35	435.5	61.3	1	2	US-08-561-521-12 Sequence 12, Appl
36	435.5	61.3	1	5	PCT-US95-01219-12 Sequence 12, Appl
37	434.5	61.1	1	1	US-08-477-877B-94 Sequence 94, Appl
38	434.5	61.1	1	2	US-08-477-877B-94 Sequence 94, Appl
39	434.5	61.1	1	2	US-08-477-877B-94 Sequence 94, Appl
40	433.5	61.0	1	3	US-08-836-561-63 Sequence 63, Appl
41	433.5	61.0	1	4	US-09-434-122-63 Sequence 63, Appl
42	433	60.9	1	1	US-08-137-117D-100 Sequence 100, App
43	433	60.9	1	2	US-08-436-717-100 Sequence 100, App
44	432	60.8	1	1	US-08-137-117D-112 Sequence 112, App
45	432	60.8	1	2	US-08-436-717-112 Sequence 112, App

## ALIGNMENTS

```
RESULT 1
US-09-025-769B-36
Sequence 36, Application
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik,
APPLICANT: Pack, Pet
APPLICANT: 11ag, Vic
APPLICANT: Ge, Limin
APPLICANT: Moroney,
APPLICANT: Plueckhu
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
ADDRESS: James F
STREET: 1251 Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FOR
MEDIUM TYPE: Flopp
COMPUTER: IBM PC C
OPERATING SYSTEM:
SOFTWARE: Patentin
CURRENT APPLICATION D
APPLICATION NUMBER:
FILING DATE: 18-PE
PRIOR APPLICATION DAT
APPLICATION NUMBER:
FILING DATE: 18-AU
ATTORNEY/AGENT INFORM
NAME: James F. Hal
REGISTRATION NUMBER
TELECOMMUNICATION INF
TELEPHONE: (212)59
TELEFAX: (212)596-
INFORMATION FOR SEQ ID
SEQUENCE CHARACTERIST
LENGTH: 120 amino
TYPE: amino acid
STRANDEDNESS: 1
TOPOLOGY: linear
MOLECULE TYPE: prote
US-09-025-769B-36
Query Match
Best Local Similarity
Matches 96; Conservat
2%; Score 485, DB 4, Length 120,
7%; Pred. No. 5.3e-39;
7; Mismatches 17; Indels 12; Gaps 1;
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QY 1 QVOLLGATATEYKKGASMKVSCMASGYPTFTSYDTSWVROAPGQGLEMMGMIISYSGNTDY 60  
1 QVOLLVQSGAEVKKPGASVKSCKASGYFTFTSYMHMVRQAPGQGLEMMGMINPNSGNTNY 60  
Db 61 AOKFOGQVMTMTDTSRRTAYMELSLRSDDTAVYYCARGDGGAYEDVWSGSEYPEYYAMD 120  
61 AOKFOGQVMTMTDTSRRTAYMELSLRSDDTAVYYCARGDGGAYEDVWSGSEYPEYYAMD 120  
QY 121 VMGQGTIVTVSS 132  
109 YMGQGTIVTVSS 120  
Db 109 YMGQGTIVTVSS 120

RESULT 2  
US-09-025-769B-59  
; Sequence 59, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckhuhn, Andreas  
; TITLE OF INVENTION: Protein/(poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-59

Query Match 68.2%; Score 485; DB 4; Length 120;  
Best Local Similarity 72.7%; Pred. No. 5,3e-39;  
Matches 96; Conservative 7; Mismatches 17; Indels 12; Gaps 1;

QY 1 QVOLLGATATEYKKGASMKVSCMASGYPTFTSYDTSWVROAPGQGLEMMGMIISYSGNTDY 60  
1 QVOLLVQSGAEVKKPGASVKSCKASGYFTFTSYMHMVRQAPGQGLEMMGMINPNSGNTNY 60  
Db 61 AOKFOGQVMTMTDTSRRTAYMELSLRSDDTAVYYCARGDGGAYEDVWSGSEYPEYYAMD 120  
61 AOKFOGQVMTMTDTSRRTAYMELSLRSDDTAVYYCARGDGGAYEDVWSGSEYPEYYAMD 120  
QY 61 AOKFOGQVMTMTDTSRRTAYMELSLRSDDTAVYYCARGDGGAYEDVWSGSEYPEYYAMD 120  
61 AOKFOGQVMTMTDTSRRTAYMELSLRSDDTAVYYCARGDGGAYEDVWSGSEYPEYYAMD 120  
Db 61 AOKFOGQVMTMTDTSRRTAYMELSLRSDDTAVYYCARGDGGAYEDVWSGSEYPEYYAMD 120  
61 AOKFOGQVMTMTDTSRRTAYMELSLRSDDTAVYYCARGDGGAYEDVWSGSEYPEYYAMD 120  
QY 121 VMGQGTIVTVSS 132  
109 YMGQGTIVTVSS 120

Db 109 YMGQGTIVTVSS: 20

RESULT 3  
US-09-025-769B-22  
; Sequence 22, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckhuhn, Andreas  
; TITLE OF INVENTION: Protein/(poly)peptide libraries  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 117 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: linear  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-22

Query Match 81.1%; Score 484.5; DB 4; Length 117;  
Best Local Similarity 72.7%; Pred. No. 5,7e-39;  
Matches 96; Conservative 5; Mismatches 16; Indels 15; Gaps 1;

QY 1 QVOLLGATATEYKKGASMKVSCMASGYPTFTSYDTSWVROAPGQGLEMMGMIISYSGNTDY 60  
1 QVOLLVQSGAEVKKPGASVKSCKASGYFTFTSYMHMVRQAPGQGLEMMGMINPNSGNTNY 60  
Db 61 AOKFOGQVMTMTDTSRRTAYMELSLRSDDTAVYYCARGDGGAYEDVWSGSEYPEYYAMD 120  
61 AOKFOGQVMTMTDTSRRTAYMELSLRSDDTAVYYCARGDGGAYEDVWSGSEYPEYYAMD 120  
QY 61 AOKFOGQVMTMTDTSRRTAYMELSLRSDDTAVYYCARGDGGAYEDVWSGSEYPEYYAMD 120  
61 AOKFOGQVMTMTDTSRRTAYMELSLRSDDTAVYYCARGDGGAYEDVWSGSEYPEYYAMD 120  
Db 61 AOKFOGQVMTMTDTSRRTAYMELSLRSDDTAVYYCARGDGGAYEDVWSGSEYPEYYAMD 120  
61 AOKFOGQVMTMTDTSRRTAYMELSLRSDDTAVYYCARGDGGAYEDVWSGSEYPEYYAMD 120  
QY 121 VMGQGTIVTVSS 132  
109 YMGQGTIVTVSS 120

RESULT 4  
US-08-264-093-3  
; Sequence 3, Application US/08264093  
; Patent No. 5639863  
; GENERAL INFORMATION:

APPLICANT: Michael D. Dan  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO  
CELL CYCLE-INDEPENDENT GLIOMA SURFACE  
TITLE OF INVENTION: ANTIGEN  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ridout & Maybee  
STREET: 2300 Richmond-Adelaide Centre  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5H 2J7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 MB storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS-DOS 6.00  
SOFTWARE: ASCII Editor  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/264,093  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA: No. 5639863 applicable  
ATTORNEY/AGENT INFORMATION:  
NAME: Lake, James R.  
REGISTRATION NUMBER: 31081  
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 868-1482  
TELEFAX: (416) 362-0823  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
STRANDEDNESS: not applicable  
TOPOLOGY: linear  
US-08-264-093-3

Query Match 67.3%; Score 478.5; DB 1; Length 121;  
Best Local Similarity 72.0%; Pred. No. 2.2e-38;  
Matches 95; Conservative 11; Mismatches 15; Indels 11; Gaps 3;

QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTFTSYDISWVRQAPGGGLEMMGWISITVSGNTDY 60  
DB 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTFTSYDISWVRQAPGGGLEMMGWISITVSGNTDY 60  
QY 61 AOKFOGRVMTTDSRTAYMELSLRSDDTAIVYCCARDGGCGAYEDVWSGEYFEYYAM 120  
DB 61 AOKFOGRVMTTDSRTAYMELSLRSDDTAIVYCCARDGGCGAYEDVWSGEYFEYYAM 120  
QY 121 VMGGCTVTVSS 132  
DB 110 VMGGCTVTVSS 121

RESULT 5  
US-08-561-521-45  
Sequence 45, Application US/08561521  
GENERAL INFORMATION:  
APPLICANT: Bendig, Mary M.  
APPLICANT: Legert, Olivier J.  
APPLICANT: Saldanha, Jose  
APPLICANT: Jones, S. Tarran  
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA

ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS/MS-DOS  
SOFTWARE: Patent In  
CURRENT APPLICATION D:  
APPLICATION NUMBER: 15/08/561,521  
FILING DATE:  
CLASSIFICATION: 42,  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE: 25-JAN 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William L.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15270-14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543,100  
TELEFAX: 415-543-5645  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 129 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-561-521-45

Query Match 0%; Score 476.5; DB 2; Length 129;  
Best Local Similarity 4%; Pred. No. 3.7e-38;  
Matches 95; Conservative 11; Mismatches 22; Indels 5; Gaps 2;

QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTFTSYDISWVRQAPGGGLEMMGWISITVSGNTDY 59  
DB 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTFTSYDISWVRQAPGGGLEMMGWISITVSGNTDY 60  
QY 60 YAKFOGRVMTTDSRTAYMELSLRSDDTAIVYCCARDGGCGAYEDVWSGEYFEYYAM 119  
DB 61 YAKFOGRVMTTDSRTAYMELSLRSDDTAIVYCCARDGGCGAYEDVWSGEYFEYYAM 119  
QY 120 DWVGCTVTVSS 32  
DB 117 DWVGCTVTVSS 29

RESULT 6  
US-08-525-539A-77  
Sequence 77, Application /08525539A  
Patent No. 6309636  
GENERAL INFORMATION:  
APPLICANT: DO COUO,  
APPLICANT: CERTANT, J.  
APPLICANT: PETERSON,  
TITLE OF INVENTION: COMBINANT PEPTIDES DERIVED FROM THE  
TITLE OF INVENTION: ANTI-B44 ANTIBODY, METHODS OF USE THEREOF, AND  
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES  
NUMBER OF SEQUENCES:  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON  
STREET: 755 Page M  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy  
COMPUTER: IBM PC  
OPERATING SYSTEM: DOS/MS-DOS  
SOFTWARE: Patent In  
CURRENT APPLICATION D:  
APPLICATION NUMBER: 5/08/525,539A  
FILING DATE: 14-SEP 1995

```

      LENGTH: 129 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      PCT-US95-01219-45

Query Match
Best Local Similarity
Matches 95; Conserved e .0%; Score 476.5; DB 5; Length 129;
                                     .4%; Pred. No. 3,76-38;
                                     e 11; Mismatches 22; Indels 5; Gaps 2

QY 1 QVOLLQSATEVK JASMKVSCMASGYPTSYDISWNRQAQGGLMMGWISITY-SGNTD 59
   |||||:|||||
Db 1 QVOLLQSGAEVK GASVKVSCKASGYTFTSYAISWNRQAQGGLMMGWINPYNGDPTN 60
   |||||:|||||
QY 60 YAAKFQGRVTMT TSRRATMELRLSRSDPTAYYYCARDDGGCAVEDVMSEGEFFYAM 119
   |||||:|||||
Db 61 YAAKFQGRVTMT TSTSTAYMELSLRSEDPTAVYYCARAPGYSGGCCYRGD---YXF 116
   |||||:|||||
QY 120 DVMGGTTVTVS 132
   |||||:|||||
Db 117 DYMGGTILVTVS 129
   |||||:|||||

RESULT 8
US-08-202-047-22
Sequence 22, Application S/08202047
Patent No. 5800815
GENERAL INFORMATION:
APPLICANT: CHEMNUT, bert W.
APPLICANT: POLLEY, garet J.
APPLICANT: PAULSON, mes C.
APPLICANT: JONES, S. arran
APPLICANT: SALDANHA, obe W.
APPLICANT: BENDIG, y M.
TITLE OF INVENTION: antibodies to P-Selectin and Their Uses
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsen and Townsend Khourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM disk
MEDIUM TYPE: Flopi ,patible
COMPUTER: IBM PC -DOS/ms-DOS
OPERATING SYSTEM: release #1.0, Version #1.25
SOFTWARE: Patentl A:
CURRENT APPLICATION NUMBER US/08/202,047
APPLICATION NUMBER: 1994
FILING DATE: 25-Feb
CLASSIFICATION: 4: ION:
ATTORNEY/AGENT INFORMATION: M. Smith, Willis
NAME: Smith, Willis 30,223
REGISTRATION NUMBER ER: 14137-77
REFERENCE/DOCKET NUMBER TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-400
TELEFAX: 415-326-2
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS: S:
LENGTH: 128 amino .ids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURES:
NAME/KEY: Protein
LOCATION: 1..128
OTHER INFORMATION: label= HUMAN_1

US-08-202-047-22
```





APPLICATION NUMBER: US/08/545,809A  
FILING DATE: 27-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/Jp93/00603  
FILING DATE: 10-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 06501/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-545-809A-105

Query Match  
Best Local Similarity 63.3%; Score 450; DB 3; Length 117;  
Matches 85; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWVRQAPGQGLEMMGWISISYSGNTDY 60  
DB 20 QVQLVQSAEYVKPKPASVYKSCKAGYFTSYGISWVRQAPGQGLEMMGWISATYNGNTNY 79

QY 61 AOKFQGRVTMTTTSRTAYWELRSLRSDDTAVYYCAR 98  
DB 80 AOKLQGRVTMTTDTSTAYWELRSLRSDDTAVYYCAR 117

RESULT 14  
US-08-253-877C-19  
Sequence 19, Application US/08253877C  
Patent No. 5773001  
GENERAL INFORMATION:  
APPLICANT: Hamann, Phillip R.  
APPLICANT: Himman, Lois  
APPLICANT: Hollander, Irwin  
APPLICANT: Holcomb, Ryan  
APPLICANT: Halleck, William  
APPLICANT: Tsou, Hwei-Ru  
APPLICANT: Weiss, Martin J.  
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Cyanamid Plaza  
CITY: Wayne  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07470-8426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/253,877C  
FILING DATE: 03-JUN-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 32,368  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-831-3246  
TELEFAX: 201-831-3305  
INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:  
LENGTH: 139 amino acids  
TYPE: amino acid  
STRANDEDNESS: sing  
TOPOLOGY: linear  
MOLECULE TYPE: prote  
US-08-253-877C-19

Query Match  
Best Local Similarity 0%; Score 448; DB 1; Length 139;  
Matches 86; Conservative 13; Mismatches 21; Indels 12; Gaps 1;

QY 1 QVOLLQSAATEVKKPGASMKVSCMASGYPTSYDISWVRQAPGQGLEMMGWISISYSGNTDY 60  
DB 20 QVQLVQSAEYVKPKPASVYKSCKAGYFTSYGISWVRQAPGQGLEMMGWIDPSGNTKY 79

QY 61 AOKFQGRVTMTTTSRTAYWELRSLRSDDTAVYYCARDDGGGAYEDVWSEFEYFYAMD 120  
DB 80 NEKFKGRVTVTVIYRTAYWELRSLRSDDTAVYYCARDDGGGAYEDVWSEFEYFYAMD 127

QY 121 VMGGQTTVTVSS 12  
DB 128 YMGQGTIVTVSS 19

RESULT 15  
US-08-452-164A-19  
Sequence 19, Application US/08452164A  
Patent No. 5877296  
GENERAL INFORMATION:  
APPLICANT: Hamann, P  
APPLICANT: Himman, L  
APPLICANT: Hollander, Irwin  
APPLICANT: Holcomb, R  
APPLICANT: Halleck, W  
APPLICANT: Tsou, Hwei-Ru  
APPLICANT: Weiss, Martin J.  
TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Cyanamid Company  
STREET: One Campus  
CITY: Parsippany  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/452,164A  
FILING DATE: 26-MAY-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 32,368-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-58  
TELEFAX: 201-683-42  
INFORMATION FOR SEQ ID 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 139 amino acids  
TYPE: amino acid  
STRANDEDNESS: sing  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-452-164A-19

Query Match  
0%; Score 448; DB 2; Length 139;

Best Local Similarity 65.2%; Pred. No. 2e-35;  
Matches 86; Conservative 13; Mismatches 21; Indels 12; Gaps 1;

```
QY      1 QVQLLOSATEVKKPGASMKVSCMASGYPTSYDISWVROAPGQGLEMGWISITYGNTDY 60
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     20 QIQLVSGAEVKKPGSSSVKVCCKASGYTFDYINMMROAPGQGLEMGWIDPGSGNTKY 79
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY     61 AQKFOGRVTMTDTSRRTAYMELRSLSDDTAVYCCARDGGGAYEDVWSGEYPEYYAMD 120
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     80 NEKFKGRVITYVDTSNTAYMELSLRSEDTAFYPCARE-----KTTYYYAMD 127
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY     121 VMGQGTTVTVSS 132
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     128 YMGGTLTVTVSS 139
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

Search completed: December 30, 2003, 11:05:31  
Job time : 13.4871 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 ; Search time 9.39399 Seconds

(without alignments)  
1003.251 Million cell updates/sec

Title: US-09-674-752-27

Perfect score: 521  
Sequence: 1 QVQLQSGATEVKKPKGASMKV.....AYMELRLSRDPTAVYYCAR 98Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summariesDatabase :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	456	87.5	98	2	S26919 Ig heavy chain V r
2	453	86.9	129	2	S36260 Ig heavy chain V r
3	451	86.6	122	2	S36271 Ig heavy chain V r
4	450	86.4	124	2	S19665 Ig heavy chain V r
5	432	82.9	131	2	S21924 Ig heavy chain V r
6	428	82.1	160	2	PL0105 anti-PR2 erythrocy
7	420	80.6	111	2	S21925 Ig heavy chain V r
8	407	78.1	98	2	S26918 Ig heavy chain V r
9	407	78.1	117	2	S18553 Ig heavy chain V r
10	407	78.1	136	2	S31600 Ig heavy chain V r
11	405	77.7	125	2	S68170 Ig heavy chain V r
12	401	77.0	98	2	S26938 Ig heavy chain V r
13	401	77.0	117	2	S31680 Ig heavy chain V r
14	401	77.0	117	2	S18551 Ig heavy chain V r
15	401	77.0	135	2	S49530 anti-sm antibody V
16	400	76.8	118	2	S36265 Ig heavy chain V r
17	397	76.2	104	2	S69899 Ig heavy chain V r
18	397	76.2	127	2	S34014 Ig heavy chain V r
19	393	75.4	98	2	S26912 Ig heavy chain V r
20	393	75.4	129	2	S46393 Ig heavy chain V r
21	391	75.0	117	2	S18552 Ig heavy chain V r
22	390	74.9	132	2	S31596 Ig heavy chain V r
23	389	74.7	110	2	PH1670 Ig heavy chain V r
24	389	74.7	123	2	D33548 Ig heavy chain V-1
25	388	74.5	98	2	S26920 Ig heavy chain V r
26	387	74.3	117	2	PT0371 Ig gamma chain pre
27	383	73.5	117	1	HVHUNG Ig heavy chain pre
28	383	73.5	148	1	S29257 Ig heavy chain V r
29	382	73.3	114	2	PH1667 Ig heavy chain V r

30	382	73.3	1	2	PH1666 Ig heavy chain V r
31	381	73.1	1	2	A32483 Ig heavy chain V r
32	380	72.9	1	2	S23623 Ig heavy chain V r
33	379	72.7	2	2	PH0871 Ig heavy chain V r
34	378	72.6	1	2	JN0295 Ig heavy chain V-D
35	377	72.4	1	2	S31657 Ig heavy chain V r
36	377	72.4	1	1	HVH05 Ig heavy chain pre
37	377	72.4	1	2	S31999 Ig heavy chain V r
38	377	72.4	1	2	B32274 Ig heavy chain pre
39	376	72.2	1	2	I44151 Ig heavy chain V r
40	372	71.4	2	2	S24680 Ig heavy chain V r
41	370	71.0	2	2	S26921 Ig heavy chain V r
42	369	70.8	1	2	PH1665 Ig heavy chain V r
43	369	70.8	1	2	PH1668 Ig heavy chain V r
44	367	70.4	2	2	S26915 Ig heavy chain V r
45	367	70.4	1	2	S31698 Ig heavy chain pre

## ALIGNMENTS

RESULT 1  
S26919  
Ig heavy chain V region (D. 4) - human (fragment)  
C:Species: Homo sapiens (m.  
C:Date: 22-Nov-1993 #sequen  
A:Accession: S26919  
R:Tolson, I.M.; Walter,  
J. Mol. Biol. 227, 776-798.  
A:Title: The repertoire of  
A:Reference number: S26885  
A:Accession: S26919  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-98 <TOM>  
A:Cross-references: EMBL:Z12316; NID:G32855; PIND:CA479186.1; PID:G32856  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 456; DB 2; Length 98;  
Best Local Similarity 87.8%; Pred. No. 1.76-39;  
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLQSGATEVKKPKGASMKVSCMASGYPTSYDSWYRQAGGLIEWYGSATNGNTHY 60  
DB 1 QVQLVQSGAEVKKPKGASVKSCASGTTFTSYGISWYRQAGGLEWYGSATNGNTY 60  
QY 61 AOKFQGRVTMTTDSRRTAYMELRLSRDPTAVYYCAR 98  
DB 61 AOKLQGRVTMTTDTSTAYMELRLSRDPTAVYYCAR 98

## RESULT 2

S36260  
Ig heavy chain V region (clone alpha-CEA4-8A) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
A:Accession: S36260  
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, A.  
EMBO J. 12, 725-734, 1993  
A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
A:Reference number: S36256; MUID:93178448; PMID:7679990  
A:Accession: S36260  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-129 <GRI>  
A:Cross-references: EMBL:Z18851; NID:G33124; PIND:CA479303.1; PID:G9339903  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.9%; Score 453; DB 2; Length 129;



Best Local Similarity 87.8%; Pred. No. 4.7e-39;  
Matches 86; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVQLQSGATVEVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWVGMSAYNGNTHY 60  
DB 1 QVQLVSGAEVKKPKGASVSKVSCASGYTFTSYGISWVRQAPGQGLEWVGMSAYNGNTHY 60

QY 61 AOKFGGRVTMTTDTSRRTAYMELRLSRSDDTAVYYCAR 98  
DB 61 AOKLQGRVTMTTDTSTSTAYMELRLSRSDDTAVYYCAR 98

RESULT 3  
S36271  
Ig heavy chain V region (clone alpha-THY-29) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
C/Accession: S36271  
R/GiFFilth, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
EMBO J. 12, 725-734, 1993  
A/Title: Human anti-self antibodies with high specificity from phage display libraries.  
A/Reference number: S36256; MUID:93178448; PMID:7679990  
A/Accession: S36271  
A/Status: preliminary; nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-122 <GRI>  
A/Cross-references: EMBL:Z18832; NID:933115; PIDN:CAA79284.1; PID:9339895  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 451; DB 2; Length 122;  
Best Local Similarity 87.6%; Pred. No. 7.1e-39;  
Matches 85; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLQSGATVEVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWVGMSAYNGNTHY 60  
DB 1 QVQLVSGAEVKKPKGASVSKVSCASGYTFTSYGISWVRQAPGQGLEWVGMSAYNGNTHY 60

QY 61 AOKFGGRVTMTTDTSRRTAYMELRLSRSDDTAVYYCA 97  
DB 61 AOKLQGRVTMTTDTSTSTAYMELRLSRSDDTAVYYCA 97

RESULT 4  
S19665  
Ig heavy chain V region (alpha-phoX15) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 20-Jun-2000  
C/Accession: S19665; S24442  
R/Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Grifflths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991  
A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage.  
A/Reference number: S19663; MUID:92085276; PMID:1748994  
A/Accession: S19665  
A/Molecule type: mRNA  
A/Residues: 1-124 <MAR>  
A/Cross-references: EMBL:X61647  
R/Jones, P.T.  
Submitted to the EMBL Data Library, October 1991  
A/Reference number: S24442  
A/Accession: S24442  
A/Molecule type: mRNA  
A/Residues: 1-40 'GLSGMDGSAITMTVQSLDK', 61-118, 'T', 120-124 <JON>  
A/Cross-references: EMBL:X61647; NID:937667; PIDN:CAA43828.1; PID:91335368  
A/Note: the difference for residues 41-60 results from misplacement of 10 bases in the  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.4%; Score 450; DB 2; Length 124;  
Best Local Similarity 86.7%; Pred. No. 9.1e-39;  
Matches 85; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLQSGATVEVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWVGMSAYNGNTHY 60  
DB 1 QVQLVSGAEVKKPKGASVSKVSCASGYTFTSYGISWVRQAPGQGLEWVGMSAYNGNTHY 60

QY 61 AOKFGGRVTMTTDTSRRTAYMELRLSRSDDTAVYYCAR 98  
DB 61 AOKLQGRVTMTTDTSTSTAYMELRLSRSDDTAVYYCAR 98

RESULT 5  
S21924  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C/Accession: S21924; S21923  
R/Friedman, D.P.  
Submitted to the EMBL Data Library, July 1991  
A/Reference number: S21923  
A/Accession: S21924  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-131 <PRI>  
A/Cross-references: EMBL:X60505; NID:933565; PIDN:CAA43025.1; PID:933566; EMBL:X60504;  
C/Genetics:  
A/Inserts: 16/1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 432; DB 2; Length 131;  
Best Local Similarity 82.7%; Pred. No. 6.5e-37;  
Matches 81; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVQLQSGATVEVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWVGMSAYNGNTHY 60  
DB 20 QVQLVSGAEVKKPKGASVSKVSCASGYTFTSYGISWVRQAPGQGLEWVGMSAYNGNTHY 79

QY 61 AOKFGGRVTMTTDTSRRTAYMELRLSRSDDTAVYYCAR 98  
DB 80 AOKLQGRVTMTTDTSTSTAYMELRLSRSDDTAVYYCAR 117

RESULT 6  
PL0105  
anti-PR2 erythrocyte autoantibody heavy chain precursor - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 26-Apr-1996  
C/Accession: PL0105  
R/Silberstein, L.E.; Litwin, S.; Carmack, C.E.  
J. Exp. Med. 169, 1631-1643, 1989  
A/Title: Relationship of variable region genes expressed by a human B cell lymphoma to  
A/Reference number: PL0106; MUID:89235583; PMID:2541221  
A/Accession: PL0105  
A/Molecule type: mRNA  
A/Residues: 1-160 <SLI>  
A/Note: the authors translated the codon GAC for residues 108 and 109 as Glu  
C/Comment: The antibody is one of the cold agglutinins that preferentially bind red b  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: autoantibody; hemagglutinin  
F/1-19/Domain: signal sequence #status predicted <SIG>  
F/34-117/Domain: immunoglobulin homology <IMM>  
F/49-54/Region: complementarity-determining 1  
F/69-84/Region: complementarity-determining 2  
F/118-131/Domain: D region <DRG>  
F/132-144/Domain: J4 segment <JSG>  
F/145-160/Domain: C region <CRG>

Query Match 82.1%; Score 428; DB 2; Length 160;  
Best Local Similarity 81.6%; Pred. No. 2.1e-36;  
Matches 80; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 QVQLQSGATVEVKKPGASMKVSCMASGYPTFSYDISWVRQAPGQGLEWVGMSAYNGNTHY 60

Db 20 QVQLVQSGAEVKKPKASVAVSCASGYFTSYGISMVNQAPQGLRWGMISAVNGNTY 79  
Oy 61 AOKFGQRYVTMTDTSRRTAYMELRSRSDDTAVVYCAR 98  
Db 80 AOKLQGRVYVTMTDTSRTAYMELRSLRSDDTAVVYCAR 117

## RESULT 7

S21925

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999

C:Accession: S21925

R:Friedman, D.F. submitted to the EMBL Data Library, July 1991

A:Reference number: S21923

A:Accession: S21925

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-111 &lt;FRI&gt;

A:Cross-references: EMBL:X60503; NID:g33626; PIDN:CAA43023.1; PID:g33627

C:Genetics:

A:introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 80.6%; Score 420; DB 2; Length 111;  
Best Local Similarity 87.0%; Pred. No. 9.1e-36;  
Matches 80; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Oy 1 QVQLQASATVEVKKPKASMKVSCMASGYPTSYDISWVROAPQGLRWGMISAVNGNTY 60  
Db 20 QVQLVQSGAEVKKPKASVAVSCASGYFTSYGISMVNQAPQGLRWGMISAVNGNTY 79  
Oy 61 AOKFGQRYVTMTDTSRRTAYMELRSRSDDTA 92  
Db 80 AOKLQGRVYVTMTDTSRTAYMELRSLRSDDTA 111

## RESULT 8

S26918

Ig heavy chain V region (DP-15) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S26918

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26918

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 &lt;TOM&gt;

A:Cross-references: EMBL:212317; NID:g32857; PIDN:CAA78187.1; PID:g32858

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 78.1%; Score 407; DB 2; Length 98;  
Best Local Similarity 78.6%; Pred. No. 1.7e-34;  
Matches 77; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Oy 1 QVQLQASATVEVKKPKASMKVSCMASGYPTSYDISWVROAPQGLRWGMISAVNGNTY 60  
Db 1 QVQLVQSGAEVKKPKASVAVSCASGYFTSYDISWVROATQGLRWGMISAVNGNTY 60  
Oy 61 AOKFGQRYVTMTDTSRRTAYMELRSRSDDTAVVYCAR 98  
Db 61 AOKFGQRYVTMTDTSRTAYMELRSLRSDDTAVVYCAR 98

## RESULT 9

S18553  
Ig heavy chain V region precursor (VI-3b) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 06-Jun-1997 #text\_change 23-Jul-1999  
C:Accession: S18553; S26916  
R:Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.;  
EMBO J. 10, 3641-3645, 1991  
A:Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus:  
A:Reference number: S18551; MUID:92037524; PMID:1935893  
A:Accession: S18553  
A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-117 &lt;SHI&gt;

A:Cross-references: EMBL:X62109

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26916

A:Molecule type: DNA

A:Residues: 20-117 &lt;TOM&gt;

A:Cross-references: EMBL:212327; NID:g32871; PIDN:CAA78197.1; PID:g32872

C:Genetics:

A:introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted &lt;SIG&gt;

F:20-117/Product: Ig heavy chain V region (VI-3b) #status predicted &lt;MAT&gt;

F:34-117/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 78.1%; Score 407; DB 2; Length 117;  
Best Local Similarity 78.6%; Pred. No. 2e-34;  
Matches 77; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Oy 1 QVQLQASATVEVKKPKASMKVSCMASGYPTSYDISWVROAPQGLRWGMISAVNGNTY 60  
Db 20 QVQLVQSGAEVKKPKASVAVSCASGYFTSYAMHVMVROAPQGLRWGMISAVNGNTY 79  
Oy 61 AOKFGQRYVTMTDTSRRTAYMELRSRSDDTAVVYCAR 98  
Db 80 SOKFGQRYVTMTDTSRTAYMELRSLRSDDTAVVYCAR 117

## RESULT 10

S31600

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S31600

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from th

A:Reference number: S31585

A:Accession: S31600

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-136 &lt;CUV&gt;

A:Cross-references: EMBL:214165; NID:g30994; PIDN:CAA78534.1; PID:g30995

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 78.1%; Score 407; DB 2; Length 136;  
Best Local Similarity 78.6%; Pred. No. 2.4e-34;  
Matches 77; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Oy 1 QVQLQASATVEVKKPKASMKVSCMASGYPTSYDISWVROAPQGLRWGMISAVNGNTY 60  
Db 20 QVQLVQSGAEVKKPKASVAVSCASGYFTSYDISWVROATQGLRWGMISAVNGNTY 79  
Oy 61 AOKFGQRYVTMTDTSRRTAYMELRSRSDDTAVVYCAR 98  
Db 80 AOKFGQRYVTMTDTSRTAYMELRSLRSDDTAVVYCAR 117





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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 5.25426 Seconds  
(without alignments)  
877.119 Million cell updates/sec

Title: US-09-674-752-27

Perfect score: 521  
Sequence: 1 QVOLLQATVEYKKGASMKV.....AYMEIRLSRSDDTAVYYCAR 98

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	383	73.5	117	1	HV1B_HUMAN
2	377	72.4	117	1	HV1G_HUMAN
3	359	68.9	147	1	HV1C_HUMAN
4	340	65.3	117	1	HV52_MOUSE
5	331	63.5	117	1	HV1A_HUMAN
6	326	62.6	114	1	HV00_MOUSE
7	326	62.6	117	1	HV14_MOUSE
8	326	62.6	120	1	HV04_MOUSE
9	325	62.4	117	1	HV04_MOUSE
10	324	62.2	140	1	HV02_MOUSE
11	319	61.2	117	1	HV09_MOUSE
12	315	60.5	118	1	HV51_MOUSE
13	314	60.3	117	1	HV06_MOUSE
14	314	60.3	120	1	HV50_MOUSE
15	313	60.1	117	1	HV05_MOUSE
16	313	60.1	117	1	HV12_MOUSE
17	313	60.1	117	1	HV13_MOUSE
18	307	58.9	139	1	HV07_MOUSE
19	300	57.6	136	1	HV15_MOUSE
20	298	57.0	117	1	HV3C_HUMAN
21	297	57.0	117	1	HV10_MOUSE
22	297	57.0	117	1	HV49_MOUSE
23	295	56.6	137	1	HV11_MOUSE
24	294	56.4	138	1	HV48_MOUSE
25	292	56.0	121	1	HV3J_HUMAN
26	290	55.7	125	1	HV1F_HUMAN
27	289	55.5	117	1	HV55_MOUSE
28	284	54.5	119	1	HV3I_HUMAN
29	282	54.1	121	1	HV01_MOUSE
30	275.5	52.9	120	1	HV1H_HUMAN
31	274	52.6	119	1	HV3P_HUMAN
32	274	52.6	112	1	HV3G_HUMAN
33	272	52.2	136	1	HV16_MOUSE

34	270	51.8	122	1	HV3A_HUMAN	P01762	homo sapien
35	270	51.8	122	1	HV3H_HUMAN	P01769	homo sapien
36	269	51.6	114	1	HV3B_HUMAN	P01763	homo sapien
37	268	51.4	119	1	HV3M_HUMAN	P01774	homo sapien
38	266	51.1	117	1	HV54_MOUSE	P18525	mus musculus
39	265.5	51.0	97	1	HV56_MOUSE	P18527	mus musculus
40	265.5	51.0	116	1	HV05_CARAU	P19181	carassius a
41	265	50.9	119	1	HV3L_HUMAN	P01773	homo sapien
42	264	50.7	126	1	HV3K_HUMAN	P01772	homo sapien
43	263.5	50.6	117	1	HV02_CARPA	P01785	caris fam11
44	263	50.5	117	1	HV03_CARPA	P19180	carassius a
45	261.5	50.2	115	1	HV3F_HUMAN	P01767	homo sapien

## ALIGNMENTS

## RESULT 1

HV1B\_HUMAN STANDARD; PRT; 117 AA.

AC P01743;

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V-I region H33 precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxId=9606;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=83144028; PubMed=6298778;

RA Reclav G., Ram D., Glazer L., Zakut R., Givol D.;

RT "Evolutionary aspects of immunoglobulin heavy chain variable region

RT (VH) gene subgroups.";

RT Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).

CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

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DR EMBL; J00240; AAA52988.1; -.

DR PIR; A02024; HVH0HG.

DR HSSP; P01772; 2PB4.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig\_MHC.

DR Pfam; PF00047; Ig\_1.

DR SMART; SM00406; IGV\_1.

DR PROSITE; PS50835; IG\_LIKE; 1.

DR Immunoglobulin V region; Signal.

KW SIGNAL

FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION H33.

FT DOMAIN 20 >117 IG-LIKE.

FT NON\_TER 117 117

SQ SEQUENCE 117 AA; 12946 MW; 203P92FC60CD1FE7 CRC64;

Query Match 73.5%; Score 383; DB 1; Length 117;

Best Local Similarity 75.5%; Pred. No. 1e-17;

Matches 74; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVOLLQATVEYKKGASMKVSCMASGYRFTSYDLSWVRQAPGQGLEWYVWISAYNGNTHY 60  
DB 20 QVOLLQATVEYKKGASVKVSCKASGYTFNSYVHWVRQAPGQGLEWYVWISAYNGNTHY 79

```

OY 61 AOKFOGRVTMTTDTSRRTAYMELRSLSRSDDTAVYYCAR 98
DB 80 AOKFOGRVTMTTDTSRRTAYMELRSLSRSDDTAVYYCAR 117

RESULT 2
ID HV1G_HUMAN STANDARD; PRT; 117 AA.
AC P23063;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
OX (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ono H., Fukushima S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus."
RL EMBL J. 7:1047-1051(1988).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC -----
CC EMBL; X07448; -; NOT_ANNOTATED_CDS.
CC PIR; S00476; HVHUS3.
CC HSSP; P01772; 2FBA4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT SIGNAL 1 19
FT DOMAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
FT NON TER 117
FT SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match 72.4%; Score 377; DB 1; Length 117;
Best Local Similarity 74.5%; Pred. No. 5.1e-37;
Matches 73; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

OY 1 QVOLLQSAATEYKVKPGASMKVSCMASGYPTFSYDISWVROAPGQGLEWVGWISAVNGNTHY 60
DB 20 QVOLLQSAATEYKVKPGASMKVSCMASGYPTFSYDISWVROAPGQGLEWVGWISAVNGNTHY 79

OY 61 AOKFOGRVTMTTDTSRRTAYMELRSLSRSDDTAVYYCAR 98
DB 80 AOKFOGRVTMTTDTSRRTAYMELRSLSRSDDTAVYYCAR 117

RESULT 3
ID HV1G_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor (fragments).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
OX (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line."
RT Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Benrich H.H., Johanson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSSP; P01789; IMCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
FT CHAIN 1 19
FT SIGNAL 1 19
FT DOMAIN 20 131 IG HEAVY CHAIN V-I REGION ND.
FT MOD RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON TER 147
FT SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 68.9%; Score 359; DB 1; Length 147;
Best Local Similarity 67.3%; Pred. No. 8.3e-35;
Matches 66; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

OY 1 QVOLLQSAATEYKVKPGASMKVSCMASGYPTFSYDISWVROAPGQGLEWVGWISAVNGNTHY 60
DB 20 QVOLLQSAATEYKVKPGASMKVSCMASGYPTFSYDISWVROAPGQGLEWVGWISAVNGNTHY 79

OY 61 AOKFOGRVTMTTDTSRRTAYMELRSLSRSDDTAVYYCAR 98
DB 80 AOKFOGRVTMTTDTSRRTAYMELRSLSRSDDTAVYYCAR 117

RESULT 4
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH58 A1/A4 precursor.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX (1)
RP SEQUENCE FROM N.A.

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RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M13787; AAA38499.1; -.
DR PIR: A02029; HWSA1.
DR HSP: P01810; 2FB4.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_V.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 65.3%; Score 340; DB 1; Length 117;
Best Local Similarity 62.2%; Pred. No. 1e-32;
Matches 61; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 1 QVQLQSGATPKVKKPGASMKVSCMASGYPFTSYDISWRQAPGQGLEWVGWISATNGNTHY 60
DB 20 QVQLQSGPELVKKGALVKISCKASGYTFSYDINWVKORPGGLEWVGWISATNGNTHY 79
QY 61 AOKFGKRVTTTDSRRRTAYMELSLRSDPTAVYYCA 98
DB 80 NEKFKGKATLTADKSSSTAYVQLSLTSENNAVYFCAR 117

RESULT 5
HVA HUMAN
ID _HVA_HUMAN STANDARD; PRT: 117 AA.
AC P01742;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
OX 11
RP SEQUENCE.
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RP DISULFIDE BOND.
RA MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
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RT Intrachain disulfide bonds.";
RL Biochemistry 9:3168-3196(1970).
CC -1 MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
CC MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
CC -1 SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A90563; G1H0U.
DR HSP: P01772; 2FB4.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_V.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Pyroglutamate carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12472 MW; 99D60ADA8BD52818 CRC64;

Query Match 63.5%; Score 331; DB 1; Length 117;
Best Local Similarity 68.0%; Pred. No. 1.2e-31;
Matches 66; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

QY 1 QVQLQSGATPKVKKPGASMKVSCMASGYPFTSYDISWRQAPGQGLEWVGWISATNGNTHY 60
DB 1 QVQLVQSGAVKVKRGSSVKKVSCKASGCTFSRAIIVWRQAPGQGLEWVGIVPFGCPNY 60
QY 61 AOKFGKRVTTTDSRRRTAYMELSLRSDPTAVYYCA 97
DB 61 AOKFGKRVTTTADGSTTATMELSLRSDPTAVYFCA 97

RESULT 6
HVOO MOUSE
ID _HVOO_MOUSE STANDARD; PRT: 114 AA.
AC P01741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region (Anti-arsenate antibody).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX 11
RP SEQUENCE.
RC STRAIN=A/J;
RA MEDLINE=79195438; PubMed=109536;
RA Capra J.D., Nisencof A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
RT mice bearing a cross-reactive idiotype.";
RL J. Immunol. 123:279-284(1979).
CC -1 MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC REGION SEQUENCE.
CC -1 SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02022; G1MSA.
DR HSP: P01772; 2FB4.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_V.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 106 IG-LIKE.
FT NON TER 114 114
```





CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.  
DR PIR: A02030; HVMS23.  
DR HSSP: P01810; 2FBJ.  
DR InterPro: IPR007110; IG\_1like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON TER 117 117  
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;  
  
Query Match 62.4%; Score 325; DB 1; Length 117;  
Best Local Similarity 62.2%; Pred. No. 5.9e-31;  
Matches 61; Conservative 15; Mismatches 22; Indels 0; Gaps 0;  
  
QY 1 QVQLQSGATEYVKKPGASMKVSCMASGYPTFTSYDISWVRQAPGQGLEWYGMISAVNGNTHY 60  
DB 20 QVQLQSGATEYVKKPGASMKVSCMASGYPTFTSYDISWVRQAPGQGLEWYGMISAVNGNTHY 79  
QY 61 AOKFGKRVMTTDTSRRTAYMELSLRSDDTAIVYYCAR 98  
DB 80 NEKFKGKTLTLVDKSSSTAYVQLSLTSEDSAVYYCAR 117  
  
RESULT 10  
HV02\_MOUSE  
ID HV02\_MOUSE STANDARD; PRT; 140 AA.  
AC P01746;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region 9367 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/J;  
RX MEDLINE=83152818; PubMed=6801765;  
RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,  
RA Capra J.D.;  
RT "Somatic mutation in genes for the variable portion of the  
RT immunoglobulin heavy chain.";  
RL Science 216:309-311(1982).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: J00493; AAA8128.1; -  
DR PIR: A94264; HVMSG7.  
DR HSSP: P01810; 2FBJ.  
DR InterPro: IPR007110; IG\_1like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IGV; 1.  
DR SMART, SM00406; IGV; 1.

DR PROSITE: PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Hybridoma; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.  
FT DOMAIN 20 139 IG-LIKE.  
FT NON TER 140 140  
SQ SEQUENCE 140 AA; 15514 MW; 25A4CB8E31DA5C8B CRC64;  
  
Query Match 62.2%; Score 324; DB 1; Length 140;  
Best Local Similarity 59.2%; Pred. No. 9.5e-31;  
Matches 58; Conservative 20; Mismatches 20; Indels 0; Gaps 0;  
  
QY 1 QVQLQSGATEYVKKPGASMKVSCMASGYPTFTSYDISWVRQAPGQGLEWYGMISAVNGNTHY 60  
DB 20 EVQLQSGAEIVRAGSSVTKVSCKASGYFTFTSYGIMWVKQRPGQGLEWYGMISAVNGNTHY 79  
QY 61 AOKFGKRVMTTDTSRRTAYMELSLRSDDTAIVYYCAR 98  
DB 80 NEKFKGKTLTLVDKSSSTAYVQLSLTSEDSAVYYCAR 117  
  
RESULT 11  
HV09\_MOUSE  
ID HV09\_MOUSE STANDARD; PRT; 117 AA.  
AC P01753; P11271;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region 186-1 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=81234548; PubMed=6788376;  
RA Boethwell A.L.M., Paekind M., Reith M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NPb family of  
RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY  
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.  
CC -----  
DR PIR: D90809; HVMS61.  
DR HSSP: P01810; 2FBJ.  
DR InterPro: IPR007110; IG\_1like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON TER 117 117  
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;  
  
Query Match 61.2%; Score 319; DB 1; Length 117;  
Best Local Similarity 60.2%; Pred. No. 2.9e-30;  
Matches 59; Conservative 15; Mismatches 24; Indels 0; Gaps 0;  
  
QY 1 QVQLQSGATEYVKKPGASMKVSCMASGYPTFTSYDISWVRQAPGQGLEWYGMISAVNGNTHY 60  
DB 20 QVQLQSGAEIVRAGSSVTKVSCKASGYFTFTSYGIMWVKQRPGQGLEWYGMISAVNGNTHY 79  
QY 61 AOKFGKRVMTTDTSRRTAYMELSLRSDDTAIVYYCAR 98



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Qy      1  QVOLLGQATEVKKRKGAKMKVSCMASGYPFPISSYIISWBRAPGGGLEMGVMSISANTYH 60
      2  |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
      3  1  QVOLLGCTELVYKRGASVNLSCKASGTFPISSYHMHIRQKPGGLEMGIGINSNOGTY 60
      4  Db
      5  Qy      61  AOKFQGVMTTDTSRRTAYMELSLRSDDTTAYYCAR 98
      6  Db      61  NEKRSKATLIVDKSSATYMWOLSTPTSEDSAYYCAR 98

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RESULT 15
HV05_MOUSE ID HV05_MOUSE STANDARD: PRT: 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig heavy chain V region 3 precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bozwell A.L.M., Paakind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1 MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
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CC -----
DR EMBL; J00536; AAA38605.1; -.
DR PIR; A02031; HVMS3.
DR HSSP; P01810; 2FBJ.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00477; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR KX Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19
FT FT 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117
SO SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

Query Match 60.1%; Score 313; DB 1; Length 117;
Best Local Similarity 59.2%; Pred. NO. 1.5e-29;
Matches 58; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

1 OVOLIQLSTEVKKPRASKMKVSCMASGYPTFTSIDYSWRQAPQGLIEWGMSAIVGNTHY 60
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
20 OVOLIQQPAELVVRPSSSVKLSTCKASGYFTSYMDWVQKRPQGLIEWGMSAIVGNTHY 79

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QY      61 A Q K F G R V T M T T D T S R T A Y M E L R S L R S D D T A V Y C A R   98
          |||:::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      80 N Q K F D K A T L T V D K S S T A Y M Q L S L S T S E D S A V Y C A R   117
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Search completed: December 30, 2003, 10:55:49  
Job time : 5.25426 sec



Db 1 EVQLVESGGAEVKPARGASVKISCSKASGTTFTGIYMHWRQAPGGGLEMMGHINPNSGTTY 60

Qy 61 AAKFGGRVTMTDTSRRTAYMELBSLSDDTATYYCAR 98  
||| ||||| ||: ||||| ||||| ||||| |||||  
Db 61 AAKVGGRVTMTDRDTTISTAYMELSRLSDDTATYYCAR 98

## RESULT 2

ID	PRELIMINARY;	PRT;	119 AA.
AC	Q9UL94;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	Wysin-reactive immunoglobulin heavy chain variable region (Fragment).		
DE			
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiina; Homo.		
OX	NCBI_TaxID=9606;		

RX	MEDLINE=98277139; PubMed=9614934;
RA	Mu X., Liu B., Van der Werwe P.L., Kalis N.N., Berney S.M.,
RA	Young D.C.;
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal
RT	fetus.";
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).
DR	EMBL; AF035020; AAD56256.1; -.
DR	HSSP; P01810; 2FBJ.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PSS0835; IG_LIKE; 1.
FT	NON_TER
FT	NON_TER
QO	SEQUENCE 119 AA; 119 119 MW; 13645F5345FA416E CRC64;

Query Match	73.7%	Score 384	DB 4	Length 119
Best Local Similarity	73.5%	Pred. NO. 8.9e-35		
Matches 72	Conservative 10	Mismatches 16	Indels 0	Gaps 0

Qy 1 QVQLLOSATEYKKPKGASMKVSCMASGYPTTSYDLSWRQRPGGLEWVGMSIAYNGNTHY 60  
:|::|||:|||:|||||:|||||:|:  
Db 1 EVQLVESGAELVKKPPGASWKVSCASGYPTTGYIHWRQRAPGGGLEMMGMINPNSMTTNY 60

```
OY      61 AQKFGQGVMTTDTSRRTAYMELRSLRSDDTAVYYCAR 98
      |||||:||||| ||||| ||||| ||||| |||||
DB      61 AQKFGQGVMTTKDTSISTAYMELRSLRSDDTAVYYCAR 98
```

### RESULT 3

ID	OEBRV0:	PRELIMINARY;	PRT;	500 AA.
AC	OEBRV0:			
DT	01-JUN-2001 (TREMBLrel_17, Created)			
DT	01-JUN-2001 (TREMBLrel_17, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel_23, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Strausberg R;			
RL	Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC005951; AA005951.1; -			
DR	HSSP; P01789; IMCP.			
DR	InterPro; IPR007110; IG-like.			

DR InterPro: IPRO03006; IG\_MHC.  
DR InterPro: IPRO03596; IG\_v.  
DR Fam: PF00047; Ig; 4.  
DR SMART: SM00406; IG\_v; 1.  
DR PROSITE: PSS0835; IG\_LIKE; 4.  
DR PROSITE: PSS0290; IG\_MHC; 1.  
KW Hypothetical protein.  
KW SEQUENCE 500 AA; 54154 MW; 0A9BF3A32A3CC6D9 CRC64;

Query Match 73.3%; Score 382; DB 4; Length 500;  
Best Local Similarity 72.4%; Pred. No. 8,2e-34;  
Matches 71; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

OY 1 QVOLLGATGVKKPAGAMKVSCHASGTPFPIISDYDSWTRQAPGGCLLEWVGWISANGNTHY 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
DB 20 QVHLVSGAALVMSPGASVRVSCSTKSFGAFHTYSILTIWRQAPGGCLEEMMGWISSPSDNTFR 79

**Oy**      61 A Q F Q G R V T M T T D S R T A Y M E L R S L R S D D T A V Y Y C A R    98  
         | : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
**Db**      80 A K F Q G R V T L T T D T S T S T V Y M E L R S L R S D D T A V Y Y C A R    117

## RESULT 4

ID	Q9UL92;	PRELIMINARY;	PRT,	124 AA.
AC	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Myosin-reactive immunoglobulin heavy chain variable region (fragment).			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE=98277139, PubMed=9614934;			
RA	Ku X., Liu B., Van der Werfe P.L., Kallis N.N., Berney S.M.,			

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus."; *Immunol. Clin.* 1998; 87:184-192 (1998).

DR HSSP; P01772; 2FB4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003006; Ig\_MHC.

DR pfam; PF00047; 1g; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.

SD SEQ

	Query Match	72.6%;	Score 378;	DB 4;	Length 124;
	Best Local Similarity	73.5%;	Pred. No. 4.	3e-34;	
Matches	72;	Conservative	10;	Mismatches	16; Indels 0; Gaps 0;
Oy	1 QVOLLQSATPEKKRGKASCMKYSCKMAGCPDFTSYDSMTWRAPRCGLGEMWGISATYNGNHY	60			
Dd	1 EVQLVESGAELVKKGKGSKVSCKASGITFSSIVTMHWAKAFQGCGLEMMGIINPSCGSTSY	60			
Oy	61 AOKFGGRVTMTDTSRRTAYMELSLRSDPTAVYYCAR	98			
Dd	61 AOKFGGRVTMTDTSTSTVMELSLRSSEDAVYYCAR	98			
RESULT 5					
ID	Q96GAG	PRELIMINARY;	PRT;	614 AA.	
AC	Q96GAG;				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				

DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=B-cell;  
 RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC009851; AA09851.1; -  
 DR InterPro; IPR000005; HTHArac.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig\_5.  
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00041; HTH\_ARAC\_FAMILY\_1; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KM Hypothetical protein.  
 SQ SEQUENCE 614 AA; 67921 MW; 55F536E77AA9BBB CRC64;

Query Match 71.2%; Score 371; DB 4; Length 614;  
 Best Local Similarity 70.4%; Pred. No. 1.7e-32;  
 Matches 69; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

OY 1 QVQLQSGATEVKKPKGASMKVSCASGYPTFSYDISVWRAPQGLBVGWISAVNGNTY 60  
 Db 20 QVQLVSGAEVKKTKGSSVSCASGYPTFTYRLHWVRQAPQALEWGMWITPFGNTY 79

OY 61 AQKFGKVTMTDTSRRTAYMELRLSRSDTAIVYCAR 98  
 Db 80 AQKFGKRVITTRDSRMTAYMELSLRSRSDTAIVYCAR 117

RESULT 6  
 Q96QSO PRELIMINARY; PRT; 159 AA.  
 ID Q96QSO;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)  
 DE Putative matrix cell adhesion molecule-3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tilson M.D.;

RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3  
 RT mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY039025; AAK82649.1; -  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 69.7%; Score 363; DB 4; Length 159;  
 Best Local Similarity 69.4%; Pred. No. 2.6e-32;  
 Matches 68; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

OY 1 QVQLQSGATEVKKPKGASMKVSCASGYPTFSYDISVWRAPQGLBVGWISAVNGNTY 60  
 Db 20 QVQLVSGAEVKKTKGSSVSCASGYPTFTYRLHWVRQAPQALEWGMWITPFGNTY 79

OY 61 AQKFGKVTMTDTSRRTAYMELRLSRSDTAIVYCAR 98  
 Db 80 AQKFGKRVITTRDSRMTAYMELSLRSRSDTAIVYCAR 117

RESULT 7  
 Q9GYZ2 PRELIMINARY; PRT; 119 AA.  
 ID Q9GYZ2;  
 AC Q9GYZ2;  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)  
 DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region  
 DE (Fragment).  
 OS Schistosoma japonicum (Blood fluke).  
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;  
 OC Schistosomatidae; Schistosomatidae; Schistosoma.  
 NCBI\_TaxID=6182;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Song X.T., Feng Z.Q., Guan X.H.;

RT "Amplification, cloning and sequence analysis of the heavy chain  
 RT variable region gene of monoclonal anti-idiotypic antibody NP30 of  
 RT Schistosoma japonicum";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF282622; AAC01452.1; -  
 DR HSP; P01772; 2F84.

DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR NON\_TER 1  
 FT NON\_TER 119  
 SQ SEQUENCE 119 AA; 13567 MW; BA893873FDSFACAB CRC64;

Query Match 68.7%; Score 358; DB 5; Length 119;  
 Best Local Similarity 68.4%; Pred. No. 6.7e-32;  
 Matches 67; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

OY 1 QVQLQSGATEVKKPKGASMKVSCASGYPTFSYDISVWRAPQGLBVGWISAVNGNTY 60  
 Db 1 QVQLVSGAEVKKTKGSSVSCASGYPTFTYRLHWVRQAPQALEWGMWITPFGNTY 79

OY 61 AQKFGKVTMTDTSRRTAYMELRLSRSDTAIVYCAR 98  
 Db 61 AQKFGKRVITTRDSRMTAYMELSLRSRSDTAIVYCAR 117

RESULT 8  
 Q8WY24 PRELIMINARY; PRT; 497 AA.  
 ID Q8WY24;  
 AC Q8WY24;  
 DT 01-MAR-2002 (TReMBLrel. 20, Created)  
 DT 01-MAR-2002 (TReMBLrel. 20, last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)  
 DE SMC66 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

RT "Identification and characterization of SMC66, a Ig-like gene which is  
 RT down-regulated in colorectal cancer";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF283666; AAL36987.1; -  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig\_4.

```
DR SMART: SM00406; IGV: 1.
DR PROSITE: PSS0835; IG_LIKE: 4.
DR PROSITE: PS00290; IG_MHC: 1.
SQ SEQUENCE 497 AA; 5365 MM; F24D08DFA5A663E5 CRC64;

Query Match
Best Local Similarity 68.5%; Score 357; DB 4; Length 497;
Matches 65; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 1 QVQLQSATVEKKKPGASMKVSCASGYPTSYDISWVROAPQGQLEWGMISAVNGNTY 60
DB 20 QEQLEQSGAEVTKPGASVSKVSCASGYPTFIADINVRQAPQGQLEWGMNPNQNTGTF 79
QY 61 AOKFGQRYMTTDSRRTAYMELRSRSDPTAVYYCA 98
DB 80 AOKFGQRLTFSRDTSINTAYMVLSTSEDSATVFCAR 117

RESULT 9
ID Q9UL89 PRELIMINARY; PRT; 116 AA.
AC Q9UL89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035025; AAD56261.1; -.
DR HSP: P01810; 2FBU.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGV: 1.
DR PROSITE: PSS0835; IG_LIKE: 1.
DR NON_TER 1
FT NON_TER 1
FT SEQUENCE 116 AA; 12605 MM; C8F9131DE13EA898 CRC64;
SQ

Query Match
Best Local Similarity 65.3%; Score 340; DB 4; Length 116;
Matches 67; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 5 LQSAIEVKKPGASMKVSCASGYPTSYDISWVROAPQGQLEWGMISAVNGNTY 64
DB 1 VQSGAEVKKPGSSVSKVSCAGTFSSYSAISWVROAPQGQLEWGMRIIPILGIANYAKF 60
QY 65 QGRVTMTDTSRRTAYMELRSRSDPTAVYYCA 97
DB 61 QGRVTITADKSTAYMELSLRSEDTAVYYCA 93

RESULT 10
ID Q925S3 PRELIMINARY; PRT; 147 AA.
AC Q925S3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MRP3.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL: AF240166; AAK43731.1; -.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGV: 1.
DR PROSITE: PSS0835; IG_LIKE: 1.
SQ SEQUENCE 147 AA; 16274 MM; 800594A12B97191F CRC64;

Query Match
Best Local Similarity 64.7%; Score 337; DB 11; Length 147;
Matches 63; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY 1 QVQLQSATVEKKKPGASMKVSCASGYPTSYDISWVROAPQGQLEWGMISAVNGNTY 60
DB 3 QVQLHSGEVEVKKPGASVSKVSCASGYPTSYDISWVROAPQGQLEWGMIPPGEGSTY 62
QY 61 AOKFGQRYMTTDSRRTAYMELRSRSDPTAVYYCA 98
DB 63 NEKFGKATLVSKSSAYMELRLTSLSEDSAVYFCAR 100

RESULT 11
ID Q91WT1 PRELIMINARY; PRT; 481 AA.
AC Q91WT1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 52.1 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC013490; AAH13490.1; -.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGV: 1.
DR PROSITE: PSS0835; IG_LIKE: 4.
DR PROSITE: PS00290; IG_MHC: 2.
KM Hypothetical protein.
SQ SEQUENCE 481 AA; 52105 MM; 97DF68D159463F65 CRC64;

Query Match
Best Local Similarity 64.3%; Score 335; DB 11; Length 481;
Matches 62; Conservative 13; Mismatches 23; Indels 0; Gaps 0;
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RL Submitted(MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC029188. AAH29188.1; -.
DR InterPro: IPR003599; IG_1like.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003597; IG_c1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG_4.
DR SMART: SM00409; IG_3.
DR SMART: SM00407; IGc1; 3.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 2.
DR SEQUENCE 480 AA; 51645 MW; 8690A63C669CDEBD CRC64;
SQ
Query Match 63.5%; Score 331; DB 11; Length 480;
Best Local Similarity 60.2%; Pred. No. 3,4e-29;
Matches 59; Conservative 18; Mismatches 21; Indels 0; Gaps 0;
Oy 1 QVOLLGSATVEKKRGASMKVSCMASGYPFTSYDISWYKRAPGGGLEWGWISAVNGTHY 60
Db 20 QVOLLGSGLVLPFGASVKSICRSGYTFSTPSIMWKORPGGPEWIGMISPDGSSEY 79
Oy 61 AOKFQGRVMTTDTSRRTAYMELRSLSDDTAVYYCAR 98
Db 80 NEKFKGKATITADKSSNTAYMHLSSLTSSENSAVYYFCAR 117
RESULT 14
Oy 1 OYVILJ PRELIMINARY; PRT; 123 AA.
AC OYVILJ;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DT Anti-DNA heavy chain (Fragment).
GN J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ-1Pr/1Pr;
RA MEDLINE=96409289; Pubmed=8814271;
RX Wlooch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gillespie G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RT anti-DNA from C3H-1Pr mice and lupus mice with nephritis."
RL Eur. J. Immunol. 26:2225-2233(1996).
DR EMBL: U59154; AAB02916.1; -.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR NON TER 1
FT NON TER 123
SQ SEQUENCE 123 AA; 13806 MW; CC0037A806E9911E CRC64;
Query Match 63.3%; Score 330; DB 11; Length 123;
Best Local Similarity 60.2%; Pred. No. 8,6e-29;
Matches 59; Conservative 19; Mismatches 20; Indels 0; Gaps 0;
Oy 1 QVOLLGSATVEKKRGASMKVSCMASGYPFTSYDISWYKRAPGGGLEWGWISAVNGTHY 60
Db 1 EIQLLGSGLVLPFGASVKSICRSGYTFSTPSIMWKORPGGPEWIGMISPDGSSEY 60
Oy 61 AOKFQGRVMTTDTSRRTAYMELRSLSDDTAVYYCAR 98
Db 61 SQKFKKATITADKSSNTAYMHLSSLTSSENSAVYYFCAR 98

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RA Venter C.J.;  
 RT "Potential virulence determinants in terminal regions of variola  
 smallpox virus genome."  
 RL Nature 366:748-751 (1993).  
 DR EMBL; L22579; AAAC0931.1; -  
 SQ SEQUENCE 1897 AA; 213641 MW; 0B3JA13F6753B08F CRC64;

Query Match 39.6%; Score 53; DB 12; Length 1897;  
 Best Local Similarity 46.2%; Pred. No. 2.3e+02;  
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 6 AYEDVWSGEYPRY 18  
 DB 1560 SYED1WKSDDPDY 1572

## RESULT 13

O934G8 PRELIMINARY; PRT; 420 AA.  
 AC O934G8;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE GlcNAc-alpha-1,4-Gal-releasing endo-beta-galactosidase.  
 GN GNGC.  
 OS Clostridium perfringens.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxId=1502;  
 RN [1]\_TaxId=1502;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC10543;  
 RA Ashida H., Anderson K., Li S., Li Y.;  
 RT "Cloning and expression of the gene encoding GlcNAc-alpha-1,4-Gal-  
 releasing endo-beta-galactosidase from Clostridium perfringens."  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBS databases.  
 DR EMBL; AB059351; BAB69460.1; -  
 FT CHAIN 18 420 POTENTIAL.  
 SQ SEQUENCE 420 AA; 49377 MW; F288D16FA0E5FB6D CRC64;

Query Match 38.8%; Score 52; DB 2; Length 420;  
 Best Local Similarity 45.5%; Pred. No. 60;  
 Matches 10; Conservative 4; Mismatches 4; Indels 4; Gaps 1;

OY 1 DGGGAYEDVWSGEYPRYAMD 22  
 DB 255 DAGSGAHNDW----PKWAIID 272

## RESULT 14

O94MR7 PRELIMINARY; PRT; 536 AA.  
 AC O94MR7;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE P52.  
 OS Bacteriophage Mx8.  
 OC Viruses.  
 OX NCBI\_TaxId=49964;  
 RN [1]\_TaxId=49964;  
 RP SEQUENCE FROM N.A.  
 RA Youderian P., Walther D., Salimi D., Magrini V., Hartzell P.L.;  
 RT "Genome organization of temperate Myxococcus phage Mx8."  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBS databases.  
 DR EMBL; AF396866; AAK94387.1; -  
 SQ SEQUENCE 536 AA; 56864 MW; 08BCA8810380E0BD CRC64;

Query Match 38.8%; Score 52; DB 9; Length 536;  
 Best Local Similarity 50.0%; Pred. No. 78;  
 Matches 10; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

OY 2 GGGAYE-----DVWSGEY 15

DB 474 GSGGTWDSITWDVWSGEY 493

## RESULT 15

O9FGH6 PRELIMINARY; PRT; 857 AA.  
 AC O9FGH6;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Na/H+ antiporter-like.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxId=3702;  
 RN [1]\_TaxId=3702;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Columbia;  
 RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI."  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBS databases.  
 DR EMBL; AB025632; BAB10261.1; -  
 DR InterPro; IPR006153; Na\_H\_porter.  
 DR Pfam; PF00999; Na\_H\_Exchange; 1.  
 SQ SEQUENCE 857 AA; 95833 MW; 5EA87F54AC2EEB73 CRC64;

Query Match 38.8%; Score 52; DB 10; Length 857;  
 Best Local Similarity 72.7%; Pred. No. 1.3e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DGGGAYEDVW 11  
 DB 253 DGGGAYISVIW 263

Search completed: December 30, 2003, 11:01:07  
 Job time : 7.6052 secs

RT "Terminal region sequence variations in variola virus DNA."  
 RL Virology 221:291-300(1996).  
 DR EMBL: U18341; AAA69465.1; -  
 SQ SEQUENCE 1896 AA; 213552 MW; 70444A0DAE289E37 CRC64;

Query Match 39.6%; Score 53; DB 12; Length 1896;  
 Best Local Similarity 46.2%; Pred. No. 2.3e+02;  
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 AYEDVWSGEYPEY 18  
 Db 1559 SYEDIWKSDMPDY 1571

## RESULT 10

ID 089096 PRELIMINARY; PRT; 1896 AA.  
 AC 089096;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
 DE DiR protein (ORF1R).  
 GN DiR.  
 OS Variola virus, and  
 OS Variola minor virus.  
 OC Viruses; daDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 NCBI\_TaxID=10255, 53258;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Variola virus; STRAIN=GARCIA-1966;  
 RA Masung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,  
 RA Totmenin A.V., Shchelkunov S.N., Esposto J.J.;  
 RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Variola minor virus; STRAIN=GARCIA-1966;  
 RA Shchelkunov S.N., Totmenin A.V., Gutov V.V., Safonov P.F.,  
 RA Masung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,  
 RA Esposto J.J., Sosnovtsev S.;  
 RL "Analysis of the complete coding sequence of DNA of alastrim variola  
 minor virus strain Garcia-1966."  
 RT Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Variola virus; STRAIN=GARCIA-1966;  
 RA Shchelkunov S.N., Blinov V.M., Totmenin A.V., Resenchuk S.M.,  
 RA Sandakhchiev L.S.;  
 RL "XhoI-I, P DNA fragments of variola minor virus strain Garcia-1966."  
 RT Submitted (JAN-1993) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U18339; AAA69405.1; -  
 DR EMBL: Y16780; CAB54796.1; -  
 DR EMBL: X70841; CA550189.1; -  
 SQ SEQUENCE 1896 AA; 213565 MW; 564F2B5276BF7D40 CRC64;

Query Match 39.6%; Score 53; DB 12; Length 1896;  
 Best Local Similarity 46.2%; Pred. No. 2.3e+02;  
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 AYEDVWSGEYPEY 18  
 Db 1559 SYEDIWKSDMPDY 1571

RESULT 11

ID 089192 PRELIMINARY; PRT; 1896 AA.  
 AC 089192;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE B26R protein.  
 GN B26R.

OS Variola virus.  
 OC Viruses; daDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 NCBI\_TaxID=10255;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=India-1967;  
 RA Blinov V.M.;  
 RL Submitted (NOV-1992) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=India-1967;  
 RX MEDLINE=9320281; PubMed=8384129;  
 RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;  
 RT "Genes of variola and vaccinia viruses necessary to overcome the host  
 protective mechanisms."  
 RL FEBS Lett. 319:80-83(1993).

RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=India-1967;  
 RX MEDLINE=95159666; PubMed=7856312;  
 RA Shchelkunov S.N., Blinov V.M., Resenchuk S.M., Totmenin A.V.,  
 RA Olenina L.V., Chirikova G.B., Sandakhchiev L.S.;  
 RT "Analysis of the nucleotide sequence of 53 kbp from the right terminus  
 of the genome of variola major virus strain India-1967."  
 RL Virus Res. 34:207-236(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=India-1967;  
 RX MEDLINE=95320969; PubMed=7597802;  
 RA Shchelkunov S.N., Totmenin A.V.;  
 RT "Two types of deletions in orthopoxvirus genomes."  
 RL Virus Genes 9:231-245(1995).

RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=India-1967;  
 RX MEDLINE=96290243; PubMed=8725113;  
 RA Shchelkunov S.N., Totmenin A.V., Sandakhchiev L.S.;  
 RT "Analysis of the nucleotide sequence of 23.8 kbp from the left  
 terminus of the genome of variola major virus strain India-1967."  
 RL Virus Res. 40:169-183(1996).  
 DR EMBL: X69198; CA449135.1; -  
 SQ SEQUENCE 1896 AA; 213498 MW; 4898B1F25E0B8456 CRC64;

Query Match 39.6%; Score 53; DB 12; Length 1896;  
 Best Local Similarity 46.2%; Pred. No. 2.3e+02;  
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 AYEDVWSGEYPEY 18  
 Db 1559 SYEDIWKSDMPDY 1571

## RESULT 12

ID 085406 PRELIMINARY; PRT; 1897 AA.  
 AC 085406;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE B22R.  
 GN B22R.  
 OS Variola major virus.  
 OC Viruses; daDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 NCBI\_TaxID=12870;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bangladesh-1975;  
 RX MEDLINE=94088747; PubMed=8264798;  
 RA Masung R.F., Esposto J.J., Liu L., Qi J., Uteerback T.R.,  
 RA Knight J.C., Aubin L., Yuzen T.E., Parsons J.M., Loparev V.N.,  
 RA Selivanov N.A., Cavaliaro K.F., Kerlavage A.R., Mahy B.W.J.,

RA McCombie W.R.:  
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC078944; AAK92619.1; -  
 DR Genbank: O34HL8; -  
 SQ SEQUENCE 221 AA; 23356 MW; 7C80178EDBA46E6 CRC64;

Query Match 39.6%; Score 53; DB 10; Length 221;  
 Best Local Similarity 62.5%; Pred. No. 22;  
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 DGGGAYEDVWSGEY 16  
 DB 6 DRGGALTEWMSGFCP 21

RESULT 6  
 ID 089230 PRELIMINARY; PRT; 1264 AA.

AC 089230:  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE (XhoI-F.O.H.P.Q genome fragment) genes.  
 OS Variola virus.  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxId=10255;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=India-1967;  
 RA Kolykhalov A.A., Blinov V.M., Gytarov V.V., Pozdnyakov S.G.,  
 RA Chizhikov V.E., Frolov I.V., Totmenin A.V., Shchelkunov S.N.,  
 RA Sandakchiev L.S.;  
 RT "Nucleotide sequence analysis of the region of Variola virus XhoI F O  
 RT H P Q genome fragment."  
 RL Submitted (Apr-1992) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=India-1967;  
 RA Shchelkunov S.N., Marenikova S.S., Totmenin A.V., Blinov V.M.,  
 RA Chizhikov V.E., Gytarov V.V., Saitonov P.F., Pozdnyakov S.G.,  
 RA Shchukhina E.M., Gashnikov P.V., Anjaparidze O.G., Sandakchiev L.S.;  
 RT "Constructions of clones of the genomic fragments of poxvirus and  
 RT study of structural and functional organization of host range viral  
 RT genes."  
 RL Doki. Akad. Nauk SSSR 321:404-406(1991).  
 DR EMBL: X67117; CAA47538.1; -  
 SQ SEQUENCE 1264 AA; 142967 MW; DBJ/E0989CB794FD CRC64;

Query Match 39.6%; Score 53; DB 12; Length 1264;  
 Best Local Similarity 46.2%; Pred. No. 1.5e+02;  
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 AYEDVWSGEY 18  
 DB 927 SYEDIMKSDMPDY 939

RESULT 7  
 ID 08927 PRELIMINARY; PRT; 1869 AA.  
 AC 08927:  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE CMP202R.  
 OS Camelopox virus (strain CP-1).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxId=203174;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=CMS;  
 RX PubMed=11907336;  
 RA Gubser C., Smith G.L.;  
 RT "The sequence of camelopox virus shows it is most closely related to  
 RT variola virus, the cause of smallpox."  
 RL J. Gen. Virol. 83:855-872(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CMS;  
 RA Gubser C., Smith G.L.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY009089; AAG37713.1; -  
 SQ SEQUENCE 1869 AA; 210470 MW; 06054FCCD94722C6 CRC64;

Query Match 39.6%; Score 53; DB 12; Length 1869;  
 Best Local Similarity 46.2%; Pred. No. 2.2e+02;  
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 AYEDVWSGEY 18  
 DB 1532 SYEDIMKSDMPDY 1544

RESULT 8  
 ID 08V2H2 PRELIMINARY; PRT; 1869 AA.

AC 08V2H2:  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE B22R-like protein.  
 OS Camelopox virus (strain CP-1).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxId=203174;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=M-96;  
 RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Zaitsev V.L.,  
 RA Kerebekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L.;  
 RT "The genome of camelopox virus."  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF438165; AAL73914.1; -  
 SQ SEQUENCE 1869 AA; 210498 MW; 64ABEF98F88237A9 CRC64;

Query Match 39.6%; Score 53; DB 12; Length 1869;  
 Best Local Similarity 46.2%; Pred. No. 2.2e+02;  
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 AYEDVWSGEY 18  
 DB 1532 SYEDIMKSDMPDY 1544

RESULT 9  
 ID 089117 PRELIMINARY; PRT; 1896 AA.  
 AC 089117:  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE B22R.  
 OS Variola virus.  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OX NCBI\_TaxId=10255;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Somalia-1977;  
 RX MEDLINE=96395428; PubMed=8661439;  
 RA Maesung R.F., Loparev V.N., Knight J.C., Totmenin A.V.,  
 RA Chizhikov V.E., Parsons J.M., Saitonov P.F., Gytarov V.V.,  
 RA Shchelkunov S.N., Espósito J.J.;

SQ SEQUENCE 168 AA; 18515 MW; 4265E315305E0657 CR; 4;  
 Query Match 44.4%; Score 59.5; DB 11; Length 168;  
 Best Local Similarity 50.0%; Pred. No. 2.1;  
 Matches 12; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

QY 1 DGGGG---AYEDVWSGEYPERYAM 21  
 DB 23 DGGGAHTWAPEDAMWGTHPKYLEM 46

RESULT 2  
 OBR3W5 PRELIMINARY; PRT; 168 AA.  
 AC OBR3W5; 1  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DE Similar to RIKEN CDNA 5730449L18 gene.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Murida; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Strusberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ data bases.  
 DR EMBL; BC024342; AAH24342.1; -  
 SQ SEQUENCE 168 AA; 18530 MW; 99DBE6E14C2FCFA0 CR; 4;

Query Match 44.4%; Score 59.5; DB 11; Length 168;  
 Best Local Similarity 50.0%; Pred. No. 2.1;  
 Matches 12; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

QY 1 DGGGG---AYEDVWSGEYPERYAM 21  
 DB 23 DGGGAHTWAPEDAMWGTHPKYLEM 46

RESULT 3  
 OBRW01 PRELIMINARY; PRT; 171 AA.  
 AC OBRW01; 1  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominda; Homo.  
 OX NCBI\_TaxId=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Testis;  
 RA Strusberg R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ data bases.  
 DR EMBL; BC022030; AAH22030.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 171 AA; 18641 MW; E728BF9A89D1FB CF; 4;

Query Match 44.4%; Score 59.5; DB 4; Length 171;  
 Best Local Similarity 50.0%; Pred. No. 2.2;  
 Matches 12; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

QY 1 DGGGG---AYEDVWSGEYPERYAM 21  
 DB 26 DGGGAPSWAPEDAMWGTHPKYLEM 49

RESULT 4  
 OBR205 PRELIMINARY; PRT; 197 AA.  
 AC OBR205; 1

DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Clorf19 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominda; Homo.  
 OX NCBI\_TaxId=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21218927; PubMed=11318611;  
 RA Sood R., Bonner T.I., Malakowska I., Stephan D.A., Robbins C.M.,  
 RA Connor T.D., Worgensesser S.D., Su K., Faruque M.U., Pinkett H.,  
 RA Graham C., Baxevanis A.D., Klingner K.W., Landes G.M., Trent J.M.,  
 RA Carpten J.D.;  
 RT "Cloning and characterization of 13 novel transcripts and the human  
 RT RGS8 gene from the 1q25 region encompassing the hereditary prostate  
 RT cancer (hpc1) locus."  
 RL Genomics 73:211-222(2001).  
 DR EMBL; AF288394; AAC60614.1; -  
 DR Genew; HGNC:16791; Clorf19.  
 FT NON TER  
 SQ SEQUENCE 197 AA; 21077 MW; 58B73731FA5E127 CRC64;

Query Match 44.4%; Score 59.5; DB 4; Length 197;  
 Best Local Similarity 50.0%; Pred. No. 2.6;  
 Matches 12; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

QY 1 DGGGG---AYEDVWSGEYPERYAM 21  
 DB 52 DGGGAPSWAPEDAMWGTHPKYLEM 75

RESULT 5  
 O94HL8 PRELIMINARY; PRT; 221 AA.  
 AC O94HL8; 1  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Hypothetical protein.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxId=4530;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Nipponbare;  
 RA Spiegel L., de la Bastide M., Nascimiento L., Kirchoff K., King L.,  
 RA Preston R., Vili M.D., Baker J., Bell M., Zutavern T., Santos L.,  
 RA Miller B., Kuit K., Rodriguez S., Cunniss D.M., Balija V., Shah R.,  
 RA Bahret A., Bal H., O'Shaughnessy A., Dedhia N., McCombie W.R.;  
 RT "Genomic Sequence for Oryza sativa, Nipponbare strain, clone  
 RT OSUNBa0089D15, from Chromosome 10, complete sequence."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Nipponbare;  
 RA McCombie W.R.;  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Nipponbare;  
 RA McCombie W.R.;  
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.  
 RN (4)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Nipponbare;  
 RA Palmer L.E., Spiegel L., de la Bastide M., Nascimiento L., Kirchoff K.,  
 RA King L., Preston R., Vili M.D., Baker J., Bell M., Zutavern T.,  
 RA Santos L., Miller B., Kuit K., Rodriguez S., Cunniss D.M., Balija V.,  
 RA Shah R., Bahret A., Bal H., O'Shaughnessy A., Dedhia N.,

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# OM protein - protein search, using sw model

Run on: December 30, 2003, 10:46:19 ; Search time 5.6052 Seconds  
(without alignments)  
1058.876 Mill on cell updates/sec

Title: US-09-674-752-30  
Perfect score: 134  
Sequence: 1 DGGCGAYEDVWSGEYPEYAMDV 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 30525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

SPRTEMBL.23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virinae:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59.5	44.4	168	11	O9CY15 mus musculus
2	59.5	44.4	168	11	O8R3W5 mus musculus
3	59.5	44.4	171	4	O8W01 homo sapien
4	59.5	44.4	197	4	O9BZQ5 homo sapien
5	53	39.6	221	10	O94HL8 oryza sativ
6	53	39.6	1264	12	O89230 variola vir
7	53	39.6	1869	12	O8Q0P27 variola vir
8	53	39.6	1869	12	O8V2H2 camelopox vi
9	53	39.6	1886	12	O89117 variola vir
10	53	39.6	1886	12	O89096 variola vir
11	53	39.6	1896	12	O89192 variola vir
12	53	39.6	1897	12	O85406 variola maj
13	52	38.8	420	2	O934G8 clostridium
14	52	38.8	420	2	O94MR7 bacterioph
15	52	38.8	857	10	O9FGH6 arabidopsis
16	52	38.8	1482	16	O8ER16 oceanobacill

17	51	38.1	187	10	O8H564	O8H564 oryza sativ
18	51	38.1	554	10	O94129	O94129 oryza sativ
19	51	38.1	800	2	O52998	O52998 escherichia
20	50.5	37.7	433	13	O91859	O91859 xenopus lae
21	50	37.3	292	5	O62458	O62458 caenorhabdi
22	50	37.3	360	16	O9RDA4	O9RDA4 streptomyces
23	50	37.3	531	10	O94B16	O94B16 vitis vinif
24	50	37.3	1933	12	O72759	O72759 cowpox viru
25	49	36.6	509	16	O9A962	O9A962 caulobacter
26	49	36.6	527	10	O9FMH4	O9FMH4 arabidopsis
27	49	36.6	1340	3	O9P3C8	O9P3C8 neurospora
28	49	36.6	1879	12	O8V407	O8V407 monkeypox v
29	48.5	36.2	166	16	O97M64	O97M64 clostridium
30	48.5	36.2	262	16	O9FC56	O9FC56 streptomyces
31	48	35.8	139	17	O96XMS	O96XMS sulfolobus
32	48	35.8	461	13	O90WQ7	O90WQ7 oncorhynch
33	48	35.8	464	13	O90W06	O90W06 oncorhynch
34	48	35.8	840	10	O9AV49	O9AV49 oryza sativ
35	47.5	35.4	178	5	O8IH71	O8IH71 drosophila
36	47.5	35.4	260	10	O8H6Q2	O8H6Q2 phycophthor
37	47.5	35.4	308	5	O8INH1	O8INH1 drosophila
38	47.5	35.4	321	5	O8MSY1	O8MSY1 drosophila
39	47.5	35.4	344	5	O9VFT6	O9VFT6 drosophila
40	47.5	35.4	558	3	O43071	O43071 schizosacch
41	47	35.1	156	4	O961F7	O961F7 homo sapien
42	47	35.1	159	4	O96E20	O96E20 homo sapien
43	47	35.1	188	4	O9B4P1	O9B4P1 diadassa ba
44	47	35.1	216	15	O9YX19	O9YX19 human immun
45	47	35.1	316	2	O9K1X4	O9K1X4 bradyrhizob

## ALIGNMENTS

### RESULT 1

ID O9CY15 PRELIMINARY; PRT; 168 AA.

AC O9CY15; 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE 5730449L1BR1K protein.  
GN 5730449L1BR1K.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Embryo;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi Y., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Glasi C., King B., Kochiwa H.,  
RA Kuenl P., Lewis S., Matsuo Y., Nikiel I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Mashio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohzuki S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL; AK017650; BAB30855.1; -;  
MGI; MGI:1913887; 5730449L1BR1K.

```
CC -----
DR EMBL; AL627275; CAD02714.1; -.
DR EMBL; AB016835; AA068065.1; -.
DR HAMAP; MF_00378; -; 1.
DR InterPro; IPR003753; Exonuc_VII_L.
DR InterPro; IPR004365; tRNA_anti.
DR Pfam; PF02601; Exonuc_VII_L; 1.
DR TIGRFAMs; TIGR00237; xseA; 1.
DR Hydrolase; Nuclease; Exonuclease; Complete proteome.
SQ SEQUENCE 449 AA; 50720 MW; 511957DEC878F5D2 CRC64;

Query Match 33.6%; Score 45; DB 1; Length 449;
Best Local Similarity 70.0%; Pred. No. 78;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGAYEDVWS 12
   |||: ||: ||
Db 206 GCGSLDPLWS 215
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Search completed: December 30, 2003, 10:55:52  
Job time : 2.23314 secs

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CC -----
DR EMBL; AF198100; AAF44578.1; -.
DR EMBL; D00295; BAA00209.1; ALT_FRAME.
DR EMBL; D00295; BAA00207.1; ALT_FRAME.
DR HSSP; P25963; INRI.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 7.
DR SMART; SM00248; ank; 6.
DR PROSITE; PS50088; ANK_REPEAT; 5.
DR PROSITE; PS50297; ANK_RBP_REGION; 1.
KW Hypothetical protein; Repeat; ANK repeat.
FT REPEAT 6 35 ANK 1.
FT REPEAT 39 68 ANK 2.
FT REPEAT 71 100 ANK 3.
FT REPEAT 103 132 ANK 4.
FT REPEAT 137 169 ANK 5.
FT REPEAT 174 202 ANK 6.
FT REPEAT 206 238 ANK 7.
FT REPEAT 242 271 ANK 8.
SQ SEQUENCE 428 AA; 49194 MW; C71BEAF74687EE8F CRC64;

Query Match 33.6%; Score 45; DB 1; Length 428;
Best Local Similarity 56.2%; Pred. No. 74;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 8 EDVMSGEYPEYVYAMDV 23
Db 133 EDGANGKYPHYAMKV 148

RESULT 14
EX7L_RICCN STANDARD; PRT; 444 AA.
AC 092G06;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
GN (Exonuclease VII large subunit).
OS XSEA OR RCI026.
OC Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiaseae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audifren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RT Science 293:2093-2098(2001).
CC -1- FUNCTION: Bidirectionally degrades single-stranded DNA into large
CC acid-insoluble oligonucleotides, which are then degraded further
CC into small acid-soluble oligonucleotides (By similarity).
CC -1- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'-
CC or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
CC -1- SUBUNIT: Heterooligomer composed of large and small subunits (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE XSEA FAMILY.
CC -----
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CC EMBL; AE008654; AAL03564.1; ALT_INIT.

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DR HAMAP; MF_00378; -. 1.
DR InterPro; IPR003753; Exonuc_VII_L.
DR InterPro; IPR004365; RNA_ant1.
DR Pfam; PF02601; Exonuc_VII_L; 1.
DR Pfam; PF01336; tRNA_ant1; 1.
DR TIGRPFAM; TIGR00237; xsea; 1.
KW Hydroxylase; Nuclease; Exonuclease; Complete proteome.
SQ SEQUENCE 444 AA; 49886 MW; CAB05BB43F476B CRC64;

Query Match 33.6%; Score 45; DB 1; Length 444;
Best Local Similarity 70.0%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 3 GCGAYEDVMS 12
Db 211 GCGSIDLWS 220

RESULT 15
EX7L_SALTI STANDARD; PRT; 449 AA.
AC 082401;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
DE (Exonuclease VII large subunit).
GN XSEA OR STY2753 OR T0345.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Baeham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jegerle K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RT Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Llou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyranni V., Schwartz D.C., Blatner F.R.;
RT "Comparative genomes of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -1- FUNCTION: Bidirectionally degrades single-stranded DNA into large
CC acid-insoluble oligonucleotides, which are then degraded further
CC into small acid-soluble oligonucleotides (By similarity).
CC -1- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'-
CC or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
CC -1- SUBUNIT: Heterooligomer composed of large and small subunits (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE XSEA FAMILY.
CC -----
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CC      SEVERAL TRANSCRIPTION FACTORS.
CC      -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC      -1- ALTERNATIVE PRODUCTS:
CC      Name=long;
CC      IsoId=O61985-1; Sequence=Displayed;
CC      Name=short;
CC      IsoId=O61985-2; Sequence=VSP_000580, VSP_000581;
CC      Note=No experimental confirmation available;
CC      -1- TISSUE SPECIFICITY: Widely expressed.
CC      -1- PTM: COULD BE DEPENDENT ON CKII PHOSPHORYLATION FOR BINDING.
CC      -1- SIMILARITY: Belongs to the bzip family. CNC subfamily.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: X78709; CAAS5362.1; -.
CC      DR      EMBL: AF015881; AAC40108.1; -.
CC      DR      PIR: I48694; I48694.
CC      DR      HSSP: P34707; ISKN.
CC      DR      MGD: MGI:99421; Nfe211.
CC      DR      InterPro: IPR004827; TF_BZIP.
CC      DR      SMART: SM00338; BRLZ; 1.
CC      DR      PROSITE: PS50217; BZIP; 1.
CC      DR      PROSITE: PS00036; BZIP_BASIC; 1.
CC      KM      DNA-binding; Nuclear protein; Phosphorylation; Alternative splicing.
CC      FT      DOMAIN 125 259
CC      FT      DOMAIN 414 447
CC      FT      DOMAIN 467 486
CC      FT      DOMAIN 467 486
CC      FT      DNA_BIND 628 643
CC      FT      DOMAIN 651 673
CC      FT      DOMAIN 730 737
CC      FT      VARSPIC 1 291
CC      FT      VARSPIC 447 583
CC      FT      VARSPIC 318 318
CC      FT      CONFLICT 387 387
CC      FT      CONFLICT 387 387
CC      SQ      SEQUENCE 741 AA; 81545 MW; C01889DD26E7CDBF CRC64;

Query Match      34.3%; Score 46; DB 1; Length 741;
Best Local Similarity 50.0%; Pred. No. 96;
Matches 10; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      4 GGAGYEDVWSGEYEPYAMDV 23
DB      210 GREEDTWSGEGEALARDL 229

RESULT 12
CIBA PAEPP      STANDARD; PRT; 675 AA.
AC      P57091;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Parasporal crystal protein cry18Ba (Parasporal delta-endotoxin
DE      CryVIIIIB(a)) (Crystalline parasporal protoxin) (76 kDa crystal
DE      protein).
GN      CRY18BA OR CRYVIIIIB(A).
OS      Paenibacillus popilliae (Bacillus popilliae).
OC      Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX      NCBI_TaxID=78057;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      STRAIN=BP3;
RA      Patel R., Yousten A.A., Rippere K.;
RT      "Detection of two new cry genes in Paenibacillus popilliae.";

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RL      Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: BINDS TO THE BRUSH BORDER MEMBRANE VESICLES OF SCARAB
CC      LARVAE AND DAMAGES THE GUT WALL SOMEHOW TO ALLOW THE VEGETATIVE
CC      CELLS OF P. POPILLIAE TO ENTER THE HEMOLYMPH (BY SIMILARITY).
CC      -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC      SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC      OF THE SPORE COAT (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: AF169250; AAF89667.1; -.
CC      DR      InterPro: IPR005638; endotoxin_C.
CC      DR      InterPro: IPR005639; endotoxin_N.
CC      DR      Pfam: PF03944; endotoxin_C; 1.
CC      DR      Pfam: PF03945; endotoxin_N; 1.
CC      KM      Toxin; Sporulation.
CC      FT      DOMAIN 101 104
CC      FT      DOMAIN 199 204
CC      FT      POLY-LEU.
CC      SQ      SEQUENCE 675 AA; 75848 MW; 823B58B84AB81DF5 CRC64;

Query Match      34.0%; Score 45.5; DB 1; Length 675;
Best Local Similarity 36.4%; Pred. No. 1e+02;
Matches 8; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

QY      2 GGAGYEDVWSGEYEPYAMDV 23
DB      455 GIGTGYASAWT-SYDPYITNI 475

RESULT 13
ID      V234 FOWPV      STANDARD; PRT; 428 AA.
AC      P14368; P14367; Q9J501;
DT      01-JAN-1990 (Rel. 13, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Putative ankyrin-repeat protein FPV234 (BamHI-ORF12/ORF13).
DE      FPV234.
OS      Fowlpox virus (FPV).
OC      Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC      Avipoxvirus.
OX      NCBI_TaxID=10261;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      MEDLINE=20193820; PubMed=10729156;
RA      Alfonso C.L., Tulman E.R., Lu Z., Zaak L., Kutish G.F., Rock D.L.;
RT      "The genome of fowlpox virus.";
RL      J. Virol. 74:3815-3831 (2000).
RN      (2)
RP      SEQUENCE OF 65-428 FROM N.A.
RC      STRAIN=FP-9 / Isolate HP-438;
RX      MEDLINE=88229622; PubMed=2836548;
RA      Tomley F., Binn M., Campbell J., Bourneall M.E.G.;
RT      "Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
RT      of fowlpox virus.";
RL      J. Gen. Virol. 69:1025-1040 (1988).
CC      -1- SIMILARITY: Contains 8 ANK repeats.
CC      -1- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
CC      in position 204, 219 and 237.
CC      -----
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RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
RN
RN SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Gurdilo B., Goldman B.S., Cao Y., Askenzi M., Halling C., Mullin L.,
RA Hounmel K., Gordon J., Vaudin M., Iarchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughy D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Seear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
-----
CC -1- FUNCTION: Catalyzes the ferrous insertion into protoporphyrin IX.
CC -1- CATALYTIC ACTIVITY: Protoporphyrin + Fe(2+) = protoheme + 2 H(+).
CC -1- PATHWAY: Protoheme biosynthesis; last step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the ferrochelatase family.
-----
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-----
CC EMBL; AE009308; AAL44581.1; -
CC EMBL; AE008306; AAK89636.1; ALT_INIT.
CC PIR; AG3020; AG3020.
DR HAMAP; MF_00323; -; 1.
DR InterPro; IPR001015; Ferrochelatase.
DR Pfam; PF00762; Ferrochelatase; 1.
DR ProDom; PD002792; Ferrochelatase; 1.
DR TIGRFAMs; TIGR00109; hemh; 1.
DR PROSITE; PS00534; FERROCHELATASE; 1.
KW Porphyrin biosynthesis; Heme biosynthesis; Lyase; Iron;
KW Complete proteome.
FT METAL 214 IRON (BY SIMILARITY).
FT METAL 295 IRON (BY SIMILARITY).
SQ SEQUENCE 344 AA; 39472 MW; 33890E7A3BA0F32 CRC64;
-----
Query Match 34.3%; Score 46; DB 1; Length 344;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
-----
QY 4 GGAYEDVWSGGEYEVY 19
DB 76 GKAYEIMWHERNESTY 91
-----
RESULT 10
YK09 CAEEL STANDARD; PRT; 643 AA.
AC PJ4304;
DT 01-FEB-1994 (Rel. 28, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C06E1.9 in chromosome III.
GN C06E1.9
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoidea; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_Taxid=6239;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RX Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RX Bonfield J., Burton J., Connell M., Copesey T., Cooper J., Coulson A.,

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RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnson L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Sime W., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterson J., Watson A., Weinstock L., Wilkinson-Sprat J.,
RA Woldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN
RN REVISIONS.
RA Waterson R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
-----
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-----
CC EMBL; L16559; AAA27929.2; -
CC WormPep; C06E1.9; CE24790.
KW Hypothetical protein.
SQ SEQUENCE 643 AA; 72354 MW; CF83BECFC880A10A CRC64;
-----
Query Match 34.3%; Score 46; DB 1; Length 643;
Best Local Similarity 46.7%; Pred. No. 83;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
-----
QY 1 DGGGAYEDVWSGEY 15
DB 537 DGGNGVDYDEYDER 551
-----
RESULT 11
NF1L MOUSE STANDARD; PRT; 741 AA.
ID NF1L_MOUSE
AC Q61985; O70234;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nuclear factor erythroid 2 related factor 1 (NFE-E2 related factor 1)
DE (NFE2-related factor 1) (Nuclear factor, erythroid derived 2, like 1).
GN NFE2L1 OR NR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RX MEDLINE=95278942; PubMed=7759107;
RX Prieasch E.E., Novotny V., Geonga R., Jaksche D., Elbe-Bueger A.,
RA Thum W., Auer M., Stingl G., Baumruker T.;
RT "A novel splice variant of the transcription factor Nrf1 interacts
RT with the tyrosine kinase and stimulates transcription."
RL Nucleic Acids Res. 26:2291-2297(1998).
CC -1- FUNCTION: THE SHORT ISOFORM INTERACTS WITH THE EXTENDED KAPPA 3
CC SITE OF THE TNF ALPHA PROMOTER AFTER FC GAMMA RI1 STIMULATION AND
CC PARTICIPATES IN THE INDUCTION OF THIS CYTOKINE. THE LONG ISOFORM
CC IS EITHER INACTIVE OR REPRESSSES THE TRANSCRIPTIONAL ACTIVATION.
CC -1- SUBUNIT: HETERODIMER (PROBABLE). IT MAY FORM A HETERODIMER WITH

```

ID AMYG CANAL STANDARD; PRT; 946 AA.  
 AC 074254;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glucosylase 1 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)  
 DE (1,4-alpha-D-glucan glucohydrolase).  
 GN GAMI OR GAI.  
 OS Candida albicans (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OX NCBI\_TaxID=5476;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SC314;  
 RX MEDLINE=99451422; PubMed=10520161;  
 RA Sturtevant J., Dixon F., Wadsworth E., Latge J.-P., Zhao X.-J.,  
 RA Calderone R.;  
 RT "Identification and cloning of GAI, a gene that encodes a cell  
 RT surface glucosylase from Candida albicans.";  
 RL Med. Mycol. 37:357-366(1999).  
 CC -1 CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-  
 CC glucose residues successively from non-reducing ends of the chains  
 CC with release of beta-D-glucose.  
 CC -1 SUBCELLULAR LOCATION: CELL WALL ASSOCIATED.  
 CC -1 SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.  
 CC -----  
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 CC -----  
 DR EMBL: AF082188; AAC1968.1; -  
 DR InterPro: IPR000322; Glyco\_hydro\_31.  
 DR Pfam: PF01055; Glyco\_hydro\_31; 1.  
 DR PROSITE: PS00129; GLYCOSYL HYDROL\_F31\_1; 1.  
 DR PROSITE: PS00707; GLYCOSYL HYDROL\_F31\_2; 1.  
 KM Hydrolyase; Glycosidase; Polysaccharide degradation; Glycoprotein;  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 946 GLUCAMYLASE 1.  
 FT ACT SITE 462 462 BY SIMILARITY.  
 FT DOMAIN 519 532 SER/THR-RICH.  
 FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 373 373 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 437 437 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 505 505 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 570 570 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 772 772 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 801 801 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 895 895 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 912 912 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 946 AA; 105804 MW; BD6B640C4EEF1F70 CRC64;

Query Match 34.7%; Score 46.5; DB 1; Length 946;  
 Best Local Similarity 45.0%; Pred. No. 1.1e+02;  
 Matches 9; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 3 GGGAYEDVSGE-YPEYAM 21  
 DB 617 GSGKYMGMGCDNADYVNM 636

RESULT 8

VG38\_BPARI  
 ID VG38\_BPARI STANDARD; PRT; 259 AA.  
 AC 09G0B4;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Receptor recognizing protein (Protein Gp38).  
 GN 38.  
 OS Bacteriophage ARI.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
 OC T4-like viruses.  
 OX NCBI\_TaxID=66711;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20485545; PubMed=11029414;  
 RA Yu S.L., Ko K.L., Chen C.S., Chang Y.C., Syu W.J.;  
 RT "Characterization of the distal tail fiber locus and determination of  
 RT the receptor for phage ARI, which specifically infects Escherichia  
 RT coli O157:H7.";  
 RL J. Bacteriol. 182:5962-5968(2000).  
 CC -1 FUNCTION: VG38 IS AT THE TIP OF THE LONG TAIL FIBERS AND SERVES  
 CC AS THE PHAGE RECOGNITION SITE FOR THE CELLULAR RECEPTOR.  
 CC -1 MISCELLANEOUS: THIS PHAGE USE OUTER MEMBRANE PROTEIN OMPA AS A  
 CC RECEPTOR.  
 CC -----  
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 CC -----  
 DR EMBL: AF208841; AAC29755.1; -  
 DR Pfam: PF05268; GP38; 1.  
 KM Fiber protein; Phage recognition.  
 SQ SEQUENCE 259 AA; 26277 MW; 042225B00128A5B CRC64;

Query Match 34.3%; Score 46; DB 1; Length 259;  
 Best Local Similarity 50.0%; Pred. No. 32;  
 Matches 8; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 2 GGGAYEDV--WSGEY 15  
 DB 154 GGGGYSQANNWAGKY 169

RESULT 9  
 HEMZ\_AGR5 STANDARD; PRT; 344 AA.  
 ID HEMZ\_AGR5  
 AC Q8U9F7;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ferrochelatase (EC 4.99.1.1) (Protoheme ferro-lyase) (Heme  
 DE synthetase).  
 GN HEMZ OR ATU3771 OR AGR L. 2129.  
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.  
 OX NCBI\_TaxID=176299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21608550; PubMed=11743193;  
 RA Wood D.W., Seubal J.C., Kaul R., Monks D.E., Kirajima J.P.,  
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F.Jr., Woo L.,  
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,  
 RA Chapman P., Clendinning J., Deachey G., Gillet W., Grant C.,  
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,  
 RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,  
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

Best Local Similarity 29.4%; Pred. No. 87;  
Matches 10; Conservative 5; Mismatches 4; Indels 15; Gaps 2;

OY 2 GCGGAYEDVWSGE-----YPEYAMD 22  
Db 212 GCGGAYEDVWSGE-----YPEYAMD 243

## RESULT 5

FAED\_ECOLI STANDARD; PRT; 812 AA.  
AC P06970;  
DT 01-APR-1988 (Rel. 07, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Outer membrane usher protein faed precursor.  
GN FAED.  
OS Escherichia coli.  
OC Plasmid pFM205.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
NCBI\_TaxID=562;  
[1]  
SEQUENCE FROM N.A.  
RX MEDLINE=86176742; PubMed=2870470;  
RA Mooi F.R., Claassen I., Bakker D., Kuipers H., de Graaf F.K.;  
RT "Regulation and structure of an Escherichia coli gene coding for an  
RT outer membrane protein involved in export of K88ab fimbriae  
RT subunit.";  
RL Nucleic Acids Res. 14:2443-2457(1986).  
[2]  
REVISIONS.  
RA Oudega B.;  
RN Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.  
[3]  
SEQUENCE FROM N.A.  
RX MEDLINE=96020654; PubMed=8577257;  
RA Valent O.A., Zaai J., de Graaf F.K., Oudega B.;  
RT "Subcellular localization and topology of the K88 usher faed in  
RT Escherichia coli.";  
RL Mol. Microbiol. 16:1243-1257(1995).  
[4]  
SEQUENCE OF 794-812 FROM N.A.  
RX MEDLINE=91312125; PubMed=1713284;  
RA Bakker D., Vader C.E.M., Roosaendaal B., Mooi F.R., Oudega B.,  
RA de Graaf F.K.;  
RT "Structure and function of periplasmic chaperone-like proteins  
RT involved in the biosynthesis of K88 and K99 fimbriae in  
RT enterotoxigenic Escherichia coli.";  
RL Mol. Microbiol. 5:875-886(1991).  
-1- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF K88AB FIMBRIAL  
SUBUNITS ACROSS THE OUTER MEMBRANE.  
-1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane  
(By similarity).  
-1- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.  
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CC  
CC EMBL; X03675; CAA27310.1; -  
CC EMBL; X56002; CAA39476.1; -  
CC EMBL; X56003; CAA39477.1; -  
CC PIR; S24931; MMECOF.  
CC InterPro; IPR000015; Fimb\_usher.  
CC Pfam; PF00577; Usher, 1.  
CC PROSITE; PS01151; FIMBRIAL\_USHER, 1.  
CC Outer membrane; Transmembrane; Fimbria; Transport; Signal; Plasmid.  
CC SIGNAL 1 35

FT CHAIN 36 812 OUTER MEMBRANE USHER PROTEIN FAED.  
FT DISULFID 793 811 POTENTIAL.  
SQ SEQUENCE 812 AA; 85496 MW; C6DAACA4AD8BDARC CRC64;

Query Match 35.1%; Score 47; DB 1; Length 812;  
Best Local Similarity 42.3%; Pred. No. 78;  
Matches 11; Conservative 4; Mismatches 7; Indels 4; Gaps 2;

OY 2 GCGGAYEDVW---SGEY-PEYAMDV 23  
Db 46 GCGGAYEDVW---SGEY-PEYAMDV 71

## RESULT 6

YG84\_METTH STANDARD; PRT; 431 AA.  
AC O27719;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein MTH1684.  
GN MTH1684.  
OS Methanobacterium thermoautotrophicum.  
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
OC Methanobacteriaceae; Methanothermobacter.  
NCBI\_TaxID=187420;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN=Delta H;  
RX MEDLINE=98037514; PubMed=9371463;  
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,  
RA Aldredge T., Bashirzadeh R., Blakey D., Cook R., Gilbert K.,  
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,  
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,  
RA Jiwani N., Caruso A., Bush D., Sater H., Patwell D., Prabhakar S.,  
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,  
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;  
RT "Complete genome sequence of Methanobacterium thermoautotrophicum  
RT deltaH: functional analysis and comparative genomics.";  
RL J. Bacteriol. 179:7135-7155(1997).  
-1- SIMILARITY: STRONG, TO M.JUNNASCHEI MJ1681.  
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-----  
CC  
CC EMBL; AE000926; AAB86156.1; -  
CC PIR; B69092; B69092.  
CC HSSP; P00198; 2FDM.  
CC InterPro; IPR001450; 4Fe4S\_ferredoxin.  
CC InterPro; IPR002708; DUF39.  
CC Pfam; PF01837; DUF39, 1.  
CC Pfam; PF00037; fer4, 2.  
CC Prodom; PD011569; DUF39, 1.  
CC PROSITE; PS00198; 4Fe4S\_FERREDOXIN, UNKNOWN\_1.  
CC Hypothetical protein; Complete proteome.  
CC SEQUENCE 431 AA; 46950 MW; 802FA39757194B85 CRC64;

Query Match 34.7%; Score 46.5; DB 1; Length 431;  
Best Local Similarity 56.2%; Pred. No. 47;

Matches 9; Conservative 2; Mismatches 0; Indels 5; Gaps 1;

OY 7 YEDVWSGE-----YPE 17  
Db 328 YEDVWSGDVRAVHPPE 343

RESULT 7  
AMYG\_CANAL

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CC -----
DR EMBL; S61875; AAB26988.1; -.
DR EMBL; S62100; AAB26989.1; -.
DR EMBL; S61875; AAB26989.1; JOINED.
DR EMBL; X62637; CAA44503.1; -.
DR EMBL; X62638; CAA44504.1; -.
DR PIR; A47369; A47369.
DR PIR; B41732; B41732.
DR PIR; B47369; B47369.
DR HSSP; P09651; 1HA1.
DR FlyBase; FBgn003498; sqd.
DR GO; GO:0005717; C:chromatin; IDA.
DR GO; GO:0016607; C:nuclear speck; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00075; rrm; 2.
DR SMART; SM00360; RRM; 2.
DR PROSITE; PS00102; RRM; 2.
DR PROSITE; PS00030; RRM_RNP_1; 2.
KW RNA-binding; Nuclear protein; Ribonucleoprotein; Alternative splicing;
FT DOMAIN 56 138 RNA-BINDING (RRM) 1.
FT DOMAIN 136 213 RNA-BINDING (RRM) 2.
FT DOMAIN 221 337 GLY-RICH.
FT VARSPLIC 286 345
FT FT
FT FT
FT VARSPLIC 286 322
FT FT
FT CONFLICT 169 169
FT FT SEQUENCE 345 AA; 36207 MM; 47.5% ID; 1; Length 345;
SO BEEST LOCAL SIMILARITY 27.8%; PRED. NO. 27;
MATCHES 10; CONSERVATIVE 3; MISMATCHES 6; INDELS 17; GAPS 1;
OY 2 GGGGAYEDVMSGE-----YPEYYA 20
Db 239 GGGGYNQMDQGSYGSGYGGYGGYGGYGGYGYA 274
RESULT 4
ITAS_XENLA STANDARD; PRT; 1050 AA.
ID ITAS_XENLA
AC 066274;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Integrin alpha-5 precursor (Fibronectin receptor alpha subunit)
DE (Integrin alpha-5) (VLA-5).
DE Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
OC Xenopodidae; Xenopus.
OC NCBI_TaxID=8355;
XX NCBI_TaxID=8355;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95344994; PubMed=7619730;
RA Joos T.O., Whitaker C.A., Meng F., Deslomme D.W., Gnan V.,
RA Hansen P.;
RT "Integrin alpha 5 during early development of Xenopus laevis.";
RL Mech. Dev. 50:187-199(1995).
RN (2)
RP SEQUENCE OF 318-393 FROM N.A.
RX MEDLINE=94008528; PubMed=8404528;
RA Whitaker C.A., Deslomme D.W.;
RT "Integrin alpha subunit mRNAs are differentially expressed in early
RT Xenopus embryos.";
CC -1- FUNCTION: INTEGRIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRONECTIN.

```

Query Match	35.4%	Score 47.5	DB 1	Length 1050
CC	IT RECOGNIZES THE SEQUENCE R-G-D IN ITS LIGANDS.			
CC	-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA			
CC	SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKED BY A			
CC	DISULFIDE BOND. ALPHA-5 ASSOCIATES WITH BETA-1.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.			
CC	-1- SIMILARITY: Contains 7 FG-GAP repeats.			
CC	-----			
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	CC or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; U12683; AAA9668.1; -			
DR	EMBL; L10191; AAA16249.1; -			
DR	PIR; I51527; I51527.			
DR	HSSP; P06756; I0V2.			
DR	InterPro; IPR000413; Integrin_alpha.			
DR	Pfam; PF01839; FG-GAP; 4.			
DR	Pfam; PF00357; Integrin_A; 1.			
DR	PRINTS; PR01185; INTEGRIN.A; 1.			
DR	SMART; SM00191; Int_alpha; 5.			
DR	PROSITE; PS00242; INTEGRIN_ALPHA; 1.			
KM	Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;			
KM	Signal; Repeat.			
FT	SIGNAL 1 32	POTENTIAL.		
FT	CHAIN 33 1050	INTEGRIN ALPHA-5		
FT	CHAIN 33 932	INTEGRIN ALPHA-5 HEAVY CHAIN (POTENTIAL).		
FT	CHAIN 933 1050	INTEGRIN ALPHA-5 LIGHT CHAIN (POTENTIAL).		
FT	DOMAIN 33 996	EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 997 1022	POTENTIAL.		
FT	DOMAIN 1023 1050	CYTOPLASMIC (POTENTIAL).		
FT	REPEAT 48 110	FG-GAP 1.		
FT	REPEAT 120 188	FG-GAP 2.		
FT	REPEAT 189 246	FG-GAP 3.		
FT	REPEAT 259 312	FG-GAP 4.		
FT	REPEAT 313 373	FG-GAP 5.		
FT	REPEAT 379 438	FG-GAP 6.		
FT	REPEAT 442 494	FG-GAP 7.		
FT	CA_BIND 324 332	POTENTIAL.		
FT	CA_BIND 390 398	POTENTIAL.		
FT	CA_BIND 454 462	POTENTIAL.		
FT	SITE 1025 1029	GFGR MOTIF.		
FT	DISULFID 90 99	BY SIMILARITY.		
FT	DISULFID 145 166	BY SIMILARITY.		
FT	DISULFID 182 195	BY SIMILARITY.		
FT	DISULFID 502 513	BY SIMILARITY.		
FT	DISULFID 519 575	BY SIMILARITY.		
FT	DISULFID 636 642	BY SIMILARITY.		
FT	DISULFID 708 721	BY SIMILARITY.		
FT	DISULFID 862 910	INTERCHAIN (BY SIMILARITY).		
FT	DISULFID 917 922	BY SIMILARITY.		
FT	CARBOHYD 75 75	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 95 95	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 98 98	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 172 172	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 287 287	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 297 297	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 306 306	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 507 507	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 515 515	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 521 521	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 600 600	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 649 649	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 714 714	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 763 763	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	CARBOHYD 861 861	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	SEQUENCE 1050 AA; 115961 MW; 10ED961535B8D918 CRC64;			

Matches 11; Conservative 2; Mismatches 6; Indels 7; Gaps 1;

OY 3 GCGAYEDVMSGEY-----PEYAM 21  
Db 42 GGGVVDVLLGHVPLGVMKHPYFLM 67

RESULT 2  
SYCL\_MYCTU STANDARD; PRT; 469 AA.

AC P96862;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Cysteine--tRNA synthetase 1 (BC 6.1.1.16) (Cysteine--tRNA ligase 1)  
DE (CYRSB 1).  
GN CYSS1 OR CYSS OR RV3580C OR MT3686 OR MTCY06G11.27C.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;  
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H37Rv;  
RX MEDLINE=98295987; PubMed=9634230;  
RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagals K., Krogan K., McLean J., Moule S., Murphy L., Oliver S., Osborne K., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skellern S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;  
RA "Deciphering the biology of Mycobacterium tuberculosis from the RT complete genome sequence."  
RT Nature 393:537-544(1998).  
RL [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=CDC 1551 / Oshkosh;  
RC Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickley B., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., DeJocher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishal W.;  
RA "Whole genome comparison of Mycobacterium tuberculosis clinical and RT laboratory strains."  
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
RL -1- CATALYTIC ACTIVITY: ATP + L-cysteine + tRNA(Cys) = AMP + diphosphate + L-cysteineyl-tRNA(Cys).  
CC -1- SUBUNIT: Monomer (by similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family. Strong, to methionyl-tRNA synthetase.  
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CC -----  
DR EMBL, Z92774; CAB07154.1; -;  
DR EMBL, AE007169; AAK4804.1; -;  
DR PIR, B70607; B70607.  
DR TIGR, MT3686; -;  
DR Tuberculin; RV3580C; -;  
DR HAMAP, MF\_00041; -; 1.  
DR InterPro, IPR002308; Cys\_tRNA-synt\_1a.  
DR InterPro, IPR001412; tRNA-synt\_1.  
DR Pfam, PF01406; tRNA-synt\_1; 1.  
DR PRINTS, PR00983; TRNASYNTHCS.  
DR TIGRFAMs, TIGR00435; cys; 1.

DR PROSITE, PS00178; AA tRNA\_LIGASE\_I, FALSE NEG.  
KM Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
KM Complete proteome.  
FT SITE 35 45 "HIGH" REGION.  
FT SITE 267 271 "KMSK" REGION.  
FT BINDING 270 270 ATP (BY SIMILARITY).  
FT CONFLICT 457 457 D -> E (IN REF. 2).  
SQ SEQUENCE 469 AA; 51854 MW; 515F9D19482ADC0E CRC64;

Query Match 35.8%; Score 48; DB 1; Length 469;  
Best Local Similarity 64.7%; Pred. No. 32;  
Matches 11; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

OY 2 GCGAYEDVMSGEYPEY 18  
Db 142 GGGVVDVLLGHVPLGVMKHPYFLM 156

RESULT 3  
SOD\_DROME STANDARD; PRT; 345 AA.

AC Q08473;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE RNA-binding protein squid (Heterogeneous nuclear ribonucleoprotein 40)  
DE (HNRNP 40).  
GN SOD OR HRP40.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RX MEDLINE=93279471; PubMed=7684991;  
RA Kelley R.L.;  
RT "Initial organization of the Drosophila dorsoventral axis depends on an RNA-binding protein encoded by the squid gene."  
RT Genes Dev. 7:948-960(1993).  
RL [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=Canton-S;  
RC MEDLINE=92112968; PubMed=1730754;  
RA Matunis E.L., Matunis M.J., Dreyfuss G.;  
RA "Characterization of the major hnRNP proteins from Drosophila melanogaster."  
RT J. Cell Biol. 116:257-269(1992).  
RL -1- FUNCTION: THIS PROTEIN IS A COMPONENT OF RIBONUCLEOSOMES. COULD BE NEEDED TO ORGANIZE A CONCENTRATION GRADIENT OF A DORSALIZING MORPHOGEN (DM) ORIGINATING IN THE GERMAL VESICLE. AT LEAST ONE OF THE ISOFORMS IS ESSENTIAL IN SOMATIC TISSUES.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC. IT IS POSSIBLE THAT SOME ISOFORMS ARE FOUND ONLY IN ONE OF THESE LOCATIONS.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing: Named isoforms=3;  
CC Comment-Additional isoforms seem to exist;  
CC Name=sqds; Synonyms=HRP40.2;  
CC IsoId=Q08473-1; Sequence=Displayed;  
CC Name=sqda; Synonyms=HRP40.1;  
CC IsoId=Q08473-2; Sequence=VSP\_005876;  
CC Name=sqdb;  
CC IsoId=Q08473-3; Sequence=VSP\_005877;  
CC -1- DISEASE: FEMALES WITH MUTATIONS IN SOD ARE STERILE AND LAY EGGS THAT DISPLAY ONLY DORSAL STRUCTURES.  
CC -1- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 1.23314 Seconds  
(without alignments)  
877.119 Million cell updates/sec

Title: US-09-674-752-30

Perfect score: 134  
Sequence: 1 DGGGAYEDVMSGEYPEYAMDV 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49.5	36.9	220	Y1CG_HAEIN	P45122 haemophilus
2	48	35.8	469	SYCL_MYCTU	P96862 mycobacteri
3	47.5	35.4	345	SOD_DROME	Q08473 drosophila
4	47.5	35.4	1050	ITAS_XENLA	Q06274 xenopus lae
5	47	35.1	812	PABD_ECOLI	P06970 escherichia
6	46.5	34.7	431	YCG4_METTH	Q27719 methanobact
7	46.5	34.7	946	AMYG_CANAL	Q74254 candida alb
8	46	34.3	259	VG38_BPAR1	Q99484 bacterioph
9	46	34.3	344	HEMZ_AGRTS	Q80917 agrobacteri
10	46	34.3	643	YKQ9_CAEL	P34304 caenorhabdi
11	46	34.0	741	NPL1_MOUSE	Q61985 mus musculu
12	45.5	34.0	675	CIBA_PABEP	P57091 paenibacill
13	45	33.6	428	V234_ROMPV	P14368 fowlpox vir
14	45	33.6	444	EX7L_RICCN	Q92966 rickettsia
15	45	33.6	449	EX7L_SALTI	Q82941 salmonella
16	45	33.6	449	EX7L_SALTY	Q82958 rickettsia
17	45	33.6	453	EX7L_RICPR	Q82958 rickettsia
18	45	33.6	456	EX7L_ECOLI	Q84994 escherichia
19	45	33.6	456	EX7L_ECOLI	Q84994 escherichia
20	45	33.6	458	EX7L_ECOLI	Q84994 escherichia
21	45	33.6	459	EX7L_YERPE	Q87664 escherichia
22	45	33.6	463	ANX7_MOUSE	Q87664 escherichia
23	45	33.6	532	EX7L_AGRIS	Q87664 escherichia
24	45	33.6	542	EX7L_BRAJA	Q87664 escherichia
25	45	33.6	1131	APCE_ANASP	P80559 anabaena sp
26	44.5	33.2	115	YAT7_RHOBL	P05450 rhodospheudo
27	44	32.8	79	RLJ1_ANASP	Q87664 escherichia
28	44	32.8	159	CUP9_DROME	Q87664 escherichia
29	44	32.8	207	ECG2_SCHJA	P27781 drosophila
30	44	32.8	210	Y593_CAMUE	Q91969 schistosoma
31	44	32.8	212	EGG1_SCHJA	Q91969 schistosoma
32	44	32.8	284	HSR4_ARATH	Q96120 arabidopsis
33	44	32.8	325	Y893_MYCTU	Q10552 mycobacteri

34	44	32.8	352	1	PRK1_SCHPO	O13958 schizosacch
35	44	32.8	466	1	ANX7_HUMAN	P20073 homo sapien
36	44	32.8	704	1	GLGB_YEAST	P32775 saccharomyc
37	44	32.8	729	1	PABD_ECO57	Q84812 e fatty oxi
38	44	32.8	729	1	PABD_ECOLI	P21177 e fatty oxi
39	44	32.8	729	1	PABD_SALTI	Q82366 s fatty oxi
40	44	32.8	729	1	PABD_SALTY	Q91615 s fatty oxi
41	44	32.8	774	1	SCA_DROME	P21520 drosophila
42	44	32.8	1173	1	DPOL_RCWMV	Q85428 rat cytoleg
43	43.5	32.5	102	1	SGP3_CHRYI	O52055 chromatiu
44	43.5	32.5	378	1	Y952_ARCFU	O23310 archaeoglob
45	43.5	32.5	451	1	EX7L_NEIMA	Q93ty8 neisseria m

## ALIGNMENTS

RESULT 1	Y1CG_HAEIN	STANDARD:	PRT:	220 AA.
ID	Y1CG_HAEIN	P45122;		
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Hypothetical protein H11240.			
GN	H11240.			
OS	Haemophilus influenzae.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;			
OC	Pasteurellaceae; Haemophilus.			
OX	NCBI_TaxId=727;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=RD / KW20 / ATCC 51907;			
RM	MEDLINE=95350630; PubMed=7542800;			
RA	Pfeilschmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,			
RA	Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,			
RA	McKenny K., Sutton G., Fitzhugh W., Fields C.A., Kelley J.M.,			
RA	Scott J.D., Shirley R., Liu L.-I., Glodex A., Kelley J.M.,			
RA	Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,			
RA	Uteerback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,			
RA	Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,			
RA	Gnehm C.L., McDonald L.A., Small K.V., Frazer C.M., Smith H.O.,			
RA	Venter J.C.;			
RT	"Whole-genome random sequencing and assembly of Haemophilus influenzae			
RT	Rd.";			
RL	Science 269:496-512(1995).			
CC	- SUBCELLULAR LOCATION: Integral membrane protein (Probable).			
CC	- SIMILARITY: BELONGS TO THE UPF0126 FAMILY. STRONG. TO E.COLI Y1CG.			
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.isb-eb.ch/announce/">http://www.isb-eb.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-eb.ch">license@isb-eb.ch</a> ).			
DR	EMBL: U32804; AAC22893.1; -			
DR	PIR: B6169; E64169.			
DR	TIGR: H11240; -			
DR	InterPro: IPR005115; UPF0126.			
DR	Pfam: PF03458; UPF0126; 2.			
KW	Hypothetical protein; Transmembrane; Complete proteome.			
FT	TRANSMEM 26	46	POTENTIAL.	
FT	TRANSMEM 65	85	POTENTIAL.	
FT	TRANSMEM 92	112	POTENTIAL.	
FT	TRANSMEM 116	136	POTENTIAL.	
FT	TRANSMEM 152	172	POTENTIAL.	
FT	TRANSMEM 175	195	POTENTIAL.	
SO	SEQUENCE 220 AA; 24228 MW; 58506FAFIC5570BF CRC64;			
Query Match	36.9%;	Score 49.5;	DB 1;	Length 220;
Best Local Similarity	42.3%;	Pred. No. 9.1;		







Best Local Similarity 69.2%; Pred. No. 18;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAYEDVWSGE 14  
| | | | |  
Db 124 GGGGAYEDVWFRE 136

## RESULT 8

E64169

conserved hypothetical protein H11240 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae  
C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 29-Sep-1999

C/Accession: E64169  
R:Platichmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kervilave, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Frazer, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630; PMID:7542800  
A:Accession: E64169  
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA  
A:Residues: 1-220 <TIGR>  
A:Cross-references: GB:U32804; GB:L42023; NID:g1574170; PIDN:AC22893.1; PID:g1574172; C:Superfamily: hypothetical protein B1832

Query Match 36.9%; Score 49.5; DB 2; Length 220;  
Best Local Similarity 42.3%; Pred. No. 16;  
Matches 11; Conservative 2; Mismatches 6; Indels 7; Gaps 1;

Qy 3 GGGAYEDVWSGEY-----PEYYAM 21  
| | | | |  
Db 42 GGGSVRVLLGHPLGKVKRPYFLM 67

## RESULT 9

H87389

conserved hypothetical protein CC1132 (imported) - Caulobacter crescentus

C:Species: Caulobacter crescentus  
C>Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001

C/Accession: H87389  
R:Merlan, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; B.; Laub, M.T.; Debey, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: H87389  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-509 <STO>  
A:Cross-references: GB:AE005673; NID:g13422446; PIDN:AAK2116.1; GSPDB:GN00148

C:Gene: CC1132  
Query Match 36.6%; Score 49; DB 2; Length 509;  
Best Local Similarity 52.6%; Pred. No. 47;  
Matches 10; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

Qy 1 DGGGAYEDVWSGEYPEY 19  
| | | | |  
Db 321 DGG----EDFWPGEYSKY 335

## RESULT 10

H96940

hypothetical protein CAC0334 (imported) - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum  
C>Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
C:Accession: H96940  
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zang, O.; Gibson, R.; Lee,

; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C  
A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: H96940  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-166 <KUR>  
A:Cross-references: GB:AE001437; PIDN:AAK78315.1; PID:g15023180; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Gene: CAC0334

Query Match 36.2%; Score 48.5; DB 2; Length 166;  
Best Local Similarity 41.7%; Pred. No. 16;  
Matches 10; Conservative 2; Mismatches 7; Indels 5; Gaps 1;

Qy 5 GAYEDVWSGEYPP-----YYAMDV 23  
| | | | |  
Db 141 GGFPCGMDPEYGRIVAYPKSV 164

## RESULT 11

B70607

probable cyts protein - Mycobacterium tuberculosis (strain H37Rv)

C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000

C/Accession: B70607  
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garfield, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feldgell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Ravidream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:9825987; PMID:9634230

A:Accession: B70607  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-469 <COL>

A:Cross-references: GB:Z92774; GB:AL123456; NID:g3261729; PIDN:CA807154.1; PID:g1877311  
A:Experimental source: strain H37Rv  
C:Gene: cyts

C:Superfamily: cysteine-tRNA ligase  
Query Match 35.8%; Score 48; DB 2; Length 469;  
Best Local Similarity 64.7%; Pred. No. 59;  
Matches 11; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

Qy 2 GGGAYEDVWSGEYPEY 18  
| | | | |  
Db 142 GGGDYVFDVLS--YPEY 156

## RESULT 12

B47369

RNA-binding protein (alternatively spliced) SqdB - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster  
C>Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 24-Sep-1999

C/Accession: B47369  
R:Kelley, R.L. Genes Dev. 7, 948-960, 1993  
A:Title: Initial organization of the Drosophila dorsoventral axis depends on an RNA-bind  
A:Reference number: A47369; MUID:93279471; PMID:7684991  
A:Accession: B47369  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-308 <XEL>

A:Cross-references: GB:S62100; NID:g385453; PIDN:AA826989.1; PID:g385455  
A>Note: sequence extracted from NCBI backbone (NCBIN:132997, NCBIN:132999, NCBI:133001)  
C:Gene: sqdB  
A:Cross-references: FlyBase:FBgn0003498









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## OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 ; Search time 12.078 Seconds

(without alignments)  
1003.251 Million cell updates/sec

Title: US-09-674-752-43

Perfect score: 665  
Sequence: 1 QVQLVQSGGGLVQPGKSLRL.....RSGVAFDIMWGCTMTVSS 126Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76: \*  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	518.5	78.0	123	2 S30532	Ig heavy chain V r
2	516.5	77.7	121	2 S31118	Ig heavy chain - h
3	516	77.6	145	2 S11239	Ig heavy chain V r
4	512	77.0	128	2 S31595	Ig heavy chain V r
5	503.5	75.7	121	2 S31104	Ig heavy chain (su
6	499.5	75.1	120	2 S36273	Ig heavy chain V r
7	477	71.7	118	2 S31105	Ig heavy chain (su
8	475.5	71.5	119	2 F36005	Ig heavy chain V r
9	475	71.4	118	2 S31116	Ig heavy chain - h
10	474	71.3	137	2 S31701	Ig heavy chain V r
11	470.5	70.8	121	2 S31966	Ig heavy chain V r
12	469.5	70.6	123	2 PC4281	Ig heavy chain V r
13	466.5	70.2	143	2 S23624	anti-SS-A/Ro 60K p
14	466	70.1	114	2 S31120	Ig heavy chain V r
15	464	69.8	120	2 S44111	Ig heavy chain - h
16	463	69.6	128	2 S48797	Ig heavy chain V r
17	463	69.6	141	2 S70442	Ig heavy chain pre
18	462.5	69.5	121	2 G36002	Ig heavy chain V r
19	462	69.5	120	2 S31112	Ig heavy chain - h
20	462	69.5	122	2 B36005	Ig heavy chain V r
21	461.5	69.4	125	2 S30531	Ig heavy chain V r
22	461	69.3	122	2 S31117	Ig heavy chain - h
23	461	69.3	128	2 S26790	Ig heavy chain V r
24	457.5	68.8	127	2 S38489	Ig heavy chain - h
25	456.5	68.6	119	2 S31108	Ig heavy chain - h
26	456.5	68.6	123	2 S26794	Ig heavy chain V r
27	454.5	68.3	138	2 S31666	Ig heavy chain V r
28	454	68.3	98	2 S26927	Ig heavy chain V r
29	454	68.3	128	2 S26786	Ig heavy chain V r

30	453.5	68.2	134	2 S31679	Ig heavy chain V r
31	453.5	68.2	139	2 I37781	Ig variable region
32	453	68.1	124	2 S20782	Ig heavy chain V r
33	452.5	68.0	123	2 S31114	Ig heavy chain - h
34	452.5	68.0	140	2 S31686	Ig heavy chain V r
35	452.5	68.0	160	2 S05271	Ig heavy chain pre
36	452	68.0	136	2 S31587	Ig heavy chain V r
37	451.5	67.9	140	2 S31588	Ig heavy chain V r
38	450.5	67.7	119	2 S31107	Ig heavy chain - h
39	450.5	67.7	135	2 S31598	Ig heavy chain V r
40	449.5	67.6	119	2 C36005	Ig heavy chain V r
41	449	67.5	132	2 PH1654	Ig heavy chain V r
42	449	67.5	139	2 S31674	Ig heavy chain V r
43	448.5	67.4	120	2 S36278	Ig heavy chain V r
44	448.5	67.4	132	2 S31603	Ig heavy chain V r
45	448	67.4	114	2 S46390	Ig heavy chain V r

## ALIGNMENTS

## RESULT 1

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996

C/Accession: S30532

R/Mariette, X.

submitted to the EMBL Data Library, October 1992

A/Reference number: S30520

A/Accession: S30532

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-123 &lt;MAR&gt;

A/Cross-references: EMBL:218318

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 78.0%; Score 518.5; DB 2; Length 123;

Best Local Similarity 78.9%; Pred. No. 1e-40; Matches 101; Conservative 11; Mismatches 9; Indels 7; Gaps 3;

QY	1 QVQLVQSGGGLVQPGKSLRLCAASGFTFGDYAIHWVROAPGSELEWVSGVTSGTIGF 60	
DB	1 EVQLVDSGGGLVQPGKSLRLCAASGFTFDYAMHWVROAPGKLEWVSGISWNSGTIGY 60	
QY	61 ADSVKGRTISRMAKNSLYLNLSLAEDTALTYCA--LPYINSSYRGRGVAFDIWQ 118	
DB	61 ADSVKGRTISRMAKNSLYLNLSLAEDTALTYCAKDTPT--SSGWSN---AFDIWGQ 115	
QY	119 GTMTVSS 126	
DB	116 GTMTVSS 123	

## RESULT 2

Ig heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999

C/Accession: S31118

R/Rapboret, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma

Eur. J. Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complen

A/Reference number: S31104; MIMD:92111633; PMID:1730252

A/Accession: S31118

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-121 &lt;RAA&gt;

A/Cross-references: EMBL:X62969

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C/Superfamily: immunoglobulin V region; immunoglobulin homology

TITLE OF INVENTION: Agents and Intermediates for Their Synthesis  
 NUMBER OF SEQUENCES: 73  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: American Cyanamid Company  
 STREET: One Cyanamid Plaza  
 CITY: Wayne  
 STATE: New Jersey  
 COUNTRY: U.S.A.  
 ZIP: 07470-8426  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATE:  
 APPLICATION NUMBER: US/08/253,877C  
 FILING DATE: 03-JUN-1994  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Barnhard, Elizabeth M.  
 REGISTRATION NUMBER: 31,088  
 REFERENCE/DOCKET NUMBER: 32,368  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-831-3246  
 TELEFAX: 201-831-3305  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 139 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 IS-08-253-877C-19

Query Match	64.4%	Score 424	DB 1	Length 139
Best Local Similarity	66.1%	Pred. No. 3.4e-39		
Matches 82; Conservative	13;	Mismatches 19;	Indels 10;	Gaps 2

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OY      1 OVOLLGSAADYKKRPGASVYVYSCASGYITSTYDINWVQAOTGGLEMMGNPNPSSGNAGF 60
Db      20 Q10LVGSAVKKPSSGASVSCASGYITTDYYINMWQAPOGLEMMGIDDPSSGNTKY 79
OY      61 AOKPGRGLTTRDSTSTAYMELRLSESDTAVVYCARCDTLLIMFGPAPYY--DSMGQ 118
Db      80 NEKRGVITITVDSTNTAYMELSLRSEDTAFYCARBKITY-----YAMDYWGQ 131
OY      119 GTLV 122
Db      132 GTLV 135

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Search completed: December 30, 2003, 11:05:34  
Job time : 12.4716 secs

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QY      60 FAQCFKGLTLTRDSTISTAVMELERLSESDPAVYYCARCDTLLIWFQPAPY-----   113
       :|::||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 YAKRFGQGVTITADPSTISATAMELSSLSASEDPAYTCAR-----AFGYSGGGGC    109

QY      114 -----DSWCGGCTLV     122
        |||||
Db      110 YRGDYXFDYMCGGTIV     125


RESULT 13
US-08-525-539A-77
; Sequence 77, Application US/0852539A
; Patent No. 6309636
GENERAL INFORMATION:
APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: MCB ANTI-BAG ANTIBODY METHODS OF USE THEREOF, AND
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525.539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-525-539A-77

Query Match          65.1%; Score 428.5; DB 4; Length 129;
Best Local Similarity 64.0%; Pred.No. 1e-39;
Matches 87; Conservative 10; Mismatches 14; Indels 25; Gaps 3

QY      1 QVOLLOSADVKKKGASVKVSCTASGYFTSYDIMNVAQTGGLEGMMGMNP-NSGNAAG 59
         |::|:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db      1 QVALVGSAEAEYKKGASVKVCCKSNGTYFTTSIAISWVDAPGQGLEMMGMIMPYANGDTN 60

QY      60 PAQCFKGLTLTRDSTISTAVMELERLSESDPAVYYCARCDTLLIWFQPAPY-----   113
       :|::||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 YAKRFGQGVTITADPSTISATAMELSSLSASEDPAYTCAR-----AFGYSGGGGC    109

QY      114 -----DSWCGGCTLV     122
        |||||
Db      110 YRGDYXFDYMCGGTIV     125


RESULT 14
PCT-US95-01219-45
Sequence 45, Application PC/TU9501219
```

```

GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leeger, Olivier J.
APPLICANT: Saldana, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-45

Query Match      65.1%; Score 428.5; DB 5; Length 129;
Best Local Similarity 64.0%; Pred. No. 1e-39;
Matches 87; Conservative 10; Mismatches 14; Indels 25; Gaps 3;

QY      1 QVQLTQSAALAVKPKGASVKISCTAASGITFTSYDINWTRQATGOGLRWGMGNP-NSNGAG 59
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 QVQLVDSGAEVKKRPGASVKISKTAASGITFTSYAISLWROAFQGLRWGMGINPYGNGDTN 60
QY      60 FAKCFKRRLTLTDPTSTSTAYMELRSESDTAYYYCARCOTLLINFGAPAY----- 113
        :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      61 YAQPFQRVITLTADTSTIAYMELSLRSEDYAYTCAR-----APGISSGGGC 109
QY      114 -----DSWGQGTLV 122
        | |||||
Db      110 YRGDYXFDYWGQGTLV 125

RESULT 15
US-08-253-877C-19
Sequence 19, Application US/08253877C
Patent No. 5773001
GENERAL INFORMATION:
APPLICANT: Hamann, Phillip R.
APPLICANT: Himman, Lois
APPLICANT: Hollander, Irwin
APPLICANT: Holcomb, Ryan
APPLICANT: Hallett, William
APPLICANT: Tesou, Hwei-Ru
APPLICANT: Weisb, Martin J.
TITLE OF INVENTION: Conjugates of Methyltrichio Antitumor

```





CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14137-77  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..128  
OTHER INFORMATION: /label= HUMAN\_1  
US-08-202-047-22

Query Match 66.1%; Score 435; DB 1; Length 128;  
Best Local Similarity 64.4%; Pred. No. 1.9e-40;  
Matches 87; Conservative 11; Mismatches 13; Indels 24; Gaps 3;

QY 1 QVOLLQSAADYKKPGASVKSCTASGYFTSYDINMVRQATGQGLEMMGMNP-NSGNAG 59  
DB 1 QVOLLQSAADYKKPGASVKSCTASGYFTSYDINMVRQATGQGLEMMGMNP-NSGNAG 59  
QY 60 FAQKFKRLTLTRDSTSTAYMELRLSEEDTAVYYCARCOTLLIMFGAP----- 111  
DB 61 YAKQFGQVITITADISTSTAYMELSLRSEDTAVYYCAR-----APGYSGGGCC 109  
QY 112 ----YDSMGQGTLY 122  
DB 110 YRGDYFDYWGQGTLY 124

RESULT 9  
US-08-964-690-22  
Sequence 22, Application US/08964690  
Patent No. 6033667  
GENERAL INFORMATION:  
APPLICANT: CHESNUT, Robert W.  
APPLICANT: POLLEY, Margaret J.  
APPLICANT: PAULSON, James C.  
APPLICANT: JONES, S. Tarran  
APPLICANT: SALDANHA, Jose W.  
APPLICANT: BENDIG, Mary M.  
TITLE OF INVENTION: Antibodies to P-selectin and Their Uses  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/964,690  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,047  
FILING DATE: 25-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 14137-77  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..128  
OTHER INFORMATION: /label= HUMAN\_1  
US-08-964-690-22

Query Match 66.1%; Score 435; DB 3; Length 128;  
Best Local Similarity 64.4%; Pred. No. 1.9e-40;  
Matches 87; Conservative 11; Mismatches 13; Indels 24; Gaps 3;

QY 1 QVOLLQSAADYKKPGASVKSCTASGYFTSYDINMVRQATGQGLEMMGMNP-NSGNAG 59  
DB 1 QVOLLQSAADYKKPGASVKSCTASGYFTSYDINMVRQATGQGLEMMGMNP-NSGNAG 59  
QY 60 FAQKFKRLTLTRDSTSTAYMELRLSEEDTAVYYCARCOTLLIMFGAP----- 111  
DB 61 YAKQFGQVITITADISTSTAYMELSLRSEDTAVYYCAR-----APGYSGGGCC 109  
QY 112 ----YDSMGQGTLY 122  
DB 110 YRGDYFDYWGQGTLY 124

RESULT 10  
US-09-049-672A-13  
Sequence 13, Application US/09049672A  
Patent No. 6135941  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Lal, Preeti  
APPLICANT: Tang, Y. Tom  
APPLICANT: Yue, Henry  
APPLICANT: Au-Young, Janice  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl J.  
APPLICANT: Baughn, Mariah R.  
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,672A  
FILING DATE: HEREWITH  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Carrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0497 US  
TELECOMMUNICATION INFORMATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/407,009  
FILING DATE: 29-MAR-1995  
APPLICATION NUMBER: 08/119,032  
FILING DATE: 09-SEP-1993  
APPLICATION NUMBER: 08/027,008  
FILING DATE: 05-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliot M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 61750-142  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 94:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: polypeptide  
FEATURE:  
NAME/KEY: Human Amu 5-3 heavy chain variable region.  
US-08-472-281A-94

Query Match 66.5%; Score 437.5; DB 2; Length 123;  
Best Local Similarity 69.7%; Pred. No. 9.7e-41;  
Matches 85; Conservative 13; Mismatches 21; Indels 3; Gaps 1;

QY 1 OVOLLOSADYKRRKGAASVCTASGYFTSYDINMTRQATGCGLEMMGMNPNISGNAGF 60  
DB 1 OVOLVQSAEYKRGASVCKASGYFTGYVMWRQAPGQGLEMMGRINPNSGCTNY 60  
QY 61 AOKFKGRLLTRDTSTSTAYMELRLSESDTAVVYCARCDTLLIMFGAPPYDSMGCGT 120  
DB 61 AOKFGRTVMTDRDISSTAYMELRLSDITAVVYCARGRTRYIV--VAEGFDYMGCGT 117  
QY 121 LV 122  
DB 118 LV 119

## RESULT 7

US-08-477-989B-94  
Sequence 94, Application US/08477989B  
Patent No. 5951983  
GENERAL INFORMATION:  
APPLICANT: Bazin, Hervy  
APPLICANT: Latine, Dominique  
APPLICANT: Kaplan, Ruth  
APPLICANT: Kiebert-Bmoch, Thomas  
APPLICANT: Poblema, Christina E.  
TITLE OF INVENTION: LO-CD2a Antibody and Uses  
TITLE OF INVENTION: Thereof for Inhibiting  
TITLE OF INVENTION: T-Cell Activation and  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
ADDRESSEE: Cecchi, Stewart & Olstein  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,989B

FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/407,009  
FILING DATE: 29-MAR-1995  
APPLICATION NUMBER: 08/119,032  
FILING DATE: 09-SEP-1993  
APPLICATION NUMBER: 08/027,008  
FILING DATE: 05-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliot M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 61750-147  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 94:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: polypeptide  
FEATURE:  
NAME/KEY: Human Amu 5-3 heavy chain variable  
US-08-477-989B-94

Query Match 66.5%; Score 437.5; DB 2; Length 123;  
Best Local Similarity 69.7%; Pred. No. 9.7e-41;  
Matches 85; Conservative 13; Mismatches 21; Indels 3; Gaps 1;

QY 1 OVOLLOSADYKRRKGAASVCTASGYFTSYDINMTRQATGCGLEMMGMNPNISGNAGF 60  
DB 1 OVOLVQSAEYKRGASVCKASGYFTGYVMWRQAPGQGLEMMGRINPNSGCTNY 60  
QY 61 AOKFKGRLLTRDTSTSTAYMELRLSESDTAVVYCARCDTLLIMFGAPPYDSMGCGT 120  
DB 61 AOKFGRTVMTDRDISSTAYMELRLSDITAVVYCARGRTRYIV--VAEGFDYMGCGT 117  
QY 121 LV 122  
DB 118 LV 119

## RESULT 8

US-08-202-047-22  
Sequence 22, Application US/08202047  
Patent No. 580815  
GENERAL INFORMATION:  
APPLICANT: CHESNUT, Robert W.  
APPLICANT: FOLLEY, Margaret J.  
APPLICANT: PAULSON, James C.  
APPLICANT: JONES, S. Tarran  
APPLICANT: SALDANHA, Jose W.  
TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,047  
FILING DATE: 25-FEB-1994

NUMBER OF SEQUENCES: 373  
 CORRESPONDENCE ADDRESS: 373  
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10021  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/025,769B  
 FILING DATE: 18-FEB-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: James F. Haley, Jr., Esq.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: MORPHO/5  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)596-9000  
 TELEFAX: (212)596-9090  
 INFORMATION FOR SEQ ID NO: 22:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 117 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-025-769B-22

Query Match 67.1%; Score 441.5; DB 4; Length 117;  
 Best Local Similarity 69.7%; Pred. No. 3.3e-41;  
 Matches 85; Conservative 11; Mismatches 17; Indels 9; Gaps 1;  
 QY 1 QVOLLGSAADVKKPGASVKVCTASGYIFTSYDINWVROATGQGLWMGMNPNPNSGNAGF 60  
 DB 1 QVOLLGSAADVKKPGASVKVCTASGYIFTSYDINWVROATGQGLWMGMNPNPNSGNAGF 60  
 QY 61 AOKFKGLTLTRDTSTSTAYMELRLSESDTAVYYCARCDTLLIWFGPAPYYDSWGQGT 120  
 DB 61 AOKFKGLTLTRDTSTSTAYMELRLSESDTAVYYCARCDTLLIWFGPAPYYDSWGQGT 120  
 QY 61 AOKFKGLTLTRDTSTSTAYMELRLSESDTAVYYCARCDTLLIWFGPAPYYDSWGQGT 120  
 DB 61 AOKFKGLTLTRDTSTSTAYMELRLSESDTAVYYCARCDTLLIWFGPAPYYDSWGQGT 120  
 QY 121 LV 122  
 DB 112 LV 113

RESULT 5  
 US-08-477-877B-94  
 Sequence 94, Application US/08477877B  
 Patent No. 5730979  
 GENERAL INFORMATION:  
 APPLICANT: Bazin, Herv  
 APPLICANT: Latime, Dominique  
 TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ  
 NUMBER OF SEQUENCES: 96  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cecchi, Byrnie, Bain, Gilfillan,  
 ADDRESSEE: Cecchi, Stewart & Olstein  
 STREET: 6 Becker Farm Road  
 CITY: Roseland  
 STATE: New Jersey  
 COUNTRY: U.S.A.  
 ZIP: 07068  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch diskette  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS

SOFTWARE: Mordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/477,877B  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/407,009  
 FILING DATE: 29-MAR-1995  
 APPLICATION NUMBER: 08/119,032  
 FILING DATE: 09-SEP-1993  
 APPLICATION NUMBER: 08/027,008  
 FILING DATE: 05-MAR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Olstein, Elliot M.  
 REGISTRATION NUMBER: 24,025  
 REFERENCE/DOCKET NUMBER: 61750-146  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-994-1700  
 TELEFAX: 201-994-1744  
 INFORMATION FOR SEQ ID NO: 94:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 123 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: polypeptide  
 FEATURE:  
 NAME/KEY: Human Amu 5-3 heavy chain variable region.  
 US-08-477-877B-94

Query Match 66.5%; Score 437.5; DB 1; Length 123;  
 Best Local Similarity 69.7%; Pred. No. 9.7e-41;  
 Matches 85; Conservative 13; Mismatches 21; Indels 3; Gaps 1;  
 QY 1 QVOLLGSAADVKKPGASVKVCTASGYIFTSYDINWVROATGQGLWMGMNPNPNSGNAGF 60  
 DB 1 QVOLLGSAADVKKPGASVKVCTASGYIFTSYDINWVROATGQGLWMGMNPNPNSGNAGF 60  
 QY 61 AOKFKGLTLTRDTSTSTAYMELRLSESDTAVYYCARCDTLLIWFGPAPYYDSWGQGT 120  
 DB 61 AOKFKGLTLTRDTSTSTAYMELRLSESDTAVYYCARCDTLLIWFGPAPYYDSWGQGT 120  
 QY 121 LV 122  
 DB 118 LV 119

RESULT 6  
 US-08-472-281A-94  
 Sequence 94, Application US/08472281A  
 Patent No. 5817311  
 GENERAL INFORMATION:  
 APPLICANT: Bazin, Herv  
 APPLICANT: Latime, Dominique  
 TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ  
 NUMBER OF SEQUENCES: 96  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cecchi, Byrnie, Bain, Gilfillan,  
 ADDRESSEE: Cecchi, Stewart & Olstein  
 STREET: 6 Becker Farm Road  
 CITY: Roseland  
 STATE: New Jersey  
 COUNTRY: U.S.A.  
 ZIP: 07068  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch diskette  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Mordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/472,281A  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 424



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## OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:45 ; Search time 12.3883 Seconds  
(without alignments)  
416.677 Million cell updates/sec

Title: US-09-674-752-40

Perfect score: 658  
Sequence: 1 OVALLOSADVKKPKGASVKV.....LLIWFGRPYDSMGQCTLV 122

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	451	68.5	120	4	US-09-025-769B-36
2	451	68.5	120	4	US-09-025-769B-59
3	449	68.2	117	3	US-08-545-809A-96
4	441.5	67.1	117	4	US-09-025-769B-22
5	437.5	66.5	123	1	US-08-477-877B-94
6	437.5	66.5	123	2	US-08-477-281A-94
7	437.5	66.5	123	2	US-08-477-989B-94
8	435	66.1	128	1	US-08-202-047-22
9	435	66.1	128	3	US-08-964-690-22
10	431	65.5	126	3	US-09-049-672A-13
11	429.5	65.3	121	1	US-08-264-093-3
12	428.5	65.1	129	2	US-08-561-521-45
13	428.5	65.1	129	4	US-08-525-539A-77
14	428.5	65.1	129	5	PCT-US95-01219-45
15	424	64.4	139	1	US-08-253-877C-19
16	424	64.4	139	2	US-08-452-164A-19
17	424	64.4	139	3	US-08-603-024-18
18	424	64.4	139	4	US-08-450-809-14
19	423	64.3	118	1	US-08-491-845-14
20	423	64.3	137	3	US-08-513-968-38
21	422.5	64.2	135	3	US-09-199-149-3
22	421.5	64.1	119	2	US-08-561-521-10
23	421.5	64.1	119	5	PCT-US95-01219-10
24	418.5	63.6	119	4	US-09-438-954-41
25	415	63.0	245	4	US-10-039-785-46
26	414.5	63.0	139	3	US-08-933-983-21
27	414	62.9	117	3	US-08-545-809A-90

28	411.5	62.5	121	1	US-08-202-047-23	Sequence 23, Appl
29	411.5	62.5	121	3	US-08-964-690-23	Sequence 23, Appl
30	406.5	61.8	119	1	US-08-478-039-65	Sequence 65, Appl
31	406.5	61.8	119	1	US-08-476-349A-65	Sequence 65, Appl
32	405.5	61.6	119	2	US-08-561-521-12	Sequence 12, Appl
33	405.5	61.6	119	5	PCT-US95-01219-12	Sequence 12, Appl
34	405.5	61.6	123	1	US-08-482-882-86	Sequence 86, Appl
35	405.5	61.6	123	2	US-08-483-389-86	Sequence 86, Appl
36	405.5	61.6	123	2	US-08-487-113D-86	Sequence 86, Appl
37	405.5	61.6	123	2	US-08-473-503-86	Sequence 86, Appl
38	405.5	61.6	123	2	US-08-483-932-86	Sequence 86, Appl
39	405.5	61.6	123	3	US-08-720-420A-86	Sequence 86, Appl
40	405.5	61.6	123	3	US-08-714-017-86	Sequence 86, Appl
41	405.5	61.6	123	3	US-08-475-680-86	Sequence 86, Appl
42	403.5	61.3	140	3	US-08-836-561-63	Sequence 63, Appl
43	403.5	61.3	140	3	US-08-569-147-82	Sequence 82, Appl
44	403.5	61.3	140	4	US-09-434-122-63	Sequence 63, Appl
45	402.5	61.2	119	1	US-08-491-845-10	Sequence 10, Appl

## ALIGNMENTS

RESULT 1  
US-09-025-769B-36  
Sequence 36, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Illag, Vic  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-025-769B-36  
Query Match 68.5%; Score 451; DB 4; Length 120;  
Best Local Similarity 71.5%; Pred. No. 3,1e-42;  
Matches 88; Conservative 9; Mismatches 18; Indels 8; Gaps 2;



```
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 204
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-204
```

```
Query Match 71.9%; Score 473; DB 12; Length 126;
Best Local Similarity 72.8%; Pred. No. 5e-41;
Matches 91; Conservative 11; Mismatches 17; Indels 6; Gaps 2;
```

```
QY 1 QVQLQSGADPVKPKGASVSVCTASGYIFTSYDINVRQATGGLMGMMNPNNSGNAGF 60
DB 1 QVQLVSGAEVKKPKGASVSVCTASGYIFTSYDINVRQATGGLMGMMNPNNSGNTGY 60
QY 61 AOKFKRLTLTRDTSTSTAYMELRLSEEDTAVYVCARCDTLLIFGAPAYY---DSWG 117
DB 61 AOKFGQRTVMTRNTSISTAYMELSLRSEDTAVYICAR---DIVVVYATDYIYGMDWVG 117
QY 118 QGTLV 122
DB 118 QGTTV 122
```

```
RESULT 13
US-10-041-860-241
Sequence 241, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 241
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-241
```

```
Query Match 71.9%; Score 473; DB 12; Length 126;
Best Local Similarity 72.8%; Pred. No. 5e-41;
Matches 91; Conservative 11; Mismatches 17; Indels 6; Gaps 2;
```

```
QY 1 QVQLQSGADPVKPKGASVSVCTASGYIFTSYDINVRQATGGLMGMMNPNNSGNAGF 60
DB 1 QVQLVSGAEVKKPKGASVSVCTASGYIFTSYDINVRQATGGLMGMMNPNNSGNTGY 60
```

```
QY 61 AOKFKRLTLTRDTSTSTAYMELRLSEEDTAVYVCARCDTLLIFGAPAYY---DSWG 117
DB 61 AOKFGQRTVMTRNTSISTAYMELSLRSEDTAVYICAR---DIVVVYATDYIYGMDWVG 117
QY 118 QGTLV 122
DB 118 QGTTV 122
```

```
RESULT 14
US-10-041-860-349
Sequence 349, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 349
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-349
```

```
Query Match 71.9%; Score 473; DB 12; Length 126;
Best Local Similarity 72.8%; Pred. No. 5e-41;
Matches 91; Conservative 11; Mismatches 17; Indels 6; Gaps 2;
```

```
QY 1 QVQLQSGADPVKPKGASVSVCTASGYIFTSYDINVRQATGGLMGMMNPNNSGNAGF 60
DB 1 QVQLVSGAEVKKPKGASVSVCTASGYIFTSYDINVRQATGGLMGMMNPNNSGNTGY 60
QY 61 AOKFKRLTLTRDTSTSTAYMELRLSEEDTAVYVCARCDTLLIFGAPAYY---DSWG 117
DB 61 AOKFGQRTVMTRNTSISTAYMELSLRSEDTAVYICAR---DIVVVYATDYIYGMDWVG 117
QY 118 QGTLV 122
DB 118 QGTTV 122
```

```
RESULT 15
US-10-041-860-38
Sequence 38, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
```



```

CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 288
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860--288

Query Match      72.0%; Score 474; DB 12; Length 126;
Best Local Similarity 74.4%; Pred.No. 3,9e-41;
Matches 93; Conservative 8; Mismatches 18; Indels 6; Gaps 2

QY      1 QVOLLGSAADVKRKGCASVKVCSTASGYIFETSYDINMVRQATGGGLMGMMNPNSGNGGF 60
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db       1 QVOLVGQAELVKKPGCASVKSCAKSGYFTSIDINMVQAATGGGLMGMMNPNSGNTCY 60
QY      61 AQKFGRLLTRDPDSTAVYMELRLRESEDDAVVYCACRDTTLILWFGAPAY---DSWG 117
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       61 AAKCGARLTMRNISISTAYMELSLRSBEDIAVVYCAREGIAVA---GTYYYYYGMDWDG 117
QY      118 QGTLV 122
        |||
Db       118 QGTTV 122

RESULT 11
US-10-041-860-40
Sequence 40, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadl
APPLICANT: Weber, Richard

```

```

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USBS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-40

Query Match
Best Local Similarity 72.9%; Score 473; DB 12; Length 126;
Matches 91; Conservative 11; Mismatches 17; Indels 6; Gaps 2

QY 1 QVQLIQSLADYKPKPASYKVSCTASGTYFTSTVDIMWPAQAGCGLEMGNNPNPSCNMGF 60
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
DB 1 QVQLVQSAEAEVAKPKPASYKVSCKASGYFTSTVDIMWVAQTQGLEMGNNPNNGNTGY 60
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

QY 61 AOKFKGRLLTRDSTSTAYMELRLSEEDTAVYYCARCDTLLIMFGPAPY---DSWG 117
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
DB 61 AOKFGGRITMRNRNISTAYMELSLRSEDTAVYYCAR---DIVVVVYATDYYGMDVWG 117
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

QY 118 QGTLV 122
   |||
DB 118 QGTLV 122
   |||

```

APPLICANT: Bezabeh, Binyam  
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
FILE REFERENCE: ABGENIX.051A  
CURRENT APPLICATION NUMBER: US/10/041.860  
CURRENT FILING DATE: 2002-01-07  
NUMBER OF SEQ ID NOS: 377  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 37  
LENGTH: 126  
TYPE: PRT  
ORGANISM: homo sapiens  
US-10-041-860-37

Query Match 72.2%; Score 475; DB 12; Length 126;  
Best Local Similarity 72.8%; Pred. No. 3.1e-41;  
Matches 91; Conservative 11; Mismatches 17; Indels 6; Gaps 2;

QY 1 QVOLLGSAADVKKFGASVKVSCYASGYIFTSYDINWVROATGQGLEWGMNPNNSGACF 60  
DB 1 QVOLLGSAEYKKGASVKVSCYASGYFTTYDINWVROATGQGLEWGMNPNNSGNTGY 60  
QY 61 AOKFKGRLLTRDTSTSTAYWELRLSEDTAVYYCARCOTLLIWFGPAPY---DSWG 117  
DB 61 AOKFGQVMTMTNTSLSTAYWELSLRSEDTAVYYCAR---DIVVVAATNYNGMDVWG 117  
QY 118 QGTLV 122  
DB 118 QGTLV 122

## RESULT 6

US-10-041-860-202  
Sequence 202, Application US/10041860  
Publication No. US20030157109A1  
GENERAL INFORMATION:  
APPLICANT: Corvalan, Jose R.F.  
APPLICANT: Jia, Xiao-Chi  
APPLICANT: Feng, Xiao  
APPLICANT: Yang, Xiao-Dong  
APPLICANT: Chen, Francine  
APPLICANT: Gazit, Gadi  
APPLICANT: Weber, Richard  
APPLICANT: Bezabeh, Binyam  
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
FILE REFERENCE: ABGENIX.051A  
CURRENT APPLICATION NUMBER: US/10/041.860  
CURRENT FILING DATE: 2002-01-07  
NUMBER OF SEQ ID NOS: 377  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 202  
LENGTH: 126  
TYPE: PRT  
ORGANISM: homo sapiens  
US-10-041-860-202

Query Match 72.2%; Score 475; DB 12; Length 126;  
Best Local Similarity 72.8%; Pred. No. 3.1e-41;  
Matches 91; Conservative 11; Mismatches 17; Indels 6; Gaps 2;

QY 1 QVOLLGSAADVKKFGASVKVSCYASGYIFTSYDINWVROATGQGLEWGMNPNNSGACF 60  
DB 1 QVOLLGSAEYKKGASVKVSCYASGYFTTYDINWVROATGQGLEWGMNPNNSGNTGY 60  
QY 61 AOKFKGRLLTRDTSTSTAYWELRLSEDTAVYYCARCOTLLIWFGPAPY---DSWG 117  
DB 61 AOKFGQVMTMTNTSLSTAYWELSLRSEDTAVYYCAR---DIVVVAATNYNGMDVWG 117  
QY 118 QGTLV 122  
DB 118 QGTLV 122

## RESULT 7

US-10-041-860-239  
Sequence 239, Application US/10041860  
Publication No. US20030157109A1  
GENERAL INFORMATION:  
APPLICANT: Corvalan, Jose R.F.  
APPLICANT: Jia, Xiao-Chi  
APPLICANT: Feng, Xiao  
APPLICANT: Yang, Xiao-Dong  
APPLICANT: Chen, Francine  
APPLICANT: Gazit, Gadi  
APPLICANT: Weber, Richard  
APPLICANT: Bezabeh, Binyam  
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
FILE REFERENCE: ABGENIX.051A  
CURRENT APPLICATION NUMBER: US/10/041.860  
CURRENT FILING DATE: 2002-01-07  
NUMBER OF SEQ ID NOS: 377  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 239  
LENGTH: 126  
TYPE: PRT  
ORGANISM: homo sapiens  
US-10-041-860-239

Query Match 72.2%; Score 475; DB 12; Length 126;  
Best Local Similarity 72.8%; Pred. No. 3.1e-41;  
Matches 91; Conservative 11; Mismatches 17; Indels 6; Gaps 2;

QY 1 QVOLLGSAADVKKFGASVKVSCYASGYIFTSYDINWVROATGQGLEWGMNPNNSGACF 60  
DB 1 QVOLLGSAEYKKGASVKVSCYASGYFTTYDINWVROATGQGLEWGMNPNNSGNTGY 60  
QY 61 AOKFKGRLLTRDTSTSTAYWELRLSEDTAVYYCARCOTLLIWFGPAPY---DSWG 117  
DB 61 AOKFGQVMTMTNTSLSTAYWELSLRSEDTAVYYCAR---DIVVVAATNYNGMDVWG 117  
QY 118 QGTLV 122  
DB 118 QGTLV 122

## RESULT 8

US-10-041-860-19  
Sequence 19, Application US/10041860  
Publication No. US20030157109A1  
GENERAL INFORMATION:  
APPLICANT: Corvalan, Jose R.F.  
APPLICANT: Jia, Xiao-Chi  
APPLICANT: Feng, Xiao  
APPLICANT: Yang, Xiao-Dong  
APPLICANT: Chen, Francine  
APPLICANT: Gazit, Gadi  
APPLICANT: Weber, Richard  
APPLICANT: Bezabeh, Binyam  
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES  
FILE REFERENCE: ABGENIX.051A  
CURRENT APPLICATION NUMBER: US/10/041.860  
CURRENT FILING DATE: 2002-01-07  
NUMBER OF SEQ ID NOS: 377  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 19  
LENGTH: 126  
TYPE: PRT  
ORGANISM: homo sapiens  
US-10-041-860-19

Query Match 72.0%; Score 474; DB 12; Length 126;  
Best Local Similarity 74.4%; Pred. No. 3.9e-41;  
Matches 93; Conservative 8; Mismatches 18; Indels 6; Gaps 2;







XX The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix,  
 CC platelet-platelet and/or cell-platelet adhesion or aggregation, for  
 CC increasing mortality of tumour or leukaemia cells, for increasing the  
 CC susceptibility of diseased cells to damage by anti-disease, anti-cancer  
 CC or anti-leukaemia agents, or for decreasing the number of tumour or  
 CC leukaemia cells in a patient, or in the manufacture of a medicament for  
 CC the above mentioned purposes. The epitopes are useful for diagnosing and  
 CC treating diseases such as cancer, leukaemia, autoimmune diseases,  
 CC inflammatory diseases, cardiovascular diseases such as myocardial  
 CC infarction, retinopathic diseases and other diseases mediated by abnormal  
 CC platelet function and diseases caused by sulphated tyrosine-dependent  
 CC protein-protein interactions. This sequence represents a human antibody  
 CC fragment of the invention.

XX Sequence 98 AA;

Query Match 68.2%; Score 449; DB 23; Length 98;  
 Best Local Similarity 84.7%; Pred. No. 8.9e-36;  
 Matches 83; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 1 QVOLLQSAADYKKPGASVKSCTASGYIFTSYDINWVROATGQGLEWGMNPNNGNAGF 60  
 DB 1 QVOLLQSAADYKKPGASVKSCTASGYIFTSYDINWVROATGQGLEWGMNPNNGNAGF 60

OY 61 AOKFKRLTLTRDTSTAYMELRLSESDTAIVYCAR 98  
 DB 61 AOKFKRLTLTRDTSTAYMELRLSESDTAIVYCAR 98

RESULT 14

ID ABG78170 standard; Protein; 98 AA.

AC ABG78170;

DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #45.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;

KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;

KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

OS Homo sapiens.

PN WO200259264-A2.

XX 01-AUG-2002.

PF 31-DEC-2001; 2001WO-US49440.

PR 29-DEC-2000; 2000US-0751181.

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

PI Plaksin D, Peretz T;

DR MPI; 2002-619166/66.

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 PT or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favour of other  
 PT cells -

XX Claim 13; Page 168-169; 232pp; English.

PS The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention.

XX Sequence 98 AA;

Query Match 68.2%; Score 449; DB 23; Length 98;  
 Best Local Similarity 84.7%; Pred. No. 8.9e-36;  
 Matches 83; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 1 QVOLLQSAADYKKPGASVKSCTASGYIFTSYDINWVROATGQGLEWGMNPNNGNAGF 60  
 DB 1 QVOLLQSAADYKKPGASVKSCTASGYIFTSYDINWVROATGQGLEWGMNPNNGNAGF 60

OY 61 AOKFKRLTLTRDTSTAYMELRLSESDTAIVYCAR 98  
 DB 61 AOKFKRLTLTRDTSTAYMELRLSESDTAIVYCAR 98

RESULT 15

ID AAR66302 standard; Protein; 117 AA.

AC AAR66302;

DT 25-MAR-2003 (updated)

DT 02-AUG-1995 (first entry)

DE Human immunoglobulin variable heavy chain #8.

XX Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;

KM cosmid; placenta; vector; pJBB1; E.coli; mammalian.

OS Homo sapiens.

PN WO9426895-A1.

XX 24-NOV-1994.

PF 10-MAY-1993; 93WO-JP00603.

PR 10-MAY-1993; 93WO-JP00603.

PA (NISB ) JAPAN TOBACCO INC.

PI Honjo T, Matsuda F;

DR MPI; 1995-006791/01.

PI N-PSDB; AAQ78946.

PT DNA fragment comprising human immunoglobulin Vh genes - for the  
 PT production of human immunoglobulin in mammalian hosts

PS Claim 17; Page 41-42; 130pp; Japanese.

XX Protein sequences (AAR66295-51) are novel human immunoglobulin heavy  
 CC chain sequences encoded by novel isolated genes. The genes  
 CC (AAQ78939-79002) were isolated and cloned from a series of cosmid

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XX PN MO9708320-A1.
XX PD 06-MAR-1997.
XX PF 19-AUG-1996; 96MO-EP036647.
XX PR 18-AUG-1995; 95EP-0113021.
XX PA (MORP-) MORPHOSYS GES PROTEINOPTIMERUNG MBH.
XX PI Ge L, Ilaag V, Knappik A, Moroney S, Pack P, Plueckthun A;
XX WPI; 1997-179277/16.
XX DR N-PSDB; AAT87949.
XX PT Preparation of human derived antibody gene library - using synthetic
PT consensus sequences, and signal consensus antibody gene as universal
PT framework for highly diverse antibody libraries
XX PS Example 1; Fig 5B; 436pp; English.
XX CC The present sequence is the human antibody heavy chain
CC variable region synthetic sequence VH1B, used in the preparation of
CC a human derived antibody gene library.
XX SQ Sequence 120 AA;

Query Match 68.5%; Score 451; DB 18; Length 120;
Best Local Similarity 71.5%; Pred. No. 7.2e-36;
Matches 86; Conservative 9; Mismatches 18; Indels 8; Gaps 2;

QY 1 QVQLVQSGAEVKKPKASVKVCTASGYIFTSYDINWVRQATGCGLEWMGMNPNNSGNAGF 60
DB 1 QVQLVQSGAEVKKPKASVKVCTASGYIFTSYDINWVRQAPGCGLEWMGMNPNNSGNTNY 60
QY 61 AOKFKGRLLITRDSTSTAYMELRLSEEDTAAYVCARCTTLIIWFGAPAY-YDSWGQG 119
DB 61 AOKFGGRVTMTSDTSTAYMELSLRSEDTAAYVCAR-----WCGDGFYAMDYWGQG 113
QY 120 TLV 122
DB 114 TLV 116

RESULT 12
AAY50958
ID AAY50958 standard; Protein; 98 AA.
XX AC AAY50958;
XX DT 23-MAR-2000 (first entry)
XX DE Human FvIII antibody A3-C1 scFv heavy chain protein DP-15.
XX KM Human; heavy chain; antibody; factor VIII; hemostatic;
KM hemophilia A; scFv; A3-C1.
XX OS Homo sapiens.
XX PN MO958680-A2.
XX PD 18-NOV-1999.
XX PF 07-MAY-1999; 99MO-NL00285.
XX PR 08-MAY-1998; 98EP-0201543.
XX PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
XX PI Voorberg JJ, Van Den Brink EN, Turenhout EAM;
XX WPI; 2000-053102/04.

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XX PS New polynucleotide, polypeptide and antibody useful for diagnosing the
XX PT presence of neutralizing antibodies against factor VIII and for
XX PT treatment of hemophilia A patients with these antibodies -
XX PS Example 8; Fig 9A; 61pp; English.
XX CC This invention describes a novel polynucleotide (I) (and complements and
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
CC coding for a human antibody with factor VIII specificity which has
CC hemostatic activity. (I) is useful a primer or probe for detecting the
CC presence of inhibitory antibodies directed against factor VIII. The
CC polypeptides of the invention and the antibodies generated from them
CC are useful in compositions for neutralizing factor VIII inhibiting
CC antibodies in hemophilia A patients. This sequence represents the human
CC factor VIII antibody A3-C1 specific scFv protein DP-15 which is used
CC in the method of the invention.
XX SQ Sequence 98 AA;

Query Match 68.2%; Score 449; DB 21; Length 98;
Best Local Similarity 84.7%; Pred. No. 8.9e-36;
Matches 83; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPKASVKVCTASGYIFTSYDINWVRQATGCGLEWMGMNPNNSGNAGF 60
DB 1 QVQLVQSGAEVKKPKASVKVCTASGYIFTSYDINWVRQATGCGLEWMGMNPNNSGNTGY 60
QY 61 AOKFKGRLLITRDSTSTAYMELRLSEEDTAAYVCAR 98
DB 61 AOKFGGRVTMTSDTSTAYMELSLRSEDTAAYVCAR 98
QY 04-DEC-2002 (first entry)
DB 04-DEC-2002 (first entry)

RESULT 13
ABG91861
ID ABG91861 standard; Protein; 98 AA.
XX AC ABG91861;
XX DT 04-DEC-2002 (first entry)
XX DE Human antibody fragment #45.
XX KM Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KM metastasis; hypervariable region; autoimmune disease; thrombosis;
KM leucemia; inflammatory disease; cardiovascular disease;
KM myocardial infarction; retinopathic disease; abnormal platelet function;
KM sulphated tyrosine-dependent protein-protein interaction.
XX OS Homo sapiens.
XX PN WO200253700-A2.
XX PD 11-JUL-2002.
XX PF 31-DEC-2001; 2001WO-US49442.
XX PR 29-DEC-2000; 2000US-258948P.
XX PR 29-DEC-2000; 2000US-0751181.
XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
XX PI Stanichon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX WPI; 2002-674776/72.
XX PT Novel isolated epitope present on cancer cells and important in
XX PT physiological phenomena such as cell rolling, metastasis and
XX PT inflammation, for treating autoimmune, inflammatory or cardiovascular
XX PT diseases, and cancer -
XX PS Disclosure; Page 246; 310pp; English.

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XX The invention relates to a novel purified preparation of a human  
 CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)  
 CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of  
 CC TIMP-1. The antibody comprises a variable heavy chain (VH)CD3 region and  
 CC a variable light chain (VL)CD3 region. An antibody preparation of the  
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiant  
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting  
 CC activity of a TIMP-1. It is especially useful for ameliorating the  
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver  
 CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary  
 CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic  
 CC pulmonary fibrosis, benign prostatic hypertrophy, lung cancer or colon  
 CC cancer. The antibody is also useful for detecting a TIMP-1 in a test  
 CC preparation, or in diagnosing a disorder in which a TIMP-1 level is  
 CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy  
 CC chain regions of a human anti-TIMP-1 antibody of the invention.

XX Sequence 230 AA;

Query Match 68.7%; Score 452; DB 24; Length 230;  
 Best Local Similarity 70.6%; Pred. No. 1.2e-35;  
 Matches 89; Conservative 11; Mismatches 18; Indels 8; Gaps 2;

OY 1 OVQLQSADYKKGASVKSCTASGYIFTSYDINMVRQATGQGLEMMGMNPNNGNAGF 60  
 1 OVQLVQSGAEVKKPGASVKVSCKASGYFTSYMMHWQAQPGQGLEMMGMNPNNGGNY 60  
 DB 1 AOKFKGRLLTRDSTSTAYMELRLSESDTAIVYCARCDTTLIMFGPAP---YYISW 116  
 61 AOKFKGRVLTMDTSISTAYMELSLRSESDTAIVYCAR---LVGIVGKPKDELILYFDW 116  
 OY 117 GGGTLV 122  
 DB 117 GGGTLV 122

RESULT 10

ABBS7555  
 ID ABB57555 standard; Peptide; 116 AA.

XX ABB57555;

DT 18-MAR-2002 (first entry)

DE HLA-DR-specific protein MS-GPC3 VH sequence.

XX Immunomodulatory human MHC class II antigen-binding protein; HLA;  
 KM human leukocyte antigen; immune system; immunosuppression; antibody;  
 KM major histocompatibility complex; antirheumatic; antiarthritic;  
 KM neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;  
 KM immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis;  
 KM thyrometetic; hepatotropic; immune response suppressor; narcolepsy;  
 KM rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulin;  
 KM Grave's disease; insulin-dependent diabetes; Hashimoto's disease;  
 KM systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;  
 KM transplant rejection; graft versus host disease; pemphigus vulgaris;  
 KM glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;  
 KM irritable bowel disease; Sjogren's syndrome.

OS Homo sapiens.  
 OS Synthetic.

PN WO200187338-A1.

PD 22-NOV-2001.

PF 14-MAY-2001; 2001WO-US15626.

PR 12-MAY-2000; 2000EP-0110063.  
 PR 06-OCT-2000; 2000US-238762P.

XX (GPCB-) GPC BIOTECH AG.

PA (MORP-) MORPHOSIS AG.

PI Nagy Z, Teasar M, Thomassen-Wolf E;

DR WPI: 2002-075289/10.

XX Composition for suppressing immune response, treating diseases of  
 PT immune system, has polypeptide comprising antibody-based  
 PT antigen-binding domain of human composition, which binds antigen  
 PT expressed on a cell surface -  
 XX Example; Fig 15; 139pp; English.

PS The present invention describes a composition (I), comprising a  
 CC polypeptide comprising an antibody-based antigen-binding domain of human  
 CC composition with binding specificity for an antigen expressed on the  
 CC surface of a cell, where treating cells expressing the antigen with the  
 CC polypeptides leads to suppression of an immune response, and the IC50 for  
 CC the suppression of immune response is 1 microm or less. (I) has  
 CC antineumatic, antiarthritic, neuroprotective, dermatological,  
 CC antidiabetic, antipsoriatic, immunosuppressive, hepatotropic activities,  
 CC antithyroid, nephrotropic, thyromimetic and hepatocytic activities, and  
 CC can be used as a suppressor of immune response. (I) is useful for  
 CC suppressing activation or proliferation of a cell of the immune system,  
 CC suppressing IL-2 secretion by a cell, the interaction of a cell of the  
 CC immune system with another cell, immunosuppressing a patient and for  
 CC killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR  
 CC on the surface of the cell, where neither cytotoxic entities nor  
 CC immunological mechanisms are needed to cause or lead to the killing.  
 CC (I) (optionally linked to cytotoxic or immunogenic agent) is useful for  
 CC preparing a pharmaceutical preparation for the treatment of rheumatoid  
 CC arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,  
 CC insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus  
 CC erythematosus, ankylosing spondylitis, transplant rejection, graft versus  
 CC host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,  
 CC glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary  
 CC cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.  
 CC ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in  
 CC the exemplification of the present invention.

XX Sequence 116 AA;

Query Match 68.5%; Score 451; DB 23; Length 116;  
 Best Local Similarity 70.5%; Pred. No. 6.9e-36;  
 Matches 86; Conservative 10; Mismatches 16; Indels 10; Gaps 1;

OY 1 OVQLQSADYKKGASVKSCTASGYIFTSYDINMVRQATGQGLEMMGMNPNNGNAGF 60  
 1 OVQLVQSGAEVKKPGASVKVSCKASGYFTSYMMHWQAQPGQGLEMMGMNPNNGGNY 60  
 DB 1 AOKFKGRLLTRDSTSTAYMELRLSESDTAIVYCARCDTTLIMFGPAPYYDSMGQGT 120  
 61 AOKFKGRVLTMDTSISTAYMELSLRSESDTAIVYCARLSTRM-----DPMGQGT 110  
 OY 121 LV 122  
 DB 111 LV 112

RESULT 11

AAW27551  
 ID AAW27551 standard; Protein; 120 AA.

AC AAW27551;

DT 23-JAN-1998 (first entry)

DE Human Ab heavy chain variable region VH1B consensus.

XX Human; antibody; preparation; library; VH1B; variable region;  
 KM heavy chain; consensus.

OS Homo sapiens.





DR WPI; 2002-114799/15.  
 XX  
 XX Antibodies against B lymphocyte Stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 PT  
 PS Claim 1; Page 1533-1534; 3148pp; English.  
 XX  
 XX This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte Stimulator (BLYS) polypeptides. BLYS is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BLYS. The antibodies bind to BLYS  
 CC and so may be used to detect and quantitate the presence of BLYS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BLYS. They may also be  
 CC administered to treat diseases associated with aberrant BLYS expression  
 CC and actively such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX  
 XX Sequence 247 AA:  
 SQ  
 Query Match 70.7%; Score 465; DB 23; Length 247;  
 Best Local Similarity 72.2%; Pred. No. 7.1e-37;  
 Matches 91; Conservative 9; Mismatches 16; Indels 10; Gaps 2;  
 QY 1 QVQLQSGADYVKKPGASVSVCTASGYIFTSYDINMVRQATGQGLEWMGMNPNNGNAGF 60  
 DB 1 QVQLVQSGAEVKKPGASVSVCKASGYITFTYGISVRQAPQGLEWMGMNPNNGNAGY 60  
 QY 61 AOKFKGRLLTTRDTSTSTAYMELRLRLESDTAIVYVCARCD---TTLTIWGPAPYDSW 116  
 DB 61 AOKFGQGVLTMTNTSISTAYMELSLRSEDTAVYVCARQGYDILTGVMFDP-----W 114  
 QY 117 GGCTLV 122  
 DB 115 GGCTLV 120  
 DB  
 RESULT 6  
 AAB62747  
 ID AAB62747 standard; Protein; 120 AA.  
 XX  
 AC AAB62747;  
 XX  
 DT 03-APR-2001 (first entry)  
 XX  
 DE Human HIV-1 monoclonal antibody SEQ ID NO: 46.  
 XX  
 KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;  
 KW envelope glycoprotein; gp120; diagnosis.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200100678-A1.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 23-JUN-2000; 2000MO-US17327.  
 XX  
 PR 30-JUN-1999; 99US-0141701.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PI  
 PT Wackins BA, Reitz MS;  
 XX  
 DR WPI; 2001-112438/12.  
 DR N-PSDB; AAF29048.  
 DR

XX  
 XX Novel human monoclonal antibody immunoreactive with human  
 PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1  
 PT in biological sample and providing passive immunotherapy to HIV-1  
 PT infected mammal -  
 XX  
 PS Claim 1; Page 51-52; 81pp; English.  
 XX  
 XX The present invention provides the protein and coding sequences for the  
 CC variable regions of human monoclonal antibodies which are immunoreactive  
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.  
 CC These can be used in diagnosis and therapy of HIV-1 infection.  
 XX  
 XX Sequence 120 AA;  
 SQ  
 Query Match 70.1%; Score 461.5; DB 22; Length 120;  
 Best Local Similarity 73.2%; Pred. No. 7e-37;  
 Matches 90; Conservative 10; Mismatches 14; Indels 9; Gaps 2;  
 QY 1 QVQLQSGADYVKKPGASVSVCTASGYIFTSYDINMVRQATGQGLEWMGMNPNNGNAGF 60  
 DB 2 EVQLQSGAEVKKPGASVSVCKASGYITFTSYDINMVRQATGQGLEWMGMNPNNGNAGY 61  
 QY 61 AOKFKGRLLTTRDTSTSTAYMELRLRLESDTAIVYVCARCDTTLTIWGPAPYDSW-WGQ 119  
 DB 62 AOKFGQGVLTMTNTSISTAYMELSLRSEDTAVYVCAR-----QSSRGVWVSWGQ 113  
 QY 120 TLV 122  
 DB 114 TLV 116  
 DB  
 RESULT 7  
 AAB45710  
 ID AAB45710 standard; Protein; 248 AA.  
 XX  
 AC AAB45710;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human Blys binding scFv SEQ ID 1721.  
 XX  
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200202641-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 15-JUN-2001; 2001WO-US19110.  
 XX  
 PR 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-876248P.  
 PR 21-MAR-2001; 2001US-877379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 PI  
 PT Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX  
 DR WPI; 2002-114799/15.  
 XX  
 XX Antibodies against B lymphocyte Stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 PT  
 XX

CC proteins and antibodies to the proteins are useful for the prevention,  
 CC treatment and diagnosis of colon disorders, such as colon cancer. The  
 CC polynucleotides may be used in diagnostics and research, such as for  
 CC chromosome identification, and as hybridization probes. The proteins  
 CC may also be used to prevent diseases such as neural disorders, immune  
 CC system disorders, muscular disorders, reproductive disorders,  
 CC gastrointestinal disorders, wounds, renal disorders, infectious  
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and  
 CC AAB54007 represent sequences used in the exemplification of the present  
 CC invention.

CC Sequence 146 AA;

Query Match 71.1%; Score 468; DB 21; Length 146;

Best Local Similarity 74.6%; Pred. No. 2e-37;

Matches 91; Conservative 10; Mismatches 19; Indels 2; Gaps 1;

QY 1 QVQLQSADPVKPKGASVSKSCSTASGYIFTSYDINMVRQATGQGLEMGMMNNSGNAGF 60  
 DB 25 QVQLVSGAEVKKPKGASVSKSCASGYFTFSYDINMVRQATGQGLEWGMNPNNSANTGY 84

QY 61 AOKFKRLTLTRDPTSTSTAYMELRLSEEDTAVYYCARCDTTLIMFGAPAPYDSWGQGT 120  
 DB 85 AOKFGQRTVMTNRTSTISTAYMELSLRSEDTAVYYCARXRMRLL--GMMDFDYWGQGT 142

QY 121 LV 122

DB 143 LV 144

RESULT 4  
 ABBP44916  
 ID ABBP44916 standard; Protein; 247 AA.

XX ABBP44916;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 927.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

XX Anticodles against B lymphocyte Stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 XX  
 PS Claim 1; Page 1508-1509; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABBP43990-ABB47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.

XX Sequence 247 AA;

Query Match 70.7%; Score 465; DB 23; Length 247;

Best Local Similarity 72.2%; Pred. No. 7.1e-37;

Matches 91; Conservative 9; Mismatches 16; Indels 10; Gaps 2;

QY 1 QVQLQSADPVKPKGASVSKSCSTASGYIFTSYDINMVRQATGQGLEMGMMNNSGNAGF 60  
 DB 1 QVQLVSGAEVKKPKGASVSKSCASGYFTFSYDINMVRQATGQGLEWGMNPNNSANTGY 60

QY 61 AOKFKRLTLTRDPTSTSTAYMELRLSEEDTAVYYCARCD---TTLIMFGAPAPYDSW 116  
 DB 61 AOKFGQRTVMTNRTSTISTAYMELSLRSEDTAVYYCARQGYDILTGYNMFD-----W 114

QY 117 GQGTIV 122

DB 115 GKGTIV 120

RESULT 5  
 ABBP44937  
 ID ABBP44937 standard; Protein; 247 AA.

XX ABBP44937;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 948.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

PT treatment of hemophilia A patients with these antibodies -  
 XX  
 PS Example 8; Fig 9B; 61pp; English.  
 XX  
 CC This invention describes a novel polynucleotide (I) (and complements and  
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence and  
 CC coding for a human antibody with factor VIII specifically which has  
 CC hemostatic activity. (I) is useful as a primer or probe for detecting the  
 CC presence of inhibitory antibodies directed against factor VIII. The  
 CC polypeptides in the invention and the antibodies generated from them  
 CC are useful in compositions for neutralizing factor VIII inhibiting  
 CC antibodies in hemophilia A patients. This sequence represents a fragment  
 CC of the human factor VIII antibody heavy chain variable region protein B38  
 CC which is used in the method of the invention.  
 XX  
 SQ Sequence 122 AA:  
 Query Match 100.0%; Score 658; DB 21; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-56;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 OVQLQSAADVKKPGASVSVCTASGYFTSYDINMVRQATGCGLEMMGMNPNNGNAGF 60  
 Db 1 OVQLQSAADVKKPGASVSVCTASGYFTSYDINMVRQATGCGLEMMGMNPNNGNAGF 60  
 QY 61 AOKFKGRLTLTRDSTSTAYMELRLLESEDTAVVYCARCDTTLIMFGPAPYDSWGQGT 120  
 Db 61 AOKFKGRLTLTRDSTSTAYMELRLLESEDTAVVYCARCDTTLIMFGPAPYDSWGQGT 120  
 QY 121 LV 122  
 Db 121 LV 122  
 DE Human FVIII antibody A3-C1 scFv heavy chain protein B38.  
 XX  
 KW Human; heavy chain; antibody; factor VIII; hemostatic;  
 KW hemophilia A; scFv; A3-C1.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9558680-A2.  
 XX  
 PD 18-NOV-1999.  
 XX  
 PF 07-MAY-1999; 99WO-NL00285.  
 XX  
 PR 08-MAY-1998; 98EP-0201543.  
 XX  
 PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.  
 XX  
 PI Vootberg JJ, Van Den Brink EN, Turenhout EM;  
 XX  
 DR WPI; 2000-053102/04.  
 XX  
 PT New polynucleotide, polypeptide and antibody useful for diagnosing the  
 PT presence of neutralizing antibodies against factor VIII and for  
 PT treatment of hemophilia A patients with these antibodies -  
 XX  
 PS Example 8; Fig 9A; 61pp; English.  
 XX  
 CC This invention describes a novel polynucleotide (I) (and complements and  
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence  
 CC coding for a human antibody with factor VIII specificity which has  
 CC hemostatic activity. (I) is useful as a primer or probe for detecting the

CC presence of inhibitory antibodies directed against factor VIII. The  
 CC polypeptides of the invention and the antibodies generated from them  
 CC are useful in compositions for neutralizing factor VIII inhibiting  
 CC antibodies in hemophilia A patients. This sequence represents the human  
 CC factor VIII antibody A3-C1 specific scFv protein B38 which is used  
 CC in the method of the invention.  
 XX  
 SQ Sequence 122 AA:  
 Query Match 95.9%; Score 631; DB 21; Length 122;  
 Best Local Similarity 96.7%; Pred. No. 3.4e-53;  
 Matches 118; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 OVQLQSAADVKKPGASVSVCTASGYFTSYDINMVRQATGCGLEMMGMNPNNGNAGF 60  
 Db 1 OVQLQSAADVKKPGASVSVCTASGYFTSYDINMVRQATGCGLEMMGMNPNNGNAGF 60  
 QY 61 AOKFKGRLTLTRDSTSTAYMELRLLESEDTAVVYCARCDTTLIMFGPAPYDSWGQGT 120  
 Db 61 AOKFKGRLTLTRDSTSTAYMELRLLESEDTAVVYCARCDTTLIMFGPAPYDSWGQGT 120  
 QY 121 LV 122  
 Db 121 LV 122  
 DE Human colon cancer antigen protein sequence SEQ ID NO:1050.  
 XX  
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KW identification; cytostatic; cardioactive; neuroprotective; vulnary;  
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;  
 KW nephrotropic; antineoplastic; antibacterial; gene therapy; wound;  
 KW neural disorder; immune system disorder; muscular disorder;  
 KW reproductive disorder; gastrointestinal disorder; renal disorder;  
 KW infectious disease; cardiovascular disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055351-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US05883.  
 XX  
 PR 12-MAR-1999; 99US-0124270.  
 XX  
 PA (HUMA-) HUMANA GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI; 2000-587534/55.  
 DR N-PSDB; AAC98267.  
 XX  
 PT Colon cancer associated gene sequences, referred to as colon cancer  
 PT antigens, useful for the treatment, prevention, and diagnosis of colon  
 PT disorders such as colon cancer -  
 XX  
 PS Claim 11; Page 1631; 2104pp; English.  
 XX  
 CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,  
 CC called human colon cancer antigens, given in AAB53334 to AAB54006. The  
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;  
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,  
 CC vulnary, nephrotropic, antineoplastic and antibacterial activities, and  
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,

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# OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 39.2461 Seconds  
(without alignments)  
493.415 Million cell updates/sec

Title: US-09-674-752-40

Perfect score: 1 QVQLQSGADVKKPKGASVKV.....LLIWFGPAPYDSWGQTLV 122

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing filter 45 summaries

Database: A\_Geneseq\_19Jun03.\*

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20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	658	100.0	122	21	AA150966 Human FVIII antibo
2	631	95.9	122	21	AA150959 Human FVIII antibo
3	468	71.1	146	21	AA153510 Human colon cancer
4	465	70.7	247	23	ABP44916 Human BLYS binding
5	465	70.7	247	23	ABP44937 Human BLYS binding
6	461.5	70.1	120	22	AA1862747 Human HIV-1 monocl
7	453.5	68.9	248	23	ABP45710 Human BLYS binding
8	452.5	68.8	245	22	AA1867619 Human Leukocyte an
9	452	68.7	230	24	ABR01514 Human anti-TIMP-1

10	451	68.5	116	23	AB157555 HLA-DR-specific pr
11	451	68.5	120	18	AA127551 Human Ab heavy cha
12	449	68.2	98	21	AA150958 Human FVIII antibo
13	449	68.2	98	23	ABG1961 Human antibody fra
14	449	68.2	98	23	ABG78170 Human Fv molecule
15	449	68.2	117	16	AB166302 Human immunoglobul
16	449	68.2	251	23	ABP45378 Human BLYS binding
17	447.5	68.0	120	24	ABP44919 Human BLYS binding
18	447	67.9	100	23	ABJ18673 Antibody library r
19	447	67.9	130	24	ABJ18719 Antibody library r
20	446	67.8	247	23	ABP45718 Human BLYS binding
21	445.5	67.7	199	20	AA134302 IGM antibody CEM 1
22	445.5	67.7	251	23	ABP45575 Human BLYS binding
23	444	67.5	241	23	ABP46020 Human BLYS binding
24	443.5	67.4	251	23	ABP45859 Human BLYS binding
25	443	67.3	249	23	ABP45624 Human BLYS binding
26	442.5	67.2	146	18	AA122841 Human anti-tumour
27	442.5	67.2	248	23	ABP45461 Human BLYS binding
28	442	67.2	228	23	ABR01526 Human anti-TIMP-1
29	442	67.2	241	23	ABP45937 Human BLYS binding
30	441.5	67.1	248	23	ABP44882 Human BLYS binding
31	441.5	67.1	248	23	ABP45860 Human BLYS binding
32	441.5	67.1	251	23	ABP45858 Human BLYS binding
33	441.5	67.1	470	23	AA174286 Anti-human AL10 m
34	440.5	66.9	251	23	ABP45727 Human BLYS binding
35	440.5	66.9	476	20	AA188464 Monoclonal antibod
36	439.5	66.8	251	23	ABP45551 Human anti-TIMP-1
37	438.5	66.6	221	24	ABR01537 Human anti-TIMP-1
38	438.5	66.6	251	23	ABP45861 Human BLYS binding
39	438	66.6	238	23	ABP45886 Human BLYS binding
40	438	66.6	249	23	ABP44908 Human BLYS binding
41	438	66.6	250	23	ABP45549 Human BLYS binding
42	437.5	66.5	133	19	AA179228 Heavy chain variab
43	437.5	66.5	248	23	ABP45866 Human BLYS binding
44	437.5	66.5	250	23	ABP45711 Human BLYS binding
45	437.5	66.5	251	23	ABP45867 Human BLYS binding

## ALIGNMENTS

RESULT 1	AA150966	AA150966 standard; Protein: 122 AA.
XX	AA150966	
AC	AA150966	
XX	23-MAR-2000	(first entry)
XX		
DE	Human FVIII antibody heavy chain variable region B38 protein fragment.	
XX		
KW	Human; heavy chain; antibody; factor VIII; hemostatic; variable region;	
KM	hemophilia A.	
XX		
OS	Homo sapiens.	
XX		
PN	W0958680-A2.	
XX		
PD	18-NOV-1999.	
XX		
XX		
PF	07-MAY-1999;	99WO-NL00285.
XX		
PR	08-MAY-1998;	98BP-0201543.
XX		
PA	(SAND-) STICHTING SANQUIN BLOEDVOORZIENING.	
XX		
PI	Voorberg JJ, Van Den Brink EN, Turenhout EM;	
XX		
DR	WPI: 2000-053102/04.	
XX		
DR	N-PSDB; AA133863.	
XX		
XX	New polynucleotide, polypeptide and antibody useful for diagnosing the	
PT	presence of neutralizing antibodies against factor VIII and for	

KA SAITO T., OKAZAKI

Search completed: December 30, 2003, 11:01:07  
Job time : 29.7319 secs

Qy		121 LV 122	
Db		135 MV 136	
 RESULT 11			
ID	095978	PRELIMINARY;	PRT; 157 AA.
AC	095978;		
DT	01-MAY-1999 (TREMBLrel. 10, Created)		
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	VH1 protein precursor (Fragment).		
GN	VH1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
CX	NCBI_TaxID=9606;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
PC	TISSUE=Peripheral blood.		
RA	Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,		
RA	Bohlen H., Diehl V., Wolf J.;		
RT	"Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a		
RT	patient with mixed cellularly Hodgkin's disease is associated with		
RT	somatic mutations within the untranslated regions of rearranged and		
RT	class switch recombined Ig genes."		
RL	Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ005570; CA006599.1; -		
DR	HSSP; P01772; 2PB4.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_v.		
DR	Pfam; PF00047; IG_1.		
DR	SMART; SMO0406; IGV_1.		
DR	PROSITE; PSS0835; IG-LIKE; 1.		
KW	Signal.		
FT	SIGNAL	1 21	POTENTIAL.
FT	NON_TER	157 157	
SO	SEQUENCE	157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;	
 Query Match 55.9%; Score 367.5; DB 4; Length 157; Best Local Similarity 59.0%; Pred.No. 8; 7e-32; Matches 72; Conservative 15; Mismatches 30; Indels 5; Gaps 1			
Qy	1 QVQLQSADYVKPKGASVKSCTASGYIFTSYDINMVRQATSGLEMMGMNPNSGNAGF 60		
Db	20 QVOLVGSAELKRPASVKNCKISGYFTSYIHMYQPRQGLEMNGIGPGVGSITMC 79		
Qy	61 AQKFGRLLTLTRDSTSTAVWELRLESEDTAVVYCARTDLLIWGPAPPYDSWGQT 120		
Db	80 AEKFGRLTMRNTSTTVYMELSLRFEDTAIVFCGRGR-----WMSGNYNGHWGQT 134		
Qy	121 LV 122		
Db	135 PV 136		
 RESULT 12			
ID	08VCX4	PRELIMINARY;	PRT; 489 AA.
AC	08VCX4;		
DT	01-MAR-2002 (TREMBLrel. 20, Created)		
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Hypothetical 53.2 kDa protein.		
GN	IGH-VU558 OR AI893585.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
CX	NCBI_TaxID=10090;		
RN	[1]		
RC	SEQUENCE FROM N.A.		

```
RC      TISSUE=Colon;
RA      Strausberg R.;
RL      Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC018322; AAH18322.1; -.
DR      MGD; MGI:96486; IGH-V0558.
DR      InterPro; IPRO07110; IG_1like.
DR      InterPro; IPRO03006; IG_MHC.
DR      InterPro; IPRO03596; IG_V.
DR      Pfam; PF00047; Ig; 4.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PSS0835; IG_LIKE; 4.
DR      PROSITE; PS00290; IG_MHC; 2.
KW      Hypothetical protein.
SQ      SEQUENCE   489 AA; 53208 MW; CC65B1194DAFEF2C CRC64;

Query Match          54.9%; Score 361.5; DB 11; Length 489;
Best Local Similarity 55.9%; Pred. No. 1.5e-30;
Matches    71; Conservative 19; Mismatches    26; Indels    11; Gaps    3

QY      1 QVQLTSGAADVKKPKGASVKRSCSTSGYIFTSYDINWVRQAATGGLEMGKMNPNNSGNAGF 60
       |||||:::||:|||||:::||:|||||:::||:|||||:::||:|||||:::||:|||||
DB      20 KVLQDSGAELVKGASVKRSCSKASGYTFSDYFLHWIKRSGOGLEWIGMNPSSGSITKF 79
QY      61 AOKFKGLTLTRPDSTSTAWNELRLSESDPAVVYCARCDT-----LLIWFGPAPYDS 115
       |||||:::||:|||||:::||:|||||:::||:|||||:::||:|||||
DB      80 NEKFKDATLTADKSSITTVMDLSRLSDESDAVYFCARHEBRGNYDGSLAF-----VI-- 133

QY      116 WQGQTIV 122
       |||||
DB      134 WQGQTIV 140

RESULT 13
Q920E8 PRELIMINARY; PRT; 120 AA.
AC      Q920E8
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Pterin-mimicking anti-idiotope heavy chain variable region
DE      (Fragment).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Actin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT      "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed
RT      in Mammalian Cells.";
RL      Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF307936; AAL09420.1; -.
DR      InterPro; IPRO07110; IG_1like.
DR      InterPro; IPRO03006; IG_MHC.
DR      InterPro; IPRO03596; IG_V.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PSS0835; IG_LIKE; 1.
DR      NON_TER
FT      NON_TER 1
SQ      SEQUENCE   120 AA; 13204 MW; DC4834AB1DBE6F3C CRC64;

Query Match          54.8%; Score 360.5; DB 11; Length 120;
Best Local Similarity 55.3%; Pred. No. 3.6e-31;
Matches    66; Conservative 25; Mismatches    23; Indels    7; Gaps    2

QY      1 QVQLTSGAADVKKPKGASVKRSCSTSGYIFTSYDINWVRQAATGGLEMGKMNPNNSGNAGF 60
       |||||:::||:|||||:::||:|||||:::||:|||||:::||:|||||
DB      1 EVQLQQSGPELEKPGASVKISKCKASGYFTSYNNMMWVQSNGKSLEWIGNDIPYGCTSY 60
QY      61 AOKFKGLTLTRPDSTSTAWNELRLSESDPAVVYCARCDTLLIWPFPAP-YYDSWGCG 119
       |||||:::||:|||||:::||:|||||:::||:|||||
DB      61 NORKRGATLTVDKSSSTAAMQLSLTYSDDSAVYCA-----VLYGNSPAMEFAVYWGCG 114
```

Oy	61 AOKKGLTLTRDSTSTAYMELRLSESDTAVVYCARCDPTLLIMFGAPAYDSMGQT	120
Dd	63 NEKKKGATLSLVSKSSSTAYMELTRLTSBDSNAVTCAGDY-----RRFPDMGQT	115
Oy	121 LV 122	
Dd	116 TV 117	

## RESULT 8

ID	Q9JUL89	PRELIMINARY	PRT	116 AA
AC	Q9JUL89			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment)			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96277139; PubMed=9614934;			
RA	Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
DR	EMBL; AF035025; AAD56261.1; -			
DR	HSSP; P01810; 2FBJ.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00406; IGV_1.			
DR	PROSITE; PSS0835; IG_LIKE; 1.			
FT	NON_TER 1 1			
FT	NON_TER 116 116			
SQ	SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;			
Query Match				
Best Local Similarity 64.4%; Pred. No.2,1e-33;				
Matches 76; Conservative 14; Mismatches 22; Indels 6; Gaps 1;				
Qy	5 IQSADVKKPGASVYVSTCAGSYFTSYDINVRQATSGLEWGMNPNNGNAFPAQK 64			
Db	1 VQSGAEVKKPGSSVKVSCASGCTPSSVAISWVRQAPGGGLEWGRITIPILGIANVAKKF 60			
Qy	65 KRRLILTRDTSTSTAYMELRLRESEDTAVYTCARCDTLLWFGAPPYDSKQCTLV 122			
Db	61 QQRVITTDKSTSTAYMELSLRSEDTAVYVCASSN-----WGPYWFIDLNGRGLTV 112			
RESULT 9				
ID	Q9GYZ2	PRELIMINARY	PRT	119 AA.
AC	Q9GYZ2			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Monoclonal anti-idiotypic antibody NP30 heavy chain variable region (Fragment)			
OS	Schistosoma japonicum (Blood fluke)			
OC	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.			
OX	NCBI_TaxId=6182;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Song X.T., Feng Z.O., Guan X.H.;			
RT	"Amplification, cloning and sequence analysis of the heavy chain variable region gene of monoclonal anti-idiotypic antibody NP30 of			

```

RT   Schistosoma japonicum";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR   EMBL; AF282622; AAC01452.1; -.
DR   HSSP; P01772; 2F84.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PSS0835; IG_LIKE; 1.
FT   NON_TER
FT   NON_TER
FT   NON_TER
SQ   SEQUENCE
      119 AA; 13567 MW; BA893873FDF5FA6AB CRC64;

Query Match          56.9%; Score 374.5; DB 5; Length 119;
Best Local Similarity 57.0%; Pred. No. 1,1e-32;
Matches 73; Conservative 15; Mismatches 21; Indels 19; Gaps 2.

```

## RESULT 10

```

096Ga6 ID 096Ga6 PRELIMINARY; PRT; 614 AA.
AC 096Ga6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISUE=B-cell;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL, BC009851, AA09851.1; -
DR InterPro; IPR000005; HTTARAC.
DR InterPro; IPR007110, IG_1like.
DR InterPro; IPR003006, IG_MHC.
DR InterPro; IPR003596, IG_V.
DR Pfam; PF00047, Ig_5.
DR SMART, SM00406, IGV_1.
DR PROSITE, PS00041; HTH_ARAC_FAMILY_1, 1.
DR PROSITE, PS08835, IG_LIKE, 5.
DR PROSITE, PS00290, IG_MHC, 3.
KW Hypothetical protein.
SQ
SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 56.8%; Score 373.5; DB 4; Length 614;
Best Local Similarity 59.8%; Pred. No. 1e-31; 26; Indels 5; Gaps 2
Matches 73; Conservative 18; Mismatches

QY 1 QVLLQSSADYVKPPASVVSCTAGYIFTSYDINMVRQATQGLQEMNGMNNPNSGNAGF 60
DB 20 QMQLVQSGAEVKKVTKSSVYKSKAGYFTTYIYLYMVAQPGQALQEMNGMIIIPFGNTNY 79
QY 61 AQKFKGRLLTRDTSTSTAYMELRLSEDTAVVYCARCDTLLIWFQAPYDYSKQGT 120
DB 80 AQKFPQDRVLTITRDRSMNTAYMELSLRSEDTAVVYCARQYS--SW---DDAFIDWGGQT 134

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Db	1	EVQLVESGAEVKKPKGASVKVSCAKSGYFTFTGYVMHWVQAPOQGLEMMGMINPNSMTNN	60
Qy	61	AQKRRGRLLTRDSTSTAYMELRLSEEDTAVYCARCDTLLIFGPAPYDSWGCGT	120
Db	61	AQKFGKRVMTKDTISISTAYMELSLRSDDTAVYCARCG-----GRGLMFPDWGCGT	113
Qy	121	LV 122	
Db	114	LV 115	
RESULT 2			
ID	Q9UL95	PRELIMINARY;	PRT; 125 AA.
AC	Q9UL95;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98277139; PubMed=9614934;		
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,		
RA	Young D.C.;		
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal		
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).		
DR	EMBL; AF035019; AAD56255.1; -.		
DR	HSSP; P01810; 2FBJ.		
DR	InterPro: IPR007110; Ig-like.		
DR	InterPro: IPR003006; Ig_MHC.		
DR	InterPro: IPR003596; Ig_V.		
DR	PIfam: PF00047; Ig; 1.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PSS0835; IG_LIKE; 1.		
FT	NON_TER 1		
FT	NON_TER 125		
SQ	SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488BAC CRG64;		
Query Match			
Best Local Similarity 63.9%; Score 420.5; DB 4; Length 125;			
Matches	80; Conservative	15; Mismatches	26; Indels 1; Gaps 1
Qy	1	QVQLQSGADPKKPGASVYSCTASGIFTSYDINNVROATGCGLEMMGMNPNNSGNAG	60
Db	1	EVQLVESGAEVKKPKGASVKVSCAKSGYFTFTGYVMHWVQAPOQGLEMMGMINPNSGTTY	60
Qy	61	AQKRRGRLLTRDSTSTAYMELRLSEEDTAVYCARCDTLLIFGPAPYDSWGCGT	120
Db	61	AQKFGKRVMTKDTISISTAYMELSLRSDDTAVYCARSGGGRI-AAAGADPDWGGT	119
Qy	121	LV 122	
Db	120	MW 121	
RESULT 3			
ID	Q9UL92	PRELIMINARY;	PRT; 124 AA.
AC	Q9UL92;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.		

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OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035022; AAD56258.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; I9_1ike.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_v.
DR Pfam; PF000047; I9_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IGV-LIKE; 1.
FT NON TER 1
FT TER 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 63.2%; Score 416; DB 4; Length 124;
Best Local Similarity 66.1%; Pred. No. 3.9e-37;
Matches 82; Conservative 16; Mismatches 20; Indels 6; Gaps 2;

QY 1 OVOLLQSAADYKKKGAAYKVSCTASGYTFPSYDINMVRQATGQGLEMMGMNPNSGNAGF 60
DB 1 EVOLVESGAEEYKKKGASVYKSCAKSGYTFPSYTMWVRQAGQGLEMMGIINPSGSGTSY 60
QY 61 AQQEKGRLLTRDPDSTFAVYVELRLLESEDPVAVYCARCDTLLIWPFPARY--YDSWQ 118
DB 61 AQQKGRATMTRDSTIVYVELSLSESDPAVYVYCARG----LYVVPAAPFSPDYVQ 116

QY 119 GTLV 122
DB 117 GTLV 120

RESULT 4
Q8WY24 PRELIMINARY; PRT; 497 AA.
AC Q8WY24;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE SMC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
RT "Identification and characterization of SMC66, a Ig-like gene which is
RL down-regulated in colorectal cancer";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF283666; AAL36987.1; -.
DR InterPro; IPR007110; I9_1like.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_v.
DR Pfam; PF00047; I9_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IGV-LIKE; 4.
DR PROSITE; PS00290; IGV_MHC; 1.
SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A63E5 CRC64;

Query Match 62.4%; Score 410.5; DB 4; Length 497;
Best Local Similarity 65.6%; Pred. No. 8e-36; Indels 1; Gaps 1
Matches 80; Conservative 13; Mismatches 28; Indels 1; Gaps 1

QY 1 OVOLLQSAADYKKKGAAYKVSCTASGYTFPSYDINMVRQATGQGLEMMGMNPNSGNAGF 60
DB 20 QOOLQSGAEAYTRKPGASVYKSCAKSGYTFIADIMWVRQAPQGLEMMGMNPNPQNTGF 79

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RL Nucleic Acids Res. 8:4839-4840(1980).
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A93708: GYMS11.
DR HSSP: P01810: 2FBJ.
DR InterPro: IPR007110: Ig-like.
DR InterPro: IPR003006: Ig_MHC.
DR InterPro: IPR003596: Ig_V.
DR Pfam: PF00047: Ig_1.
DR SMART: SM00406: IGV; 1.
DR PROSITE: PS50835: IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC656ED0BF CRC64;

Query Match 51.1%; Score 336.5; DB 1; Length 121;
Best Local Similarity 50.8%; Pred. No. 2.8e-29;
Matches 61; Conservative 23; Mismatches 31; Indels 5; Gaps 1;

Qy 1 OVQLQSADVKKPGASVYVSGTASGYFTSYDINMVRQATGQGLEMMGMNPNSGNAQF 60
Db 1 EOQLQSGAEIVRPGSVKISCAAGYFTTNWIGWKEPBGLEWIGDIIYPGGFTNY 60

Qy 61 AQKFKGRLLTRDTSTSTAYMELRLRLESEDTAVVYVCARCDTLLIFGPAPYDSWGQST 120
Db 61 NNLMKGKALTITDTSSTAYIQLSLTSDSAIYHCARG-----IYNSSPFDSWGQST 115

RESULT 15
HV11 MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Peckind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00539; AAA8172.1; -.
DR PIR: A02038; G2MS43.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047: Ig_1.
DR SMART: SM00406: IGV; 1.
DR PROSITE: PS50835: IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19

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FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 50.6%; Score 333; DB 1; Length 137;
Best Local Similarity 54.2%; Pred. No. 7.8e-29;
Matches 65; Conservative 17; Mismatches 30; Indels 8; Gaps 1;

Qy 1 OVQLQSADVKKPGASVYVSGTASGYFTSYDINMVRQATGQGLEMMGMNPNSGNAQF 60
Db 20 OVQLQDPGAEFVKPGASVYLSCKASGYFTSTLMVMNVRPGRGLEWIGRIDPNSGCTTY 79

Qy 61 AQKFKGRLLTRDTSTSTAYMELRLRLESEDTAVVYVCARCDTLLIFGPAPYDSWGQST 120
Db 80 NEHFRSKALTITDKPSSSTAYVQLSLTSDSAVYVCAR-----YRLGRYFDYWGQST 131

Search completed: December 30, 2003, 10:55:53
Job time : 7.54102 secs

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QY 61 AOKFKGRLTLTRDSTSTAYMELRLSEEDTAVVYCARCDTTLIIFGPAPYDSWGCGT 120  
 DB 61 AOKFGGRLTLTRDSTSTAYMELRLSEEDTAVVYCARCDTTLIIFGPAPYDSWGCGT 112  
 QY 121 LV 122  
 DB 113 LV 114

## RESULT 12

HVS2\_MOUSE  
 ID HVS2\_MOUSE STANDARD; PRT; 117 AA.  
 AC P06327;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region VH58 A1/A4 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8509340; PubMed=2578321;  
 RA Yancopoulos G.D., Alt F.W.;  
 RT "Developmentally controlled and tissue-specific expression of  
 RL Cell 40:271-281 (1985).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC DR EMBL\_M13787; AAA18499.1; -  
 CC PIR: A02029; HYMSA1.  
 CC HSSP: P01810; 2FBJ.  
 CC InterPro: IPR007110; Ig\_Like.  
 CC InterPro: IPR003006; Ig\_MHC.  
 CC InterPro: IPR003596; Ig\_V.  
 CC Pfam: PF00047; Ig\_1.  
 CC SMART: SM00406; IGV; 1.  
 CC PROSITE: PS50835; Ig\_Like; 1.  
 CC Immunoglobulin V region; Signal.  
 CC FT SIGNAL 1 19  
 CC FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH58 A1/A4.  
 CC FT DOMAIN 20 49 FRAMEWORK-1.  
 CC FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 CC FT DOMAIN 55 68 FRAMEWORK-2.  
 CC FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 CC FT DOMAIN 86 117 FRAMEWORK-3.  
 CC FT DISULFID 41 115 BY SIMILARITY.  
 CC FT NON TER 117 117  
 CC SQ SEQUENCE 117 AA; 12971 MW; 880BC13885DFC9D CRC64;

Query Match 51.8%; Score 341; DB 1; Length 117;  
 Best Local Similarity 63.3%; Pred. No. 9e-30;  
 Matches 62; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 QVQLQSGADYKPKGASVKSCCTASGYSIFTSYDINVRQATGGLTGMGMNPNSSNAGF 60  
 DB 20 QVQLQSGPELVKPGALVKISCKASGYTFTSYDINVKRPPGGLGIMIGYDGSTYK 79  
 QY 61 AOKFKGRLTLTRDSTSTAYMELRLSEEDTAVVYCAR 98  
 DB 80 NEKFKGRLTLTRDSTSTAYMELRLSEEDTAVVYCAR 117

RESULT 13

HVS0\_MOUSE  
 ID HVS0\_MOUSE STANDARD; PRT; 120 AA.  
 AC P06329;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region AC38 15.3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=84182519; PubMed=6201362;  
 RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;  
 RT "A V region determinant (idiotope) expressed at high frequency in B  
 RT lymphocytes is encoded by a large set of antibody structural genes."  
 RL EMO J 3:517-523 (1984).  
 DR PIR: A02037; MEMS15.  
 DR HSSP: P01810; 2FBJ.  
 DR InterPro: IPR007110; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; Ig\_Like; 1.  
 CC Immunoglobulin V region.  
 CC FT DOMAIN 1 98 V SEGMENT.  
 CC FT DOMAIN 99 105 D SEGMENT.  
 CC FT DOMAIN 106 120 J SEGMENT.  
 CC FT DISULFID 22 96 BY SIMILARITY.  
 CC FT NON TER 120 120  
 CC SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 51.5%; Score 339; DB 1; Length 120;  
 Best Local Similarity 53.3%; Pred. No. 1.5e-29;  
 Matches 65; Conservative 18; Mismatches 33; Indels 6; Gaps 1;

QY 1 QVQLQSGADYKPKGASVKSCCTASGYSIFTSYDINVRQATGGLTGMGMNPNSSNAGF 60  
 DB 1 QVQLQSGPELVKPGALVKISCKASGYTFTSYDINVKRPPGGLGIMIGYDGSTYK 60  
 QY 61 AOKFKGRLTLTRDSTSTAYMELRLSEEDTAVVYCARCDTTLIIFGPAPYDSWGCGT 120  
 DB 61 NEKFKGRLTLTRDSTSTAYMELRLSEEDTAVVYCARCDTTLIIFGPAPYDSWGCGT 114  
 QY 121 LV 122  
 DB 115 TV 116

## RESULT 14

HV01\_MOUSE  
 ID HV01\_MOUSE STANDARD; PRT; 121 AA.  
 AC P01745;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region MPC 11.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81053741; PubMed=6253904;  
 RA Zakut R., Cohen J., Givol D.;  
 RT "Cloning and sequence of the cDNA corresponding to the variable  
 RT region of immunoglobulin heavy chain MPC11."  
 RL Nucleic Acids Res. 8:3591-3601 (1980).  
 RN [2]  
 RP REVISIONS.  
 RA Zakut R., Cohen J., Givol D.;

RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,  
 RA Hood L.E.;  
 RT "Complete amino acid sequence of a mouse mu chain: homology among  
 RT heavy chain constant region domains.";  
 RL Biochemistry 21:5415-5424(1982).  
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA  
 CC PROTEIN HAS ALSO BEEN DETERMINED.  
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02039; MEMS4E.  
 DR HSSP; P01789; IMCP.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG LIKE; 1.  
 KM Immunoglobulin V region; Glycoprotein.  
 FT DOMAIN 1 116  
 FT DISULFID 22 96  
 FT CARBOHYD 55 55  
 FT NON TER 117 117  
 SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE47E41 CRC64;  
 Query Match 52.7%; Score 346.5; DB 1; Length 117;  
 Best Local Similarity 55.7%; Pred. No. 2.3e-30;  
 Matches 68; Conservative 17; Mismatches 28; Indels 9; Gaps 2;  
 QY 1 OVQLLOSADVKKPGASVKSCTASGYIFTSYDINWVRQATGQGLEMGMMNPNSGNAGF 60  
 DB 1 EVQLQSGPELVKPGASVKSKCSAGYTFDYWKWKQSHGKSLKLEIGINPNNGTSTY 60  
 QY 61 AQKFKRLTLTRDTSTSTAYMELRLLESEPTAVYVCARCDTLLIWFGPAPYYDSMGQGT 120  
 DB 61 NQKFKKATLTVDKSSSTAYMQLSLTPEFAVYCARSD-----GYDWMFYWG 111  
 QY 121 LV 122  
 DB 112 TV 113  
 RESULT 10  
 HV48\_MOUSE  
 ID HV48\_MOUSE STANDARD; PRT; 138 AA.  
 AC P03980;  
 DT 23-OCT-1986 (Rel. 02, Created)  
 DT 23-OCT-1986 (Rel. 02, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region TEPC 1017 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=64248078; PubMed=6429663;  
 RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,  
 RA Tucker P.W.;  
 RT "Illegitimate recombination generates a class switch from C mu to C  
 RT delta in an Igd-secreting plasmacytoma.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).  
 DR PIR; A02033; HVMST7.  
 DR HSSP; P01810; 2FBJ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG LIKE; 1.  
 KM Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 138  
 FT DOMAIN 21 49  
 IG HEAVY CHAIN V REGION TEPC 1017.  
 FRAMEWORK-1.

FT DOMAIN 50 54  
 FT DOMAIN 55 68  
 FT DOMAIN 69 85  
 FT DOMAIN 86 117  
 FT DOMAIN 118 127  
 FT DOMAIN 128 138  
 FT DISULFID 41 115  
 FT NON TER 138 138  
 SQ SEQUENCE 138 AA; 15576 MW; 748157E4C69078BE CRC64;  
 Query Match 52.4%; Score 344.5; DB 1; Length 138;  
 Best Local Similarity 55.2%; Pred. No. 4.6e-30;  
 Matches 69; Conservative 17; Mismatches 26; Indels 13; Gaps 2;  
 QY 1 OVQLLOSADVKKPGASVKSCTASGYIFTSYDINWVRQATGQGLEMGMMNPNSGNAGF 60  
 DB 20 OVQLQPGAEVLVPGASVQLSCASGHTFTNYIHVKKRPGQGLEMGIGINPNDRSNV 79  
 QY 61 AQKFKRLTLTRDTSTSTAYMELRLLESEPTAVYVCARCDTLLIWFGPAPYYD---SWG 117  
 DB 80 NEKFKKATLTVDKSSSTAYMQLSLTPEFAVYCARSD-----GYDWMFYWG 129  
 QY 118 QGTLV 122  
 DB 130 QGTLV 134  
 RESULT 11  
 HV00\_MOUSE  
 ID HV00\_MOUSE STANDARD; PRT; 114 AA.  
 AC P01741;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region (Anti-arsenate antibody).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=A/J;  
 RX MEDLINE=79195438; PubMed=109536;  
 RA Capra J.D., Nisonoff A.;  
 RT "Structural studies on induced antibodies with defined idiotypic  
 RT specificities. VII. The complete amino acid sequence of the heavy  
 RT chain bearing a cross-reactive idiotype.";  
 RL J. Immunol. 123:279-284(1979).  
 CC -1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF  
 CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V  
 CC REGION SEQUENCE.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02022; GIMSA.  
 DR HSSP; P01772; 2FBA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG LIKE; 1.  
 KM Immunoglobulin V region.  
 FT DOMAIN 1 106  
 FT NON TER 114 114  
 SQ SEQUENCE 114 AA; 12555 MW; 99D8F0B6A69F4BE CRC64;  
 Query Match 52.3%; Score 344; DB 1; Length 114;  
 Best Local Similarity 55.7%; Pred. No. 4.2e-30;  
 Matches 68; Conservative 23; Mismatches 23; Indels 8; Gaps 2;  
 QY 1 OVQLLOSADVKKPGASVKSCTASGYIFTSYDINWVRQATGQGLEMGMMNPNSGNAGF 60  
 DB 1 EVQLQSGAEVLVPGASVKSCKATGYTFSSYELVWVROAPGGLDGLVYSSSSAYPNV 60

FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DOMAIN 118 124 D SEGMENT.  
FT DOMAIN 125 139 JH2 SEGMENT.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON TER 139 139  
SQ SEQUENCE 139 AA; 15419 MW; 1857DD4FD00C9F465 CRC64;

Query Match 54.1%; Score 356; DB 1; Length 139;  
Best Local Similarity 57.5%; Pred. No. 2.7e-31;

Matches 69; Conservative 20; Mismatches 25; Indels 6; Gaps 2;

QY 1 OVOLLOASADYKKPGASVYKSCASGYFTSYDINMWAOATGOGLEMMGNPNNGNAGF 60  
DB 20 OVOLLOQPGAEVLKPGASVYKSCASGYFTSYDINMWAOATGOGLEMMGNPNNGNAGF 79  
QY 61 AOKFKGRLTLTRDSTSTAYMELRLRLESEDTAVVYCARCDTTLTIWFGPAPYDSWGCGT 120  
DB 80 NEKFKSKATLTVDKSSATYVQSLTSEDSAVVYCARCD-----YVG-SSYFDVWGCGT 133

## RESULT 7

HV51\_MOUSE  
ID HV51\_MOUSE STANDARD; PRT; 118 AA.  
AC P06310;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region AC38 205.12.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP MEDLINE=84182519; PubMed=6201362;  
RX "A V region determinant (idiotope) expressed at high frequency in B lymphocytes is encoded by a large set of antibody structural genes.";  
RT EMBL J. 3:517-523(1984).  
RL PIR; A02040; MMS38.  
DR HSSP; P01789; IMCP.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 98 V SEGMENT.  
FT DOMAIN 99 104 D SEGMENT.  
FT DOMAIN 105 118 J SEGMENT.  
FT DISULFID 22 96 BY SIMILARITY.  
FT NON TER 118 118  
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 53.5%; Score 352; DB 1; Length 118;  
Best Local Similarity 56.6%; Pred. No. 6e-31;  
Matches 69; Conservative 17; Mismatches 28; Indels 8; Gaps 2;

QY 1 OVOLLOASADYKKPGASVYKSCASGYFTSYDINMWAOATGOGLEMMGNPNNGNAGF 60  
DB 1 EVOLLOQSGPELVKPGASVYKSCASGYFTSYDINMWAOATGOGLEMMGNPNNGNAGF 60

QY 61 AOKFKGRLTLTRDSTSTAYMELRLRLESEDTAVVYCARCDTTLTIWFGPAPYDSWGCGT 120  
DB 61 NOKFKSKATLTVDKSSATYVQSLTSEDSAVVYCARCD-----GYGIDP-FDVWGCGT 112

QY 121 LV 122

DB 113 TV 114

## RESULT 8

HV13\_MOUSE  
ID HV13\_MOUSE STANDARD; PRT; 117 AA.  
AC P01757;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region J558.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP MEDLINE=80078170; PubMed=6765983;  
RX Schilling J., Clevinger B., Davie J.M., Hood L.;  
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements in heavy chain V-region gene segments.";  
RL Nature 283:35-40(1980).  
CC -I- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN THE D AND J SEGMENTS.  
CC -I- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.  
CC PIR; A26242; MMS35.  
DR HSSP; P01789; IMCP.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 116 IG-LIKE.  
FT DISULFID 22 96 BY SIMILARITY.  
FT NON TER 117 117  
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 52.8%; Score 347.5; DB 1; Length 117;  
Best Local Similarity 55.7%; Pred. No. 1.8e-30;

Matches 68; Conservative 17; Mismatches 28; Indels 9; Gaps 2;

QY 1 OVOLLOASADYKKPGASVYKSCASGYFTSYDINMWAOATGOGLEMMGNPNNGNAGF 60  
DB 1 EVOLLOQSGPELVKPGASVYKSCASGYFTSYDINMWAOATGOGLEMMGNPNNGNAGF 60

QY 61 AOKFKGRLTLTRDSTSTAYMELRLRLESEDTAVVYCARCDTTLTIWFGPAPYDSWGCGT 120  
DB 61 NOKFKSKATLTVDKSSATYVQSLTSEDSAVVYCARCD-----RYW-----YFDVWGAGT 111

QY 121 LV 122  
DB 112 TV 113

## RESULT 9

HV12\_MOUSE  
ID HV12\_MOUSE STANDARD; PRT; 117 AA.  
AC P01756;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region M0PC 104E.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP MEDLINE=83075344; PubMed=6816276;

QY 121 LV 122

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8311846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RT "Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT "idiotype response of the strain A mouse.";
RL Bur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE. THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSSP: P01789; IMCP.
DR InterPro: IPR003110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGv_1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 56.8%; Score 373.5; DB 1; Length 120;
Best Local Similarity 58.0%; Pred. No. 3e-33;
Matches 69; Conservative 22; Mismatches 23; Indels 5; Gaps 1;

QY 2 VQLQGSADYKPKGASVYKSCASGYITFTSYDINWVROATGGLGEMWGMNPNNSGNAGFA 61
DB 1 VQLQGSAGELVYRAGSSVYKMSCKASGYFTSYGINWVKORPGGLEWIGYINPGNGTKYN 60
QY 62 QKFKGRLTLTRDPTSTAYMELRLSESDTAVYVCARCDTLLIFGPAPYDSMGCGT 120
DB 61 EKFKGKTLTLVDKSSSTAYMQLRSLTSEDSAVYFCARSH-----YVGGSYDFDYGCGT 114

RESULT 5
HVO2_MOUSE STANDARD; PRT; 140 AA.
ID HVO2_MOUSE
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbits T.H., Bates P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; J00493; AAA38128.1; -.
CC PIR; A94264; HWMSC7.

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DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGv_1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE3D1A5CE8 CRC64;

Query Match 55.1%; Score 362.5; DB 1; Length 140;
Best Local Similarity 56.7%; Pred. No. 5.4e-32;
Matches 68; Conservative 22; Mismatches 25; Indels 5; Gaps 1;

QY 1 OVQLQGSADYKPKGASVYKSCASGYITFTSYDINWVROATGGLGEMWGMNPNNSGNAGF 60
DB 20 EVQLQGSAGELVYRAGSSVYKMSCKASGYFTSYGINWVKORPGGLEWIGYINPGNGTKYN 79
QY 61 AOKFKGRLTLTRDPTSTAYMELRLSESDTAVYVCARCDTLLIFGPAPYDSMGCGT 120
DB 80 NEKFKGKTLTLVDKSSSTAYMQLRSLTSEDSAVYFCARSH-----YVGGSYDFDYGCGT 134

RESULT 6
HVO7_MOUSE STANDARD; PRT; 139 AA.
ID HVO7_MOUSE
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region B1-8/16e-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botthwell A.L.M., Paskind M., Reih M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN mRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
CC (NPB ANTIBODIES).
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CC -----
CC EMBL; J00529; AAA38170.1; -.
CC PIR; A90809; MMS318.
CC PDB; 1A6U; 27-MAY-98.
CC PDB; 1A6W; 15-JUL-98.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGv_1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/16e-2.

```





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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 6.54102 Seconds  
(without alignments)  
877.119 Million cell updates/sec

Title: US-09-674-752-40

Perfect score: 658  
Sequence: 1 QVQLQSADVKKPGASVYV.....LTIWGPARYDSWGQGLV 122

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Swisprot\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	392	59.6	117	1 HV1G_HUMAN	P23083 homo sapien
2	390	59.3	117	1 HV1B_HUMAN	P01743 homo sapien
3	385	58.5	117	1 HV1C_HUMAN	P01744 homo sapien
4	373.5	56.8	120	1 HV03_MOUSE	P01747 mus musculu
5	362.5	55.1	140	1 HV02_MOUSE	P01746 mus musculu
6	356	54.1	139	1 HV07_MOUSE	P01751 mus musculu
7	352	53.5	118	1 HV01_MOUSE	P06330 mus musculu
8	347.5	52.8	117	1 HV13_MOUSE	P01757 mus musculu
9	346.5	52.7	117	1 HV12_MOUSE	P01756 mus musculu
10	344.5	52.4	138	1 HV48_MOUSE	P03980 mus musculu
11	344	52.3	114	1 HV00_MOUSE	P01741 mus musculu
12	341	51.8	117	1 HV52_MOUSE	P01747 mus musculu
13	339	51.5	120	1 HV50_MOUSE	P06329 mus musculu
14	336.5	51.1	121	1 HV01_MOUSE	P01745 mus musculu
15	333	50.6	137	1 HV11_MOUSE	P01745 mus musculu
16	329	50.0	117	1 HV09_MOUSE	P01753 mus musculu
17	323	49.1	117	1 HV14_MOUSE	P01758 mus musculu
18	322	48.9	117	1 HV1A_HUMAN	P01742 homo sapien
19	319.5	48.6	125	1 HV1F_HUMAN	P06326 homo sapien
20	316	48.0	117	1 HV06_MOUSE	P01750 mus musculu
21	315.5	47.9	136	1 HV15_MOUSE	P01759 mus musculu
22	315	47.9	117	1 HV04_MOUSE	P01748 mus musculu
23	307	46.7	117	1 HV10_MOUSE	P01754 mus musculu
24	307	46.7	117	1 HV49_MOUSE	P06328 mus musculu
25	303	46.0	117	1 HV05_MOUSE	P01749 mus musculu
26	301	45.7	120	1 HV1H_HUMAN	P0421 homo sapien
27	300.5	45.7	119	1 HV31_HUMAN	P01770 homo sapien
28	299	45.4	119	1 HV37_MOUSE	P01807 mus musculu
29	296.5	45.1	121	1 HV3J_HUMAN	P01771 homo sapien
30	294	44.7	119	1 HV38_MOUSE	P01808 mus musculu
31	293	44.5	117	1 HV3O_HUMAN	P01776 homo sapien
32	291.5	44.3	120	1 HV3E_HUMAN	P01766 homo sapien
33	291	44.2	119	1 HV4O_MOUSE	P01810 mus musculu

34	290	44.1	122	1 HV3G_HUMAN	P01768 homo sapien
35	290	44.1	122	1 HV3H_HUMAN	P01769 homo sapien
36	290	44.1	136	1 HV16_MOUSE	P01783 mus musculu
37	289	43.9	120	1 HV3U_HUMAN	P01782 homo sapien
38	284	43.2	114	1 HV3B_HUMAN	P01763 homo sapien
39	282	42.9	126	1 HV3K_HUMAN	P01772 homo sapien
40	281	42.7	114	1 HV01_CANFA	P01784 canis fami
41	280.5	42.6	115	1 HV3D_HUMAN	P01765 homo sapien
42	278	42.2	119	1 HV3P_HUMAN	P01777 homo sapien
43	278	42.2	124	1 HV1E_HUMAN	P01761 homo sapien
44	276.5	42.0	117	1 HV42_MOUSE	P01812 mus musculu
45	275	41.8	119	1 HV3M_HUMAN	P01774 homo sapien

## ALIGNMENTS

## RESULT 1

ID HV1G\_HUMAN STANDARD; PRT; 117 AA.  
 AC P23083;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-I region V35 precursor.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 ON NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88296408; PubMed=2841108;  
 RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zeng S.Q.,  
 RA Ono H., Fukushima S., Honjo T.;  
 RT "Dispersed localization of D segments in the human immunoglobulin  
 heavy-chain locus."  
 RL EMBO J. 7:1047-1051(1988).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

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 CC -----  
 CC EMBL: X07448; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; S00476; HVH03.  
 DR HSSP; P01772; 2FB4.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; P:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.  
 FT DOMAIN 20 >117 IG-LIKE.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA: 13009 MW, BE61CE63F8CE97BD CRC64;

Query Match 59.6%; Score 392; DB 1; Length 117;

Best Local Similarity 75.5%; Pred. No. 3e-35;

Matches 74; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 QVQLQSADVKKPGASVYVSCASGYITFTSYDINVRQATGGLPMGMNNSNGAGF 60  
 DB 20 QVQLVSGALVKKPGASVYVSCASGYITFTGYIMHWVRQAPGGGLPMGRINPSGCTNY 79





[illegible]

	Query Match	65.6%	Score 431.5;	DB 2;	Length 122;
	Best Local Similarity	68.9%	Pred. No. 2,9e-34;		
	Matches 84;	Conservative 13;	Mismatches 24;	Indels 1;	Gaps 1;
OY	1 QVOLLGSADVDKKPGASVKVSCTAAGSYIFTSYDINWVRQATGGCLEMGNNPNPISNAGF	60			
	:   :   :   :   :   :   :   :   :				
Db	1 QVOLVGSAEAVKPKKGASIVKSKSGASTFTPSYGISTSWRAOPGCGLEMGMIISAAYGNNTY	60			
OY	61 AOKRGRLLTLTRDTSTAYAMELRLSESDPAVVYCARCDPTLLIMFGAPAYDSWGQGT	120			
	:   :   :   :   :   :   :   :   :				
Db	61 AOKRGQGVWTMTTDPSTSTAWEMLSLSSDDTAIYYCA-ADTGRIIDDFMSGINFDMWGQGT	119			

C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 465.5; DB 2; Length 127;  
Best Local Similarity 71.9%; Pred. No. 1.7e-37;  
Matches 92; Conservative 10; Mismatches 15; Indels 11; Gaps 3;

QY 1 QVQLQSAADYVKPKGASVYKVSCTASGIFTSYDINMWROATGCGLEMMGMNPNNSGNAGF 60  
DB 1 QVQWVSGAEVKKPKGASVYKVSCKASGYTFTSYDINMWROATGCGLEMMGMNPNNSGNAGF 60  
QY 61 AOKFKGRLTLTRDTSTSTAYMELRLSESDTAIVYCARCDTLLIWFGPAPYDYSNGGCT 114  
DB 61 AOKFKGRLTLTRDTSTSTAYMELRLSESDTAIVYCARCDTLLIWFGPAPYDYSNGGCT 114  
QY 115 SWGGCTLV 122  
DB 116 VMGGCTTV 123

## RESULT 3

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31596

R:Clutiner, A.M.; Gauchier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31596

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-132 <CUI>

A:Cross-references: EMBL:214166; NID:g30996; PIDN:CAA78535.1; PID:g30997

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 68.7%; Score 453; DB 2; Length 132;  
Best Local Similarity 71.3%; Pred. No. 3.4e-36;  
Matches 87; Conservative 12; Mismatches 9; Indels 14; Gaps 2;

QY 1 QVQLQSAADYVKPKGASVYKVSCTASGIFTSYDINMWROATGCGLEMMGMNPNNSGNAGF 60  
DB 20 QVQLVSGAEVKKPKGASVYKVSCKASGYTFTSYDINMWROATGCGLEMMGMNPNNSGNAGF 79  
QY 61 AOKFKGRLTLTRDTSTSTAYMELRLSESDTAIVYCARCDTLLIWFGPAPYDYSNGGCT 120  
DB 80 AOKFKGRLTLTRDTSTSTAYMELRLSESDTAIVYCARCDTLLIWFGPAPYDYSNGGCT 120  
QY 121 LV 122  
DB 126 MV 127

## RESULT 4

Ig heavy chain V region (DP-15) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S26918

R:Tominson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

A:Title: The repertoire of human germline VH sequences reveals about fifty groups of V

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26918

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TM>

A:Cross-references: EMBL:212317; NID:g32857; PIDN:CAA78187.1; PID:g32858

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 449; DB 2; Length 98;  
Best Local Similarity 84.7%; Pred. No. 4.9e-36;  
Matches 83; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLQSAADYVKPKGASVYKVSCTASGIFTSYDINMWROATGCGLEMMGMNPNNSGNAGF 60  
DB 1 QVQLVSGAEVKKPKGASVYKVSCKASGYTFTSYDINMWROATGCGLEMMGMNPNNSGNAGF 60  
QY 61 AOKFKGRLTLTRDTSTSTAYMELRLSESDTAIVYCAR 98  
DB 61 AOKFKGRLTLTRDTSTSTAYMELRLSESDTAIVYCAR 98

## RESULT 5

S49530

anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human

C:Species: Homo sapiens (man)

C:Date: 01-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 23-Jul-1999

C:Accession: S49530

R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.

A:Description: Molecular characterization of natural human anti-Sm autoantibodies.

A:Reference number: S48797

A:Accession: S49530

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-135 <MAH>

A:Cross-references: EMBL:246348; NID:g560839; PIDN:CAA66467.1; PID:g560840

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.9%; Score 447; DB 2; Length 135;  
Best Local Similarity 69.7%; Pred. No. 1e-35;  
Matches 85; Conservative 11; Mismatches 16; Indels 10; Gaps 1;

QY 1 QVQLQSAADYVKPKGASVYKVSCTASGIFTSYDINMWROATGCGLEMMGMNPNNSGNAGF 60  
DB 20 QVQLVSGAEVKKPKGASVYKVSCKASGYTFTSYDINMWROATGCGLEMMGMNPNNSGNAGF 79  
QY 61 AOKFKGRLTLTRDTSTSTAYMELRLSESDTAIVYCARCDTLLIWFGPAPYDYSNGGCT 120  
DB 80 AOKFKGRLTLTRDTSTSTAYMELRLSESDTAIVYCARCDTLLIWFGPAPYDYSNGGCT 129  
QY 121 LV 122  
DB 130 LV 131

## RESULT 6

Ig heavy chain V region precursor - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999

C:Accession: S23623

R:Olée, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defeo, M.; Kozin, F.; Carson, D.A.;

J. Exp. Med. 175, 831-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from

A:Reference number: S23623; MUID:92156804; PMID:1740665

A:Accession: S23623

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-171 <OLE>

A:Cross-references: EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID:g32011

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 443; DB 2; Length 171;  
Best Local Similarity 65.6%; Pred. No. 3.2e-35;  
Matches 84; Conservative 15; Mismatches 17; Indels 12; Gaps 2;

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 ; Search time 11.6946 Seconds

(without alignments)  
1003.251 Million cell updates/sec

Title: US-09-674-752-40

Sequence: 1 QVQLVQSGADVKKPKGASVKV.....LLIMFGPAPYDSWGQCTLV 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR:76:.\*  
2: PIR:.\*  
3: PIR:.\*  
4: PIR:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	72.5	136	2	S31600
2	465.5	70.7	127	2	S34014
3	452	68.7	132	2	S31596
4	449	68.2	98	2	S26918
5	447	67.9	135	2	S49530
6	443	67.3	171	2	S23623
7	442	67.2	110	2	PH1670
8	441	67.0	118	2	S36265
9	436.5	66.3	123	2	D33548
10	431.5	65.6	122	2	S36271
11	430.5	65.4	129	2	S46393
12	429.5	65.3	129	2	S36260
13	421.5	64.1	129	2	A33548
14	420	63.8	124	2	S19665
15	417.5	63.4	121	2	S20783
16	416.5	63.3	142	2	S19245
17	414	62.9	98	2	S26938
18	414	62.9	117	2	S31680
19	414	62.9	117	2	S18551
20	413.5	62.8	142	2	A32483
21	410.5	62.4	109	2	PH1668
22	408.5	62.1	148	2	S29257
23	407.5	61.9	160	2	PL0105
24	406	61.7	98	2	S26912
25	406	61.7	132	2	S46394
26	405	61.6	116	2	PH0959
27	402.5	61.2	125	2	PH0957
28	401	60.9	104	2	S69899
29	401	60.9	114	2	PH1667

30	400	60.8	120	2	PH0962	Ig heavy chain V r
31	399	60.6	98	2	S26919	Ig heavy chain V r
32	398.5	60.6	126	2	I44151	Ig heavy chain V r
33	398	60.5	110	2	PH1669	Ig heavy chain V r
34	397.5	60.4	125	2	S68170	Ig heavy chain V r
35	397	60.3	128	2	PH0952	Ig heavy chain V r
36	397	60.3	132	2	PH0954	Ig heavy chain V r
37	395.5	60.1	111	2	S26792	Ig heavy chain V r
38	395	60.0	98	2	S26920	Ig heavy chain V r
39	394	59.9	118	2	PH1666	Ig heavy chain V r
40	393.5	59.8	133	2	C33548	Ig heavy chain V-1
41	393.5	59.8	627	2	S14683	Ig mu chain precur
42	393	59.7	117	2	S18553	Ig heavy chain V r
43	393	59.7	122	2	PH0958	Ig heavy chain V r
44	392	59.6	117	1	HVH035	Ig heavy chain pre
45	392	59.6	136	2	PH0960	Ig heavy chain V r

## ALIGNMENTS

## RESULT 1

S31600  
Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S31600

R:Clisnir, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31600

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-136 &lt;CUI&gt;

A:Cross-references: EMBL:Z14165; NID:G30994; PIDN:CAA78534.1; PID:G30995

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 72.5% Score 477; DB 2; Length 136;

Best Local Similarity 74.6% Pred. No. 1.4e-38;

Matches 91; Conservative 9; Mismatches 12; Indels 10; Gaps 2;

QY 1 QVQLVQSGADVKKPKGASVKVCTASGVIPTSYDINVRQATGQGLEWGMGNPNSGNAF 60

Db 20 QVQLVQSGAEVKKPKGASVKVCSASGVTFTSYDINVRQATGQGLEWGMGNPNSGNTGY 79

QY 61 AQKFKGRITITRTSTSTAMELRLESEDTAVYCCARCDTLLIMFGPAPYDSWGQGT 120

Db 80 AQKFGKRVITRTSTSTAMELRLESEDTAVYCCAR-----W---RDARDIWQGT 129

QY 121 LV 122

Db 130 MV 131

## RESULT 2

S34014  
Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996

C:Accession: S34014; S30535

R:Marlette, X.; Teapla, A.; Broquet, J.C.

Eur. J. Immunol. 23, 846-851, 1993

A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal

A:Reference number: S34001; WUID:93209281; PMID:7681398

A:Accession: S34014

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-127 &lt;MAR&gt;

A:Cross-references: EMBL:Z18321

C:Superfamily: Immunoglobulin V region; immunoglobulin homology





Query Match 33.2%; Score 44.5; DB 4; Length 105;  
Best Local Similarity 50.0%; Pred. No. 23;  
Matches 8; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 DGGGAYEDVWSGEYP 16  
||||| : : : :  
6 DGGGGG---IMGGWMP 18

Db 6 DGGGGG---IMGGWMP 18

RESULT 11  
US-09-252-991A-19413  
; Sequence 19413, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 19413  
; LENGTH: 217  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-19413

Query Match 33.2%; Score 44.5; DB 4; Length 217;  
Best Local Similarity 38.5%; Pred. No. 54;  
Matches 10; Conservative 3; Mismatches 6; Indels 7; Gaps 1;

QY 3 GGGAYEDVWSGEY-----PEYYAM 21  
||||| : : : :  
53 GGGSVRDMLGHVPLTWHRHPEYAL 78

Db 53 GGGSVRDMLGHVPLTWHRHPEYAL 78

RESULT 12  
US-09-343-011B-1  
; Sequence 1, Application US/09343011B  
; Patent No. 6300473  
; GENERAL INFORMATION:  
; APPLICANT: Stephanie Richard  
; TITLE OF INVENTION: SLIM-1 AND SLIM-2; NOVEL  
; FILE REFERENCE: A32561  
; CURRENT APPLICATION NUMBER: US/09/343.011B  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: CA 2265271  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 349  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-343-011B-1

Query Match 33.2%; Score 44.5; DB 4; Length 349;  
Best Local Similarity 36.7%; Pred. No. 93;  
Matches 11; Conservative 2; Mismatches 6; Indels 11; Gaps 2;

QY 1 DGGGAYEDVWSGEY-----PEY 19  
||||| : : : :  
274 DGYGYDDQTYEAYDNSYVTPQSVPEY 303

Db 274 DGYGYDDQTYEAYDNSYVTPQSVPEY 303

RESULT 13  
US-09-157-370-1  
; Sequence 1, Application US/09157370A

Patent No. 6262238  
; GENERAL INFORMATION:  
; APPLICANT: STEINBACHER, Stefan  
; APPLICANT: STEINBACHER, Stefan  
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES  
; FILE REFERENCE: P8341-8072  
; CURRENT APPLICATION NUMBER: US/09/157,370A  
; PRIOR FILING DATE: 1998-09-21  
; EARLIER APPLICATION NUMBER: 08/765,179  
; EARLIER FILING DATE: 1997-01-14  
; EARLIER APPLICATION NUMBER: PCT/EP95/02626  
; EARLIER FILING DATE: 1995-07-06  
; EARLIER APPLICATION NUMBER: DE/P44 25 115.7  
; EARLIER FILING DATE: 1994-07-15  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-157-370-1

Query Match 32.8%; Score 44; DB 3; Length 117;  
Best Local Similarity 70.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGAYEDVW 11  
||||| : : : :  
98 GGGGGYFDYW 107

Db 98 GGGGGYFDYW 107

RESULT 14  
US-09-328-352-5411  
; Sequence 5411, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5411  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5411

Query Match 32.8%; Score 44; DB 4; Length 229;  
Best Local Similarity 57.1%; Pred. No. 67;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGGAYEDVWSGEYP 16  
||||| : : : :  
57 GGGSVRDVLDGHVP 70

Db 57 GGGSVRDVLDGHVP 70

RESULT 15  
US-08-526-136-13  
; Sequence 13, Application US/08526136  
; Patent No. 6107089  
; GENERAL INFORMATION:  
; APPLICANT: Towle, Christine A. et al.  
; TITLE OF INVENTION: ANNEXIN XI  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804

NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/020,846  
FILING DATE: 09-FEB-1998  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 9-027015  
FILING DATE: 10-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-024045  
FILING DATE: 09-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Wegner, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 053466/0225  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 421 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-020-846-68

Query Match 33.6%; Score 45; DB 4; Length 421;  
Best Local Similarity 62.5%; Pred. No. 98;  
Matches 10; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

Qy 1 DGG--GGAEDVWSGE 14  
Db 82 DGGCGGAYDIRGSGE 97

RESULT 10  
US-09-205-258-745  
Sequence 745, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,890  
FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876

EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
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EARLIER APPLICATION NUMBER: 60/048,974  
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EARLIER APPLICATION NUMBER: 60/048,898  
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EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 745  
LENGTH: 105  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-745

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/ LENGTH: 285
/ TYPE: PRT
/ ORGANISM: Acinetobacter baumannii
US-09-328-352-7483

Query Match          33.6%; Score 45; DB 4; Length 285;
Best Local Similarity 42.9%; Pred. No. 62;
Matches 9; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCGAYEDVWSGEYPEYAMDV 23
   ||| ||| ||| ||| |||
Db 68 GHGRSSQVWDGHDMDHYADDV 88

RESULT 6
US-09-252-991A-31155
; Sequence 31155, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31155
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31155

Query Match          33.6%; Score 45; DB 4; Length 338;
Best Local Similarity 42.9%; Pred. No. 76;
Matches 9; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCGAYEDVWSGEYPEYAMDV 23
   ||| ||| ||| ||| |||
Db 121 GHGRSSQVWDGHDMDHYADDV 141

RESULT 7
US-09-020-846-69
; Sequence 69, Application US/09020846
; Patent No. 6322965
; GENERAL INFORMATION:
; APPLICANT: YAMAGUCHI, Kenjiro
; APPLICANT: KASHIWAKUMA, Tomiko
; APPLICANT: CHIBA, Yukie
; APPLICANT: YAGI, Shintaro
; APPLICANT: HASEGAWA, Akira
; TITLE OF INVENTION: CHIMERA ANTIGEN PEPTIDE
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,846
; FILING DATE: 09-FEB-1998
; CLASSIFICATION: 424
```

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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 9-027015
/ FILING DATE: 10-FEB-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 8-024045
/ FILING DATE: 09-FEB-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wegner, Harold C.
/ REGISTRATION NUMBER: 25,258
/ REFERENCE/DOCKET NUMBER: 053466/0225
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 672-5300
/ TELEFAX: (202) 672-5399
/ INFORMATION FOR SEQ ID NO: 69:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 396 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-020-846-69

Query Match          33.6%; Score 45; DB 4; Length 396;
Best Local Similarity 62.5%; Pred. No. 91;
Matches 10; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 DGG--GAYEDVWSGE 14
   ||| ||| ||| ||| |||
Db 67 DGGCAGAYDVIGSGE 82

RESULT 8
US-09-252-991A-30606
; Sequence 30606, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30606
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30606

Query Match          33.6%; Score 45; DB 4; Length 410;
Best Local Similarity 34.5%; Pred. No. 95;
Matches 10; Conservative 5; Mismatches 8; Indels 6; Gaps 1;

QY 1 DGGGAYE-----DVWSGEYPEYAMDV 23
   ||| ||| ||| ||| |||
Db 337 DGDGDHDMPLMLCSVWTGSGFLYKLDL 365

RESULT 9
US-09-020-846-68
; Sequence 68, Application US/09020846
; Patent No. 6322965
; GENERAL INFORMATION:
; APPLICANT: YAMAGUCHI, Kenjiro
; APPLICANT: KASHIWAKUMA, Tomiko
; APPLICANT: CHIBA, Yukie
; APPLICANT: YAGI, Shintaro
; APPLICANT: HASEGAWA, Akira
; TITLE OF INVENTION: CHIMERA ANTIGEN PEPTIDE
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ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29606

Query Match 34.3% Score 46; DB 4; Length 1287;  
Best Local Similarity 42.1%; Pred. No. 2,6e+02;  
Matches 8; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 2 GGGAYEDVMSGEYPEYVA 20  
DB 326 GGGTTGTCGWDGTFEAYS 344

RESULT 3  
US-07-882-329-2  
Sequence 2, Application US/07882329

Patent No. 5108765

GENERAL INFORMATION:

APPLICANT: Ozaki, Eiji

APPLICANT: Sakimae, Akihiro

APPLICANT: Numazawa, Ryozo

TITLE OF INVENTION: ESTERASE GENES, ESTERASE, RECOMBINANT

TITLE OF INVENTION: PLASMIDS AND TRANSFORMANTS CONTAINING THE RECOMBINANT

TITLE OF INVENTION: PLASMID AND METHODS OF PRODUCING OPTICALLY ACTIVE

TITLE OF INVENTION: CARBOXYLIC ACIDS AND THEIR ENANTIOMERIC ESTERS USING SAID

TITLE OF INVENTION: TRANSFORMANTS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/882,329

FILING DATE: 19920513

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Mierock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7005-046-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 276 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Pseudomonas putida

STRAIN: MR-2068 (FERM BP-3846)

US-07-882-329-2

Query Match 33.6% Score 45; DB 1; Length 276;  
Best Local Similarity 42.9%; Pred. No. 60;  
Matches 9; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 3 GGGAYEDVMSGEYPEYVADV 23  
DB 59 GGGSSQVWDGDMHDYADV 79

RESULT 4  
US-08-183-213-2

Sequence 2, Application US/08183213  
Patent No. 5482847

GENERAL INFORMATION:

APPLICANT: Ozaki, Eiji

APPLICANT: Sakimae, Akihiro

APPLICANT: Numazawa, Ryozo

TITLE OF INVENTION: ESTERASE GENES, ESTERASE, RECOMBINANT

TITLE OF INVENTION: PLASMIDS AND TRANSFORMANTS CONTAINING THE RECOMBINANT

TITLE OF INVENTION: PLASMID AND METHODS OF PRODUCING OPTICALLY ACTIVE

TITLE OF INVENTION: CARBOXYLIC ACIDS AND THEIR ENANTIOMERIC ESTERS USING SAID

TITLE OF INVENTION: TRANSFORMANTS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/183,213

FILING DATE: 14-JAN-1994

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US 07/882,329

FILING DATE: 13-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: Mierock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7005-046-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 276 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Pseudomonas putida

STRAIN: MR-2068 (FERM BP-3846)

US-08-183-213-2

Query Match 33.6% Score 45; DB 1; Length 276;  
Best Local Similarity 42.9%; Pred. No. 60;  
Matches 9; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 3 GGGAYEDVMSGEYPEYVADV 23  
DB 59 GGGSSQVWDGDMHDYADV 79

RESULT 5  
US-09-328-352-7483

Sequence 7483, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7483

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## OM protein - protein search, using SW model

Run on: December 30, 2003, 10:47.45 ; Search time 2.3355 Seconds  
(Without alignments)  
416.677 Million cell updates/sec

Title: US-09-674-752-30

Perfect score: 134  
Sequence: 1 DGGGAYEDVSGEYPEYAMDV 23Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCtUS.COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	46	34.3	659 4 US-09-562-737-12	Sequence 12, Appl
2	46	34.3	1287 4 US-09-252-991A-29606	Sequence 29606, A
3	45	33.6	276 1 US-07-882-329-2	Sequence 2, Appl1
4	45	33.6	276 1 US-08-183-213-2	Sequence 2, Appl1
5	45	33.6	285 4 US-09-328-352-7483	Sequence 7483, Ap
6	45	33.6	338 4 US-09-252-991A-31155	Sequence 31155, A
7	45	33.6	396 4 US-09-020-846-69	Sequence 66, Appl
8	45	33.6	410 4 US-09-252-991A-30606	Sequence 30606, A
9	45	33.6	421 4 US-09-020-846-68	Sequence 68, Appl
10	44.5	33.2	105 4 US-09-205-258-745	Sequence 745, A
11	44.5	33.2	217 4 US-09-252-991A-19413	Sequence 19413, A
12	44.5	33.2	349 4 US-09-343-0118-1	Sequence 1, Appl1
13	44	32.8	117 3 US-09-157-370-1	Sequence 1, Appl1
14	44	32.8	229 4 US-09-328-352-9411	Sequence 5411, Ap
15	44	32.8	466 3 US-08-526-136-13	Sequence 13, Appl
16	44	32.8	659 4 US-09-562-737-13	Sequence 13, Appl
17	44	32.8	1220 3 US-08-930-996A-2	Sequence 2, Appl1
18	43.5	32.5	473 4 US-08-914-375C-71	Sequence 71, Appl
19	43.5	32.5	476 4 US-08-914-375C-69	Sequence 69, Appl
20	43.5	32.5	499 4 US-09-252-991A-25819	Sequence 25819, A
21	43.5	32.5	548 3 US-08-688-988-41	Sequence 41, Appl
22	43	32.1	16 1 US-08-133-011-130	Sequence 130, App
23	43	32.1	16 3 US-08-907-739-130	Sequence 130, App
24	43	32.1	16 4 US-09-729-597-130	Sequence 130, App
25	43	32.1	70 1 US-08-315-695-3	Sequence 3, Appl1
26	43	32.1	197 1 US-08-044-621D-29	Sequence 29, Appl
27	43	32.1	197 1 US-08-709-912-9	Sequence 9, Appl1

28	43	32.1	197 2 US-09-047-370-9	Sequence 9, Appl1
29	43	32.1	217 4 US-09-229-583A-6	Sequence 6, Appl1
30	43	32.1	261 2 US-07-857-224B-59	Sequence 59, Appl
31	43	32.1	270 2 US-08-859-201-4	Sequence 4, Appl1
32	43	32.1	275 2 US-08-701-191A-36	Sequence 36, Appl
33	43	32.1	299 4 US-09-205-258-265	Sequence 265, App
34	43	32.1	314 2 US-08-859-201-8	Sequence 8, Appl1
35	43	32.1	461 4 US-09-134-001C-3316	Sequence 3316, Ap
36	43	32.1	462 1 US-08-458-023B-2	Sequence 2, Appl1
37	43	32.1	463 3 US-09-111-556A-2	Sequence 2, Appl1
38	43	32.1	463 3 US-08-360-758-2	Sequence 2, Appl1
39	43	32.1	485 4 US-09-107-532A-4797	Sequence 4797, Ap
40	43	32.1	603 4 US-09-396-149-8	Sequence 8, Appl1
41	43	32.1	659 4 US-09-562-737-11	Sequence 11, Appl
42	43	32.1	660 3 US-08-819-177-1	Sequence 1, Appl1
43	43	32.1	714 2 US-08-859-201-2	Sequence 2, Appl1
44	43	32.1	800 4 US-09-175-928-10	Sequence 10, Appl
45	42.5	31.7	817 4 US-09-252-991A-25598	Sequence 25598, A

## ALIGNMENTS

RESULT 1  
US-09-562-737-12  
; Sequence 12, Application US/09562737  
; Patent No. 6428967  
; GENERAL INFORMATION:  
; APPLICANT: Hertz, Joachim  
; TITLE OF INVENTION: LDL Receptor Signaling Pathways  
; FILE REFERENCE: UTSW0708  
; CURRENT APPLICATION NUMBER: US/09/562, 737  
; CURRENT FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 132  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 659  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Sequence  
US-09-562-737-12

Query Match 34.3%; Score 46; DB 4; Length 659;  
Best Local Similarity 34.6%; Pred. No. 1.2e+02;  
Matches 9; Conservative 3; Mismatches 4; Indels 10; Gaps 1;

Qy 8 EDVWSGEY-----PEYAMDV 23  
Db 517 EDVWGAYNRTGARHVFPAYVAIEI 542

RESULT 2  
US-09-252-991A-29606  
; Sequence 29606, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252, 991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074, 788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094, 190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29606  
; LENGTH: 1287  
; TYPE: PRT

QY 6 AYEDVMSGEYPEYAMDV 23  
DB 102 AYYDILTYLYYYMDV 119

## RESULT 14

US-10-062-254-246  
Sequence 246, Application US/10062254  
Publication No. US20020138882A1  
GENERAL INFORMATION:  
APPLICANT: Cahoon, Edgar B  
APPLICANT: Cahoon, Rebecca E  
APPLICANT: Falco, Saverio Carl  
APPLICANT: Fang, Yiwen  
APPLICANT: Hantke, Sabine S.  
APPLICANT: Lee, Jian-Ming  
APPLICANT: Li, Zhongsen  
APPLICANT: Miao, Guo-Hua  
APPLICANT: Morgente, Michele  
APPLICANT: Niu, Xiping  
APPLICANT: Odell, Joan  
APPLICANT: Rafalski, Antoni  
APPLICANT: Sakai, Hajime  
APPLICANT: Zheng, Peizhong  
APPLICANT: Zhu, Qun  
TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved in Plant Metabolism  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/062,254  
CURRENT FILING DATE: 2002-02-01  
PRIOR APPLICATION NUMBER: 09/630,346  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: 60/146511  
PRIOR FILING DATE: 1999-07-30  
PRIOR APPLICATION NUMBER: 60/156006  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: 60/156899  
PRIOR FILING DATE: 1999-09-30  
PRIOR APPLICATION NUMBER: 60/157287  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/169767  
PRIOR FILING DATE: 1999-12-09  
PRIOR APPLICATION NUMBER: 60/171054  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: 60/172958  
PRIOR FILING DATE: 1999-12-21  
PRIOR APPLICATION NUMBER: 60/171515  
PRIOR FILING DATE: 1999-12-22  
PRIOR APPLICATION NUMBER: 60/173535  
PRIOR FILING DATE: 1999-12-29  
NUMBER OF SEQ ID NOS: 375  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 246  
LENGTH: 389  
TYPE: PRT  
ORGANISM: Zea mays  
US-10-062-254-246

Query Match 36.6%; Score 49; DB 14; Length 389;  
Best Local Similarity 50.0%; Pred. No. 84;  
Matches 11; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 DGGGAYED-VMSGEYPEYVA 20  
DB 359 NSGGGFGRCDFWSPQYAYVA 380

RESULT 15  
US-09-840-459-77  
Sequence 77, Application US/09840459  
Patent No. US20020150576A1  
GENERAL INFORMATION:  
APPLICANT: LaRosa, Gregory J.  
APPLICANT: Horvath, Christopher

APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-012  
CURRENT APPLICATION NUMBER: US/09/840,459  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FaalSeq for Windows Version 3.0  
SEQ ID NO 77  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (1)...(128)  
OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-840-459-77

Query Match 36.2%; Score 48.5; DB 10; Length 128;  
Best Local Similarity 66.7%; Pred. No. 32;  
Matches 10; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 9 DVMSCGEYPEYAMDV 23  
DB 104 DFWSGXY-YTGMADV 117

Search completed: December 30, 2003, 11:45:23  
Job time : 4.93258 secs

Db 99 GAYVDILTGYYP--YGM DV 115

## RESULT 10

US-09-880-748-1695  
; Sequence 1695, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1695  
; LENGTH: 252  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1695

Query Match 38.8%; Score 52; DB 11; Length 252;  
Best Local Similarity 57.9%; Pred. No. 21;  
Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

Qy 5 GAYEDVWSGEYPEYAMD V 23  
Db 99 GAYVDILTGYYP--YGM DV 115

## RESULT 11

US-09-880-748-1698  
; Sequence 1698, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1698  
; LENGTH: 252  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1698

Query Match 38.8%; Score 52; DB 11; Length 252;  
Best Local Similarity 57.9%; Pred. No. 21;  
Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;  
Qy 5 GAYEDVWSGEYPEYAMD V 23

Db 99 GAYVDILTGYYP--YGM DV 115

## RESULT 12

US-09-880-748-2172  
; Sequence 2172, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2172  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2172

Query Match 37.3%; Score 50; DB 11; Length 21;  
Best Local Similarity 55.6%; Pred. No. 3.1;  
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 6 AYEDVWSGEYPEYAMD V 23  
Db 4 AYVDILTGYLYYYAMD V 21

## RESULT 13

US-09-880-748-839  
; Sequence 839, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 839  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-839

Query Match 37.3%; Score 50; DB 11; Length 256;  
Best Local Similarity 55.6%; Pred. No. 40;  
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

RESULT 6  
US-09-880-748-926  
; Sequence 926, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 926  
; LENGTH: 249  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-926

Query Match 38.8%; Score 52; DB 11; Length 249;  
Best Local Similarity 57.9%; Pred. No. 21;  
Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 5 GAYEDVWSGEYPEYAMDV 23  
|||:|:|:|:|  
DB 99 GAYYDILTGYP--YGMVDV 115

RESULT 7  
US-09-880-748-1394  
; Sequence 1394, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1394  
; LENGTH: 252  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1394

Query Match 38.8%; Score 52; DB 11; Length 252;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 6 AYEDVWSGEYPEYAMDV 23  
:|:|:|:|:|:|  
DB 101 SYDILITGYVHYGMVDV 118

RESULT 8  
US-09-880-748-1646  
; Sequence 1646, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1646  
; LENGTH: 252  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1646

Query Match 38.8%; Score 52; DB 11; Length 252;  
Best Local Similarity 57.9%; Pred. No. 21;  
Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 5 GAYEDVWSGEYPEYAMDV 23  
|||:|:|:|:|  
DB 102 GAYYDILTGYP--YGMVDV 118

RESULT 9  
US-09-880-748-1674  
; Sequence 1674, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1674  
; LENGTH: 252  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1674

Query Match 38.8%; Score 52; DB 11; Length 252;  
Best Local Similarity 57.9%; Pred. No. 21;  
Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 5 GAYEDVWSGEYPEYAMDV 23  
|||:|:|:|:|



## US-09-880-748-1777

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/ Sequence 1777, Application US/09880748
/ Publication No. US2003005937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1777
/ LENGTH: 253
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-1777
```

Query Match 41.4%; Score 55.5; DB 11; Length 253;

Best Local Similarity 54.5%; Pred. No. 7;

Matches 12; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

```
QY 2 GCGGAEVDWVGSEYPEYAMDV 23
DB 99 GDFG DY-DILTGYYPVYGGMDV 119
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## RESULT 3

```
US-09-880-748-2860
/ Sequence 2860, Application US/09880748
/ Publication No. US2003005937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2860
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-2860
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Query Match 38.8%; Score 52; DB 11; Length 17;

Best Local Similarity 57.9%; Pred. No. 1.3;

Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

```
QY 5 GAYEDVWVGSEYPEYAMDV 23
DB 1 GAYYDILTYGP--YGMDV 17
```

## RESULT 4

```
US-09-880-748-2743
/ Sequence 2743, Application US/09880748
/ Publication No. US2003005937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2743
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-2743
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Query Match 38.8%; Score 52; DB 11; Length 20;

Best Local Similarity 50.0%; Pred. No. 1.6;

Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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QY 6 AYEDVWVGSEYPEYAMDV 23
DB 3 SYVDILTYGVYHYGGMDV 20
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## RESULT 5

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US-09-880-748-918
/ Sequence 918, Application US/09880748
/ Publication No. US2003005937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 918
/ LENGTH: 249
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-918
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Query Match 38.8%; Score 52; DB 11; Length 249;

Best Local Similarity 57.9%; Pred. No. 2.1;

Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

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QY 5 GAYEDVWVGSEYPEYAMDV 23
DB 99 GAYYDILTYGP--YGMDV 115
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OM protein - protein search, using sw model

Run on: December 30, 2003, 11:01:15 ; Search time 4.93258 Seconds

(without alignments)  
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Title: US-09-674-752-30

Perfect score: 134

Sequence: 1 DGGGAYEDVWVGSEPEYVAMDV 23

Scoring table:

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Searched: 724715 seqs, 199017464 residues

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55.5	41.4	21	11	US-09-880-748-13082
2	55.5	41.4	253	11	US-09-880-748-1777
3	52	38.8	17	11	US-09-880-748-2860
4	52	38.8	20	11	US-09-880-748-2743
5	52	38.8	249	11	US-09-880-748-918
6	52	38.8	249	11	US-09-880-748-926
7	52	38.8	252	11	US-09-880-748-1394
8	52	38.8	252	11	US-09-880-748-1546
9	52	38.8	252	11	US-09-880-748-1674
10	52	38.8	252	11	US-09-880-748-1695
11	52	38.8	252	11	US-09-880-748-1698
12	50	37.3	21	11	US-09-880-748-2172
13	50	37.3	256	11	US-09-880-748-839
14	49	36.6	389	14	US-10-062-254-246
15	48.5	36.2	128	10	US-09-840-459-77

16	48.5	36.2	128	10	US-09-840-459-79	Sequence 79, App1
17	48.5	36.2	477	12	US-10-169-493-8940	Sequence 8940, App
18	47.5	35.4	22	11	US-09-880-748-2761	Sequence 2761, App
19	47.5	35.4	253	11	US-09-880-748-938	Sequence 938, App
20	47	35.1	19	11	US-09-880-748-2987	Sequence 2987, App
21	47	35.1	254	11	US-09-880-748-1625	Sequence 1625, App
22	46.5	34.7	552	9	US-09-815-028-2	Sequence 2, App1
23	46.5	34.7	552	12	US-10-137-870-196	Sequence 196, App
24	46.5	34.7	552	12	US-10-140-018-196	Sequence 196, App
25	46.5	34.7	552	12	US-10-140-021-196	Sequence 196, App
26	46.5	34.7	552	12	US-10-140-021-196	Sequence 196, App
27	46.5	34.7	552	12	US-10-140-274-196	Sequence 196, App
28	46.5	34.7	552	12	US-10-140-807-196	Sequence 196, App
29	46.5	34.7	552	12	US-10-140-807-196	Sequence 196, App
30	46.5	34.7	552	12	US-10-140-922-196	Sequence 196, App
31	46.5	34.7	552	12	US-10-140-924-196	Sequence 196, App
32	46.5	34.7	552	12	US-10-140-928-196	Sequence 196, App
33	46.5	34.7	552	12	US-10-141-698-196	Sequence 196, App
34	46.5	34.7	552	12	US-10-141-702-196	Sequence 196, App
35	46.5	34.7	552	12	US-10-141-704-196	Sequence 196, App
36	46.5	34.7	552	12	US-10-142-421-196	Sequence 196, App
37	46.5	34.7	552	12	US-10-142-433-196	Sequence 196, App
38	46.5	34.7	552	12	US-10-143-033-196	Sequence 196, App
39	46.5	34.7	552	12	US-10-144-994-196	Sequence 196, App
40	46.5	34.7	552	12	US-10-145-631-196	Sequence 196, App
41	46.5	34.7	552	12	US-10-145-628-196	Sequence 196, App
42	46.5	34.7	552	12	US-10-145-633-196	Sequence 196, App
43	46.5	34.7	552	12	US-10-145-746-196	Sequence 196, App
44	46.5	34.7	552	12	US-10-145-748-196	Sequence 196, App
45	46.5	34.7	552	12	US-10-145-823-196	Sequence 196, App

## ALIGNMENTS

RESULT 1  
US-09-880-748-13082  
Sequence 13082, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PFS3  
CURRENT APPLICATION NUMBER: US/09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3082  
LENGTH: 21  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-13082  
Query Match 41.4%, Score 55.5, DB 11, Length 21;  
Best Local Similarity 54.5%, Pred. No. 0.56;  
Matches 12; Conservative 2; Mismatches 7; Indels 1; Gaps 1;  
QY 2 DGGGAYEDVWVGSEPEYVAMDV 23  
DB 1 GDFGDI-DILGDIYPTVYAMDV 21  
RESULT 2

AC	ABP45684:
XX	
DT	19-AUG-2002 (first entry)
DE	Human Blyts binding scfv SEQ ID 1695.
XX	
KW	Blyts; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM	tumour necrosis factor; B cell proliferation; B cell differentiation;
KM	immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KM	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM	common variable immunodeficiency; acquired immunodeficiency syndrome.
XX	
OS	Homo sapiens.
XX	
PN	WO200202641-A1.
PD	10-JAN-2002.
PF	15-JUN-2001; 2001WO-US19110.
PR	16-JUN-2000; 2000US-212210P.
PR	17-OCT-2000; 2000US-240816P.
PR	16-MAR-2001; 2001US-276248P.
PR	21-MAR-2001; 2001US-277379P.
PR	25-MAY-2001; 2001US-293499P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX	
F1	Ruben SM, Baraeh SC, Choi GH, Vaughan T, Hilbert D,
DR	WPI; 2002-114799/15.
PT	Antibodies against B Lymphocyte Stimulating polypeptides, useful for
FT	the diagnosis and treatment of cancers and immune disorders -
XX	
PS	Claim 1; Page 2425-2426; 3148pp; English.
CC	This invention describes novel antibodies that immunospecifically bind to
CC	B Lymphocyte Stimulator (Blyts) polypeptides. Blyts is a member of the
CC	tumour necrosis factor (TNF) super family and induces B cell
CC	proliferation and differentiation. The antibodies of the invention have
CC	cyclostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC	antineumatic and antiAIDS activity and can be used in vaccines to
CC	inhibit the expression and activity of Blyts. The antibodies bind to Blyts
CC	and so may be used to detect and quantitate the presence of Blyts in
CC	biological samples and may be used in this way to diagnose disease
CC	associated with aberrant expression of Blyts. They may also be
CC	administered to treat diseases associated with aberrant Blyts expression
CC	and actively such as cancer, immune, and autoimmune disorders and
CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC	the antibodies and fragments of the antibodies described in the method
CC	of the invention.
XX	
SQ	Sequence 252 AA.
Query Match	38.8%; Score 52; DB 23; Length 252;
Best Local Similarity	57.9%; Pred. No. 22;
Matches 11; Conservative	2; Mismatches 4; Incls 2; Gaps 1
OY	5 GAYEDVMSGEYPPEYAMDY 23     :       DB 99 GAYYDILTGYP--YGMDV 115
RESULT 15	
ID	ABP45687 standard; Protein; 252 AA.
XX	

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AC ABP45687;
XX
XX DT 19-AUG-2002 (first entry)
DE Human Blys binding ecFv SEQ ID 1698.
XX
XX BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
PN WO200202641-A1.
XX
XX PD 10-JAN-2002.
XX
PE 15-JUN-2001; 2001WO-US19110.
XX
XX PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HDMA-) HUMAN GENOME SCI INC.
PA (CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 2428-2429; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and actively such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SQ Sequence 252 AA;
XX
QY Query Match 38.8%; Score 52; DB 23; Length 252;
Best Local Similarity 57.9%; Pred. No. 22;
Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1
DB 99 GAYDIULTGYYP--YGMDV 115

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ID	ABP45635
AC	ABP45635 standard; Protein; 252 AA.
XX	
XX	ABP45635;
DT	19-AUG-2002 (first entry)
DE	
Human Blys binding scFv SEQ ID 1646.	
XX	
Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunosuppressant; immunomodulatory; antineumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.	
OS	Homo sapiens.
PX	
WO200202641-A1.	
PD	
XX	
10-JAN-2002.	
PF	
PE	
PR	15-JUN-2001; 2001WO-US19110.
PP	
PR	16-JUN-2000; 2000US-212210P. 17-OCT-2000; 2000US-240816P. 16-MAR-2001; 2001US-276248P. PR 21-MAY-2001; 2001US-277379P. PR 25-MAY-2001; 2001US-293499P.
XX	
(HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.	
PA	
Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D; WPI: 2002-114799/15.	
DR	
Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders - Claim 1; Page 2367-2368; 3148pp; English.	
PS	
This invention describes novel antibodies that nonspecifically bind to B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytotoxic, immunosuppressive, immunostimulant, immunomodulatory, antineumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of Blys. The antibodies bind to Blys and so may be used to detect and quantitate the presence of Blys in biological samples and may be used in this way to diagnose disease associated with aberrant expression of Blys. They may also be administered to treat diseases associated with aberrant Blys expression and actively such as cancer, immune, and autoimmune disorders and diseases, e.g., systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g., common variable immunodeficiency (CVID), and acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention.	
CC	
Sequence      252 AA;	
SQ	
Query Match                  38.8%; Score 52; DB 23; Length 252; Best Local Similarity        57.9%; Pred. No. 22; Matches     11; Conservative   2; Mismatches     4; Indels     2; Gaps     11	
OY	5 GAIEDVMSGEYPEYYAMDV 23    :::-        DB        102 GAVYDILGYYP--YGMDV 118
RESULT 13	
ABP45663	

```

ID   ABP45663 standard; Protein; 252 AA.
AC
XX   ABP45663;
XX
XX   19-AUG-2002 (first entry)
XX
XX   Human BlyS binding scFv SEQ ID 1674.
XX
XX   BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX   tumour necrosis factor; B cell proliferation; B cell differentiation;
XX   immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
XX   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX   Homo sapiens.
XX
XX   OS
XX   PN   WO200202641-A1.
XX
XX   PD   10-JAN-2002.
XX
XX   PF   15-JUN-2001; 2001WO-US19110.
XX
XX   PR   16-JUN-2000; 2000US-212210P.
XX   PR   17-OCT-2000; 2000US-240816P.
XX   PR   16-MAR-2001; 2001US-276248P.
XX   PR   21-MAR-2001; 2001US-277379P.
XX   PR   25-MAY-2001; 2001US-293499P.
XX
XX   PA   (HUMA-) HUMAN GENOME SCI INC.
XX   PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX   PI   Ruben SM, Baraash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX   DR   WPI; 2002-114799/15.
XX
XX   PT   Antibodies against B lymphocyte Stimulating polypeptides, useful for
XX   the diagnosis and treatment of cancers and immune disorders -
XX
XX   PS   Claim 1; Page 2400-2401; 3148pp; English.
XX
XX   PP   This invention describes novel antibodies that immunospecifically bind to
XX   B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
XX   tumour necrosis factor (TNF) super family and induces B cell
XX   proliferation and differentiation. The antibodies of the invention have
XX   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX   antineumatic and antiAIDS activity and can be used in vaccines to
XX   inhibit the expression and activity of BlyS. The antibodies bind to BlyS
XX   and so may be used to detect and quantitate the presence of BlyS in
XX   biological samples and may be used in this way to diagnose disease
XX   associated with aberrant expression of BlyS. They may also be
XX   administered to treat diseases associated with aberrant BlyS expression
XX   and activity such as cancer, immune, and autoimmune disorders and
XX   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX   acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
XX   the antibodies and fragments of the antibodies described in the method
XX   of the invention.
XX
XX   SQ   Sequence 252 AA;
XX
XX   Query Match 38.8%; Score 52; DB 23; Length 252;
XX   Best Local Similarity 57.9%; Pred. No. 22;
XX   Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
XX
XX   5 GAYEDWWSGGEPEYKAMDV 23
XX   ||| : : |||
XX   DB 99 GAYYDILTYGYP--YGMDV 115

```

```

RESULT 10
ABP44915
ID ABP44915 standard; Protein; 249 AA.
XX
AC ABP44915;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 926.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 1507-1508; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SO Sequence 249 AA;
XX
Query Match 38.8%; Score 52; DB 23; Length 249;
Best Local Similarity 57.9%; Pred. No. 22;
Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
OY 5 AYEDVWSGEYPPYAMDV 23
DB 99 GAYYDILTGYPP--YGMDDV 115

```

```

RESULT 11
ABP45383
ID ABP45383 standard; Protein; 252 AA.
XX
AC ABP45383;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1394.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US19110.
XX
PR 16-JUN-2000; 2000US-212210P.
PR 17-OCT-2000; 2000US-240816P.
PR 16-MAR-2001; 2001US-276248P.
PR 21-MAR-2001; 2001US-277379P.
PR 25-MAY-2001; 2001US-293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
PS Claim 1; Page 2066-2067; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
SO Sequence 252 AA;
XX
Query Match 38.8%; Score 52; DB 23; Length 252;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
OY 6 AYEDVWSGEYPPYAMDV 23
DB 101 SYDILTGYVHYHGMDDV 118

```

RESULT 12



QY 2 GCGAYEDVMSGEYPEYAMDV 23  
 Db 1 GDFGDY-DILTGYPVYYGMDV 21

RESULT 6  
 ID ABP45766 standard; Protein; 253 AA.

AC ABP45766;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1777.

KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

XX Antibodies against B lymphocyte stimulating polypeptides, useful for

PT the diagnosis and treatment of cancers and immune disorders -

PS Claim 1; Page 2522-2523; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.

SQ Sequence 253 AA;

Query Match 41.4%; Score 55.5; DB 23; Length 253;  
 Best Local Similarity 54.5%; Pred. No. 7.2;  
 Matches 12; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

QY 2 GCGAYEDVMSGEYPEYAMDV 23

Db 99 GDFGDY-DILTGYPVYYGMDV 119

RESULT 7  
 ID ABP46849 standard; peptide; 17 AA.

AC ABP46849;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv VH CDR3 SEQ ID 2860.

KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

XX Antibodies against B lymphocyte stimulating polypeptides, useful for

PT the diagnosis and treatment of cancers and immune disorders -

PS Claim 2; Page 3066; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.

SQ Sequence 17 AA;

Query Match 38.8%; Score 52; DB 23; Length 17;  
 Best Local Similarity 57.9%; Pred. No. 1.1;  
 Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 5 GAYEDVMSGEYPEYAMDV 23

XX DE Human gene 22-encoded secreted protein fragment, SEQ ID NO:236.  
 XX KW Human; secreted protein; proliferative disorder; cancer;  
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
 KW cardiovascular disorder; angiotensin disorder; kidney disorder;  
 KW gastrointestinal disorder; pregnancy-related disorder; tumour;  
 KW endocrine disorder; infection; wound healing; veneral;  
 KW cell culture; chemotaxis; food additive; expression;  
 KW binding partner identification.  
 XX KW Homo sapiens.  
 OS  
 XX MO200132910-A2.  
 PN 10-MAY-2001.  
 PD 25-OCT-2000; 2000MO-US29362.  
 PF 29-OCT-1999; 99US-0162240.  
 PR 30-JUN-2000; 2000US-0215131.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Ruben SM, Komatoullis GA, Birse CE, Ni J, Soppet DR;  
 PI WPI; 2001-335835/35.  
 DR  
 XX Novel 27 isolated human secreted proteins and polynucleotides encoding  
 PT them useful for treating, diagnosing, preventing Alzheimer's disease,  
 PT Parkinson's disease, AIDS, rheumatoid arthritis, asthma  
 XX Disclosure; Page 62; 594pp; English.  
 PS  
 XX AAH19170-AAH19250 represent cDNAs corresponding to 27 human secreted  
 CC protein genes, and AAG62156-AAG62235 represent the proteins they encode.  
 CC AAG62236-AAG62293 represent human secreted protein fragments. The genes  
 CC and their corresponding secreted proteins are useful for preventing,  
 CC treating or ameliorating medical conditions, e.g., by protein or gene  
 CC therapy. Pathological conditions can be diagnosed by determining the  
 CC amount of the new protein in a sample or by determining the presence of  
 CC mutations in the new genes. Specific uses are described for each of the  
 CC 52 genes, based on the tissues in which they are most highly expressed,  
 CC and include developing products for the diagnosis or treatment of  
 CC proliferative disorders, cancer, tumours, foetal and developmental  
 CC abnormalities, haematopoietic disorders, diseases of the immune system,  
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,  
 CC Alzheimer's disease, Parkinson's disease, cognitive disorders, schizophrenia, asthma,  
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,  
 CC cardiovascular disorders, angiotensin disorders, kidney disorders,  
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine  
 CC disorders, and infections. The proteins can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues, to identify their  
 CC cognate ligands or binding partners, and in chemotaxis, and can be used  
 CC as a food additive or preservative to modify storage properties.  
 CC Antibodies specific for a protein of the invention can be used in  
 CC alleviating symptoms associated with the disorders mentioned above, and  
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked  
 CC immunosorbent assay (ELISA). The present sequence represents a human  
 CC secreted protein fragment referred to in the disclosure of the invention.  
 XX  
 XX Sequence 129 AA:  
 Query Match 44.4%; Score 59.5; DB 22; Length 129;  
 Best Local Similarity 50.0%; Pred. No. 0.92;  
 Matches 12; Conservative 2; Mismatches 7; Indels 3; Gaps 1;

QY 1 DGGGG---AYEDWSCGEYPTAM 21  
 Db 26 DGGGAPSWAPEDAMWGTHTPELEM 49  
 RESULT 5  
 ABP47071  
 ID ABP47071 standard; peptide; 21 AA.  
 XX  
 AC ABP47071;  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human Blys binding scFv VH CDR3 SEQ ID 3082.  
 XX  
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX  
 OS Homo sapiens.  
 PN MO200202641-A1.  
 PD 10-JAN-2002.  
 PF 15-JUN-2001; 2001MO-US19110.  
 PR 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX WPI; 2002-114799/15.  
 DR  
 XX AntiBodies against B Lymphocyte Stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 PS Claim 2; Page 3111-3112; 3148pp; English.  
 XX  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antineumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX  
 XX Sequence 21 AA:  
 Query Match 41.4%; Score 55.5; DB 23; Length 21;  
 Best Local Similarity 54.5%; Pred. No. 0.43;  
 Matches 12; Conservative 2; Mismatches 7; Indels 1; Gaps 1;



XX Example 4; Fig 4C; 61pp; English.  
 XX This invention describes a novel polynucleotide (I) (and complements and  
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence  
 CC coding for a human antibody with factor VIII specifically which has  
 CC hemostatic activity. (I) is useful a primer or probe for detecting the  
 CC presence of inhibitory antibodies directed against factor VIII. The  
 CC polypeptides of the invention and the antibodies generated from them  
 CC are useful in compositions for neutralizing factor VIII inhibiting  
 CC antibodies in hemophilia A patients. This sequence represents the human  
 CC anti-factor VIII antibody VH IT-2 protein CDR3 fragment which is used  
 CC in the method of the invention.  
 XX  
 SQ Sequence 23 AA;  
 Query Match 100.0%; Score 134; DB 21; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-12;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 DGGGAGYEDVWSGGEYPEYAMDV 23  
 1 DGGGAGYEDVWSGGEYPEYAMDV 23  
 Db 1 DGGGAGYEDVWSGGEYPEYAMDV 23  
 RESULT 2  
 AAY50950  
 ID AAY50950 standard; Protein; 132 AA.  
 XX  
 AC AAY50950;  
 XX  
 DT 23-MAR-2000 (first entry)  
 XX  
 PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.  
 XX  
 PI Voorberg JJ, Van Den Brink EN, Turenhout EM;  
 XX  
 DR WPI; 2000-053102/04.  
 XX  
 PT New polynucleotide, polypeptide and antibody useful for diagnosing the  
 PT presence of neutralizing antibodies against factor VIII and for  
 PT treatment of hemophilia A patients with these antibodies -  
 XX  
 Example 4; Fig 4A; 61pp; English.  
 XX  
 CC This invention describes a novel polynucleotide (I) (and complements and  
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence  
 CC coding for a human antibody with factor VIII specificity which has  
 CC hemostatic activity. (I) is useful a primer or probe for detecting the  
 CC presence of inhibitory antibodies directed against factor VIII. The  
 CC polypeptides of the invention and the antibodies generated from them  
 CC are useful in compositions for neutralizing factor VIII inhibiting  
 CC antibodies in hemophilia A patients. This sequence represents the human  
 CC anti-factor VIII antibody clone IT-2 protein which is used in the method  
 CC of the invention.  
 XX  
 SQ Sequence 132 AA;  
 Query Match 100.0%; Score 134; DB 21; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-12;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 DGGGAGYEDVWSGGEYPEYAMDV 23  
 1 DGGGAGYEDVWSGGEYPEYAMDV 121  
 Db 99 DGGGAGYEDVWSGGEYPEYAMDV 121  
 RESULT 4  
 AAG62284  
 ID AAG62284 standard; Protein; 129 AA.  
 XX  
 AC AAG62284;  
 XX  
 DT 18-JUL-2001 (first entry)

Query Match 100.0%; Score 134; DB 21; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 DGGGAGYEDVWSGGEYPEYAMDV 23  
 99 DGGGAGYEDVWSGGEYPEYAMDV 121  
 Db 99 DGGGAGYEDVWSGGEYPEYAMDV 121  
 RESULT 3  
 AAY50953  
 ID AAY50953 standard; Protein; 132 AA.  
 XX  
 AC AAY50953;  
 XX  
 DT 23-MAR-2000 (first entry)  
 XX  
 PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.  
 XX  
 PI Voorberg JJ, Van Den Brink EN, Turenhout EM;  
 XX  
 DR WPI; 2000-053102/04.  
 XX  
 PT New polynucleotide, polypeptide and antibody useful for diagnosing the  
 PT presence of neutralizing antibodies against factor VIII and for  
 PT treatment of hemophilia A patients with these antibodies -  
 XX  
 Example 4; Fig 4B; 61pp; English.  
 XX  
 CC This invention describes a novel polynucleotide (I) (and complements and  
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence  
 CC coding for a human antibody with factor VIII specificity which has  
 CC hemostatic activity. (I) is useful a primer or probe for detecting the  
 CC presence of inhibitory antibodies directed against factor VIII. The  
 CC polypeptides of the invention and the antibodies generated from them  
 CC are useful in compositions for neutralizing factor VIII inhibiting  
 CC antibodies in hemophilia A patients. This sequence represents the human  
 CC anti-factor VIII antibody VH IT-2 protein which is used in the method  
 CC of the invention.  
 XX  
 SQ Sequence 132 AA;  
 Query Match 100.0%; Score 134; DB 21; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 DGGGAGYEDVWSGGEYPEYAMDV 23  
 99 DGGGAGYEDVWSGGEYPEYAMDV 121  
 Db 99 DGGGAGYEDVWSGGEYPEYAMDV 121  
 RESULT 4  
 AAG62284  
 ID AAG62284 standard; Protein; 129 AA.  
 XX  
 AC AAG62284;  
 XX  
 DT 18-JUL-2001 (first entry)

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# OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 7.39886 Seconds  
(without alignments)  
493.415 Million cell updates/sec

Title: US-09-674-752-30  
Perfect score: 134  
Sequence: 1 DGGGAGYEDVWSEGYEPTAMDV 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*  
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	134	100.0	23	21	AA150957 Human anti-factor
2	134	100.0	132	21	AA150950 Human anti-factor
3	134	100.0	132	21	AA150953 Human anti-factor
4	59.5	44.4	129	22	AA62284 Human gene 22-enco
5	55.5	41.4	21	23	ABP47071 Human Blys binding
6	55.5	41.4	253	23	ABP45766 Human Blys binding
7	52	38.8	17	23	ABP46849 Human Blys binding
8	52	38.8	20	23	ABP46732 Human Blys binding
9	52	38.8	249	23	ABP44907 Human Blys binding

10	52	38.8	249	23	ABP44915 Human Blys binding
11	52	38.8	252	23	ABP45383 Human Blys binding
12	52	38.8	252	23	ABP45635 Human Blys binding
13	52	38.8	252	23	ABP45663 Human Blys binding
14	52	38.8	252	23	ABP45684 Human Blys binding
15	52	38.8	252	23	ABP45687 Human Blys binding
16	50.5	37.7	475	24	ABJ36921 Anti-CD4 monoclon
17	50	37.3	21	23	ABP46161 Human heavy chain
18	50	37.3	44	23	ABG31313 Anti-CD4 monoclon
19	50	37.3	151	24	ABJ36993 Human Blys binding
20	50	37.3	256	23	ABP44828 Human ORF198 prot
21	49	36.6	123	23	ABP34925 Human heavy chain
22	48.5	36.2	128	22	AAE07014 Novel human diago
23	48	35.8	124	22	ABG09454 Human polypeptide
24	48	35.8	304	22	AA442096 H. pylori lactofer
25	48	35.8	528	23	ABB07347 Human Blys binding
26	47.5	35.4	22	23	ABP46750 Human Blys binding
27	47.5	35.4	253	23	ABP44927 Human Blys binding
28	47	35.1	19	23	ABP46976 Human Blys binding
29	47	35.1	108	21	AA441476 Human ORF1240
30	47	35.1	158	23	ABP31473 Human ORF446 prote
31	47	35.1	254	23	ABP31473 Human Blys binding
32	47	35.1	331	21	AA613982 Arabidopsis thalia
33	47	35.1	331	21	AA650644 Arabidopsis thalia
34	47	35.1	333	21	AA613981 Arabidopsis thalia
35	47	35.1	333	21	AA650643 Arabidopsis thalia
36	47	35.1	383	23	AAU72500 Arabidopsis thalia
37	47	35.1	401	21	AA613980 Arabidopsis thalia
38	47	35.1	401	21	AA650642 Arabidopsis thalia
39	47	35.1	1579	23	ABP91088 Hericidially activ
40	46.5	34.7	305	22	ABG25421 Novel human diago
41	46.5	34.7	357	21	AA402978 Human ORF ORF2742
42	46.5	34.7	552	22	AAU09026 Human novel glycos
43	46.5	34.7	552	22	AAU12269 Human PRO394 poly
44	46.5	34.7	552	22	AAU06620 Human protein protel
45	46.5	34.7	552	23	ABP97254 Novel human protel

## ALIGNMENTS

RESULT 1	AA150957 standard; Protein; 23 AA.
AA150957	
XX	AA150957;
AC	23-MAR-2000 (first entry)
XX	
DE	Human anti-factor VIII antibody VH protein VH IT-3 CDR3 fragment.
XX	
KW	Human; heavy chain; antibody; factor VIII; hemostatic;
KW	hemophilia A; VH protein.
OS	Homo sapiens.
XX	
PN	WO9558680-A2.
XX	
PD	18-NOV-1999.
XX	
PF	07-MAY-1999; 99MO-NL00285.
XX	
PR	08-MAY-1998; 98BP-0201543.
XX	
PA	(SANC-) STICHTING SANQUIN BLOEDVOORZIENING.
XX	
PI	Voorberg JJ, Van Den Brink EN, Turehout EAM;
XX	
DR	WPI; 2000-053102/04.
XX	
PT	New polynucleotide, polypeptide and antibody useful for diagnosing the
PT	presence of neutralizing antibodies against factor VIII and for
PT	treatment of hemophilia A patients with these antibodies -



GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 30, 2003, 10:46:19 ; Search time 30.7067 Seconds  
(without alignments)  
1058.876 Million cell updates/sec

Title: US-09-674-752-43

Perfect score: 665  
Sequence: 1 QVQLVQSGGGLVQPGKSLRL.....RRGVAAPDIWGQGTMTVYSS 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_protein:\*
- 12: sp\_virus:\*
- 13: sp Vertebrate:\*
- 14: sp Unclassified:\*
- 15: sp\_rv1rus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	502	75.5	573	4	Q8WU38
2	479	72.0	613	4	Q8WU38
3	459	69.0	118	4	Q8WU38
4	457.5	68.8	121	4	Q9UL71
5	456	68.6	112	4	Q9HCC1
6	450	67.7	471	4	Q8TC77
7	446.5	67.1	597	4	Q96BB9
8	443.5	66.7	116	4	Q9UL93
9	439.5	66.1	499	4	Q8NSK4
10	437.5	65.8	113	4	Q9UL90
11	427	64.2	147	4	Q9Y509
12	420	63.2	122	4	Q9UL84
13	419.5	63.1	493	4	Q8NCL6
14	419	63.0	118	4	Q9UL72
15	417	62.7	494	4	Q96K68
16	415	62.4	473	11	Q91205

17	409.5	61.6	104	4	Q9UL87	Q9UL87	mus	sapien
18	397	59.7	487	11	Q9YKA4	Q9YKA4	mus	muscult
19	384.5	57.8	119	11	Q920E7	Q920E7	mus	muscult
20	381.5	57.4	131	4	Q9UL88	Q9UL88	mus	sapien
21	381.5	57.4	479	11	Q91WP5	Q91WP5	mus	muscult
22	378	56.8	469	11	Q8R3V9	Q8R3V9	mus	muscult
23	376	56.5	95	4	Q9UL86	Q9UL86	mus	sapien
24	374.5	56.3	486	11	Q91207	Q91207	mus	muscult
25	371	55.8	484	11	Q8VEA0	Q8VEA0	mus	muscult
26	365	54.9	298	11	Q9QYF0	Q9QYF0	mus	muscult
27	358.5	53.9	521	4	Q8N4Y9	Q8N4Y9	mus	sapien
28	351.5	52.9	480	11	Q91XE1	Q91XE1	mus	muscult
29	342	51.4	437	11	Q9R1A4	Q9R1A4	mus	muscult
30	339.5	51.1	112	4	Q9UGP3	Q9UGP3	mus	sapien
31	337	50.7	124	4	Q9UL92	Q9UL92	mus	sapien
32	333	50.1	124	6	Q9N0M4	Q9N0M4	orycto	laque
33	330	49.6	124	6	Q9N0M6	Q9N0M6	orycto	laque
34	330	49.6	482	11	Q91X92	Q91X92	mus	muscult
35	327.5	49.2	614	4	Q96GAB	Q96GAB	mus	sapien
36	325.5	48.9	125	4	Q9UL95	Q9UL95	mus	muscult
37	325.5	48.9	484	11	Q9UL96	Q9UL96	mus	muscult
38	319	48.0	121	11	Q99NG4	Q99NG4	mus	muscult
39	313	47.1	159	4	Q96C50	Q96C50	mus	sapien
40	313	47.1	500	4	Q9BRV0	Q9BRV0	mus	sapien
41	310.5	46.7	142	11	Q924Q1	Q924Q1	mus	muscult
42	308.5	46.4	119	4	Q9UL94	Q9UL94	mus	sapien
43	304	45.7	241	11	Q921A6	Q921A6	mus	muscult
44	303.5	45.6	150	4	Q9Y298	Q9Y298	mus	sapien
45	302.5	45.5	146	11	Q924R8	Q924R8	mus	muscult

## ALIGNMENTS

### RESULT 1

ID Q8WU38 PRELIMINARY; PRT; 573 AA.

AC Q8WU38; 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Tonsil;

RA Strausberg R.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC021276; AAH21276.1; -

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_V.

DR Pfam; PF00047; Ig\_1.

DR SMART; SM00406; IGV; 4.

DR PROSITE; PSS00835; IG\_LIKE; 2.

DR PROSITE; PSS00290; IG\_MHC; 2.

KW Hypothetical protein.

SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 75.5%; Score 502; DB 4; Length 573;

Best Local Similarity 76.2%; Pred. No. 16-42;

Matches 96; Conservative 12; Mismatches 16; Indels 2; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDIAIHVRQAPAEGLRWVGSGTTIGF 60

DB 20 EVQLVESGGGLVQPGKSLRLSCAASGFTFDYAMHWROAPKGLRWVGSGISWNSGIST 79

QY 61 ADSVGRFTISPDNKNKSLYLTMNLSRAPDTLALYCALPYINSSNVRQVAAPDIWGQGT 120

DB 80 ADSVGRFTISPDNKNKSLYLTMNLSRAPDTLALYCALPYINSSNVRQVAAPDIWGQGT 137



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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RX MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
RT 1A2 immunoglobulin of the A2m (2) allotype";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02050; AZHUBU.
DR HSSP; P01789; IMCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 1 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DC64 CRC64;

Query Match 59.3%; Score 394.5; DB 1; Length 115;
Best Local Similarity 60.3%; Pred. No. 5.9e-34;
Matches 76; Conservative 24; Mismatches 15; Indels 11; Gaps 2;

DR PIR; A02047; H3H026.
DR PDB; 1H0U; 23-DEC-99.
DR Genew; HGNC:5545; IGHV0.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-II REGION VH26.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CE0F1 CRC64;

Query Match 59.5%; Score 396; DB 1; Length 117;
Best Local Similarity 76.3%; Pred. No. 4.2e-34;
Matches 74; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

OY 1 QVQLVSGGGLVQPGKSLRLSCAASGFTPDYAIHWYRQAPGEGLEWVSQVTTSGTTCF 60
DB 20 EVQLLESGGGLVQPGKSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSATISGSGSTYY 79
OY 61 ADSVKGFTISRDNKNSLYLNMSLRAPDTALYYCA 97
DB 80 GDSVKGFTISRDNKNTLYLNMSLRAPDTALYYCA 116

RESULT 12
HV3F HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region BU1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RX MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
RT 1A2 immunoglobulin of the A2m (2) allotype";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02050; AZHUBU.
DR HSSP; P01789; IMCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 1 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DC64 CRC64;

Query Match 59.3%; Score 394.5; DB 1; Length 115;
Best Local Similarity 60.3%; Pred. No. 5.9e-34;
Matches 76; Conservative 24; Mismatches 15; Indels 11; Gaps 2;

OY 1 QVQLVSGGGLVQPGKSLRLSCAASGFTPDYAIHWYRQAPGEGLEWVSQVTTSGTTCF 60
DB 1 EVQLLESGGGLVQPGKSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSATISGSGSTYY 59
OY 61 ADSVKGFTISRDNKNSLYLNMSLRAPDTALYYCA 97
DB 60 GDSVKGFTISRDNKNTLYLNMSLRAPDTALYYCA 109

RESULT 13
HV3F HUMAN STANDARD; PRT; 115 AA.
AC P01765;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region TIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RX MEDLINE=7805528; PubMed=409716;
RA Wang A.-C., Wang I.Y., Fudenberg H.H.;
RT "Immunoglobulin structure and genetics. Identity between variable
RT regions of a mu and a gamma2 chain.";
RL J. Biol. Chem. 252:7192-7199(1977).
CC -1- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
CC OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
CC GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
CC IDENTICAL.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02048; H3H02L.
DR HSSP; P01772; 2PB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.

```

```

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region TIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RX MEDLINE=7805528; PubMed=409716;
RA Wang A.-C., Wang I.Y., Fudenberg H.H.;
RT "Immunoglobulin structure and genetics. Identity between variable
RT regions of a mu and a gamma2 chain.";
RL J. Biol. Chem. 252:7192-7199(1977).
CC -1- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
CC OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
CC GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
CC IDENTICAL.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02048; H3H02L.
DR HSSP; P01772; 2PB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.

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RP SEQUENCE OF 17-136.
RX MEDLINE=7100368; PubMed=401950;
RA Adeyugo K., Milestein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@1sb-sib.ch).
CC -----
DR EMBL: J00522; AAD15290.1; -.
DR PIR: B90809; G1MS21.
DR PDB: 1IGC; 03-JUN-95.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT NON_TER 1
FT SIGNAL 1
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78
FT CONFLICT 89 90 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 115 115 DN -> ND (IN REF. 2).
FT CONFLICT 120 120 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON_TER 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDF7016 CRC64;

Query Match 61.5%; Score 409; DB 1; Length 136;
Best Local Similarity 62.0%; Pred. No. 2,3e-35;
Matches 80; Conservative 16; Mismatches 19; Indels 14; Gaps 2;

QY 2 VOLVSGGGVOPGKSLRLSCAASGFTFGDVAIHWRQAPGEGLEWVSGVTWSGTTIGFA 61
DB 18 VOLVESGGGVOPGSGRKLSCAASGFTFSFGHWRQAPGEGLEWVAIYSSGSLHYA 77
QY 62 DSVYKGRFTISRDNAKNSLYLYNNSLRAEDTALYYCA-----LPYINSNRRGAAADING 117
DB 78 DTVYKGRFTISRDNPKNLTFLQMTSLRSEDTAMVYCARMGNYPRY-----ANDYWG 127
QY 118 OGTMVTYSS 126
DB 128 QGTSVTYSS 136

RESULT 10
HVC HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SBP-2003 (Rel. 42, Last annotation update)
DR IG heavy chain V-II region KOL.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
OX 1;
RN SEQUENCE, AND DISULFID BONDS.
RP MEDLINE=83289131; PubMed=6864994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).

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RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marduari M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
RT and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02055; G1HUKL.
DR PDB: 2PB4; 12-JUL-89.
DR PDB: 2IG2; 12-JUL-89.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT TURN 58 60
FT STRAND 62 64
FT HELIX 65 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT STRAND 107 108
FT STRAND 109 109
FT STRAND 113 116
FT STRAND 120 124
FT NON_TER 126
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 59.8%; Score 398; DB 1; Length 126;
Best Local Similarity 59.3%; Pred. No. 2,8e-34;
Matches 80; Conservative 18; Mismatches 19; Indels 18; Gaps 2;

QY 1 OVOLVSGGGVOPGKSLRLSCAASGFTFGDVAIHWRQAPGEGLEWVSGVTWSGTTIGF 60
DB 1 OVOLVESGGGVOPGSRKLSCSSSGFTFSYAHTWRQAPGEGLEWVAIIMDDGSDOHY 60
QY 61 ADSVYKGRFTISRDNAKNSLYLYNNSLRAEDTALYYCALPYINSNRRGVAAF----- 113
DB 61 ADSVYKGRFTISRDNSKNTLFLQMDSLRPDGTGVYCA-----RDGSGHFCSSASCF 111
QY 114 --DIWGGTMVTYSS 126
DB 112 GPDYWGQGTPTVYSS 126

RESULT 11
HVC HUMAN STANDARD; PRT; 117 AA.
AC P01764;

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QY 61 ADVKGRFTISRDNKNSLYLYMNSLRADPTALYYCALPYINSSNYRGRVAAPDIWGQGT 120  
 DB 61 AASVKGRTTISRBSKRTMYLBNMSLRADPTALYYCA----RSGIALGSAVAGTDYWGQGT 116  
 QY 121 MVTVSS 126  
 DB 117 LVTIVSS 122

## RESULT 7

HV3B\_HUMAN STANDARD; PRT; 114 AA.  
 ID HV3B\_HUMAN P01763;  
 AC P01763;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region WEA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_Taxid=9606;  
 RX MEDLINE=83273707; PubMed=6410398;  
 RN SEQUENCE.  
 RP Goni F., Frangione B.;

RT "Amino acid sequence of the Fv region of a human monoclonal IgM (protein WEA) with antibody activity against 3,4-pyruvylated galactose in Klebsiella polysaccharides K30 and K33."  
 RT Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH WALDENSTROM'S MACROGLOBULINEMIA.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02046; M3HUM.  
 DR HSSP; P01772; 2FB4.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Pyroliidone carboxylic acid.  
 FT MOD\_RES 1 112 PYRROLIDONE CARBOXYLIC ACID.  
 FT NON\_TER 114 114  
 SO SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;

Query Match 62.3%; Score 414; DB 1; Length 114;  
 Best Local Similarity 65.1%; Pred. No. 5, 6e-36;  
 Matches 82; Conservative 18; Mismatches 14; Indels 12; Gaps 1;

QY 1 QVQLVDSGGGLVPGGSLRLSCAASGFTGDYAIHWVRAPGEGLEWVSQVTGTTIGF 60  
 DB 1 QVQLVDSGGGLVPGGSLRLSCAASGFTGSANDMVRAPGEGLEWVSFTIGSGSTIY 60  
 QY 61 ADVKGRFTISRDNKNSLYLYMNSLRADPTALYYCALPYINSSNYRGRVAAPDIWGQGT 120  
 DB 61 ADVKGRFTISRDNKNSLYLYMNSLRADPTALYYCALPYINSSNYRGRVAAPDIWGQGT 108  
 QY 121 MVTVSS 126  
 DB 109 LVTIVSS 114

RESULT 8  
 HV3A\_HUMAN STANDARD; PRT; 122 AA.  
 ID HV3A\_HUMAN P01762;  
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region TRO.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_Taxid=9606;  
 RX MEDLINE=76023781; PubMed=809331;  
 RN SEQUENCE (MYELOMA PROTEIN TRO).  
 RP Kratzin H., Altevogt P., Ruban E., Kortt A., Starosck K., Hilschmann N.;

RT "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.), RT II. The amino acid sequence of the H-chain, alpha-type, subgroup III; RT structure of the complete IgA-molecule."  
 RT Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).  
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02045; A1HUTR.  
 DR HSSP; P01772; 2FB4.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Pyroliidone carboxylic acid.  
 FT MOD\_RES 1 108 IG-LIKE.  
 FT NON\_TER 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SO SEQUENCE 122 AA; 13472 MW; 2E21A11DA04D80F9 CRC64;

Query Match 62.0%; Score 412; DB 1; Length 122;  
 Best Local Similarity 59.5%; Pred. No. 9, 8e-36;  
 Matches 75; Conservative 24; Mismatches 23; Indels 4; Gaps 1;  
 QY 1 QVQLVDSGGGLVPGGSLRLSCAASGFTGDYAIHWVRAPGEGLEWVSQVTGTTIGF 60  
 DB 1 QVQLVDSGGGLVPGGSLRLSCAASGFTGSANDMVRAPGEGLEWVSFTIGSGSTIY 60  
 QY 61 ADVKGRFTISRDNKNSLYLYMNSLRADPTALYYCALPYINSSNYRGRVAAPDIWGQGT 120  
 DB 61 ADVKGRFTISRDNKNSLYLYMNSLRADPTALYYCA----TBFPMSTSLBYWGZGB 116  
 QY 121 MVTVSS 126  
 DB 117 LVTIVSS 122

## RESULT 9

HV16\_MOUSE STANDARD; PRT; 136 AA.  
 ID HV16\_MOUSE P01783;  
 AC P01783;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region MOPC 21 precursor (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_Taxid=10090;  
 RX MEDLINE=81234548; PubMed=6788376;  
 RA Bothwell A.L.M., Paekind M., Reth M., Imantsht-Karl T., Rajewsky K., Baltimore D.;

RT "Heavy chain variable region contribution to the NPB family of RT antibodies; somatic mutation evident in a gamma 2a variable region."  
 RT Cell 24:625-637(1981).  
 RN [2]





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RESULT 2
HV3U_HUMAN          STANDARD;          PRT;          120 AA.
ID   HV3U_HUMAN
AC   P01782;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-II region DOB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RP   SEQUENCE.
RX   MEDLINE=80020921; PubMed=114209;
RA   Steiner L.A., Garcia Pardo A., Margolies M.N.;
RT   "Amino acid sequence of the heavy-chain variable region of the
RL   crystallizable human myeloma protein Dob."
RL   Biochemistry 18:4068-4080(1979).
[2]
RN   RP
RP   CRYSTALLIZATION.
RX   MEDLINE=80020920; PubMed=114208;
RA   Steiner L.A.; Lopes A.D.;
RT   "The crystallizable human myeloma protein Dob has a hinge-region
RT   deletion."
RL   Biochemistry 18:4054-4067(1979).
CC   -1- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE
CC   HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN
CC   DISULFIDE BONDS.
CC   -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   PIR; A50431; GIH0DB.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; P:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig_Like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; Ig_V.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN 1 112 IG-LIKE.
FT   NON TER 120 120
SQ   SEQUENCE 120 AA; 13440 MW; 880DDE307C4B2627 CRC64;

Query Match 65.7%; Score 437; DB 1; Length 120;
Best Local Similarity 65.1%; Pred. No. 2.5e-38;
Matches 82; Conservative 18; Mismatches 20; Indels 6; Gaps 1;

QY 1 OVQLVSGGGLVQPGKSLRLSCAAGFTGDAIHVRQAQPGCLEWVSGVTIGTGF 60
DB 1 EVQLVSGGGLVQPGKSLRLSCAAGFTGDAIHVRQAQPGCLEWVSGVTIGTGF 60
QY 61 ADSVKGRTISRDNAKNSLYLNMSLRPEDTALYYCALPYINSSNYRQVAAPFDIWGQGT 120
DB 61 ADSVKGRTISRDNAKNSLYLNMSLRPEDTALYYCALPYINSSNYRQVAAPFDIWGQGT 120
QY 121 MVTVSS 126
DB 115 LVTVSS 120

RESULT 3
HV3I_HUMAN          STANDARD;          PRT;          119 AA.
ID   HV3I_HUMAN
AC   P01770;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-II region NIB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OX   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN   RP
RP   SEQUENCE.
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponsstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a
RT   monoclonal IgG1 immunoglobulin (myeloma protein Nle). II. The
RT   chymotryptic peptides of the H-chain, alignment of the tryptic
RT   peptides and discussion of the complete structure."
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
[2]
RN   RP
RP   DISULFIDE BOND.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreher L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nle). I: Purification and
RT   characterization of the protein, the L- and H-chains, the
RT   cyanogen bromide cleavage products, and the disulfide bridges."
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC   -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG01 MYELOMA
CC   PROTEIN.
CC   -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   PIR; A51668; GIH0NT.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; P:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig_Like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; Ig_V.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN 1 112 IG-LIKE.
FT   MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID 22 96
FT   NON TER 119 119
SQ   SEQUENCE 119 AA; 13242 MW; C96935A655E1658 CRC64;

Query Match 64.0%; Score 425.5; DB 1; Length 119;
Best Local Similarity 66.7%; Pred. No. 3.8e-37;
Matches 84; Conservative 14; Mismatches 21; Indels 7; Gaps 1;

QY 1 OVQLVSGGGLVQPGKSLRLSCAAGFTGDAIHVRQAQPGCLEWVSGVTIGTGF 60
DB 1 EVQLVSGGGLVQPGKSLRLSCAAGFTGDAIHVRQAQPGCLEWVSGVTIGTGF 60
QY 61 ADSVKGRTISRDNAKNSLYLNMSLRPEDTALYYCALPYINSSNYRQVAAPFDIWGQGT 120
DB 61 ADSVKGRTISRDNAKNSLYLNMSLRPEDTALYYCALPYINSSNYRQVAAPFDIWGQGT 113
QY 121 MVTVSS 126
DB 114 LVTVSS 119

RESULT 4
HV3T_HUMAN          STANDARD;          PRT;          116 AA.
ID   HV3T_HUMAN
AC   P01781;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V-II region GAL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN   RP
RP   SEQUENCE.
RX   MEDLINE=75059123; PubMed=4803843;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 6.75548 Seconds  
(Without alignments)  
877.119 Million cell updates/sec

Title: US-09-674-752-43

Sequence: 1 QVQLVQSGGGLVPGKSLRL.....RRGVAFDIWGQGTMTVSS 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	444	66.8	122	1	HV3G_HUMAN
2	437	65.7	120	1	HV3U_HUMAN
3	425.5	64.0	119	1	HV3I_HUMAN
4	424	63.8	116	1	HV3T_HUMAN
5	422.5	63.5	121	1	HV3J_HUMAN
6	419	63.0	122	1	HV3H_HUMAN
7	414	62.3	114	1	HV3B_HUMAN
8	412	62.0	122	1	HV3A_HUMAN
9	409	61.5	126	1	HV3K_HUMAN
10	398	59.8	136	1	HV16_MOUSE
11	396	59.5	117	1	HV3C_HUMAN
12	394.5	59.3	115	1	HV3F_HUMAN
13	392.5	59.0	115	1	HV3D_HUMAN
14	386.5	58.1	119	1	HV3L_HUMAN
15	382	57.4	114	1	HV01_CANFA
16	379	57.0	119	1	HV3M_HUMAN
17	379	57.0	122	1	HV20_MOUSE
18	378.5	56.9	120	1	HV3E_HUMAN
19	377.5	56.8	116	1	HV3R_HUMAN
20	377	56.7	119	1	HV38_MOUSE
21	376	56.5	119	1	HV37_MOUSE
22	373	56.1	119	1	HV40_MOUSE
23	372.5	56.0	123	1	HV18_MOUSE
24	372	55.9	117	1	HV3O_HUMAN
25	369	55.5	122	1	HV21_MOUSE
26	368.5	55.4	123	1	HV19_MOUSE
27	367.5	55.3	116	1	HV05_CARAU
28	367	55.2	119	1	HV3N_HUMAN
29	365.5	55.0	123	1	HV22_MOUSE
30	365.5	55.0	123	1	HV23_MOUSE
31	363.5	54.7	117	1	HV02_CANFA
32	362	54.4	111	1	HV35_MOUSE
33	360.5	54.2	115	1	HV32_MOUSE

34	360	54.1	119	1	HV3P_HUMAN
35	358.5	53.9	113	1	HV30_MOUSE
36	358.5	53.9	117	1	HV41_MOUSE
37	356	53.5	98	1	HV57_MOUSE
38	355.5	53.5	113	1	HV34_MOUSE
39	354.5	53.3	117	1	HV17_MOUSE
40	354.5	53.3	123	1	HV24_MOUSE
41	354.5	53.3	142	1	HV01_RAT
42	353.5	53.2	113	1	HV01_MOUSE
43	353.5	53.2	118	1	HV39_MOUSE
44	352.5	53.0	115	1	HV33_MOUSE
45	350.5	52.7	123	1	HV25_MOUSE

## ALIGNMENTS

RESULT 1  
ID HV3G\_HUMAN STANDARD; PRT; 122 AA.  
AC P01768;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DE Ig heavy chain V-III region CAM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN  
RP  
RX MEDLINE=01013859; PubMed=6774332;  
RA Lehman D.W., Putnam F.W.;  
RT "Amino acid sequence of the variable region of a human mu chain:  
RL location of a possible JH segment."  
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).  
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A  
CC PATIENT WITH MACROGLOBULINEMIA.  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A02051; M3HUM.  
DR HSSP; P01772; 2PB4.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IgV\_1.  
DR PROSITE; PS50835; IG\_Like; 1.  
KW Immunoglobulin V region; Pyroglutamate carboxylic acid.  
FT DOMAIN 1 112 IG-LIKE.  
FT MOD RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
FT NON TER 122  
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 66.8%; Score 444; DB 1; Length 122;

Best Local Similarity 65.1%; Pred. No. 4.8e-39; Indels 4; Gaps 1;

Matches 82; Conservative 23; Mismatches 17; Indels 4; Gaps 1;

Qy	1	QVQLVQSGGGLVPGKSLRLCAASGFTFGDVAIHWRQAPGSGLEWVSGVTSGTTIGF 60
Db	1	QVQLVSGGGLVPGKSLRLCAASGFTFGDVAIHWRQAPGSGLEWVAVISVGBBKXY 60
Qy	61	ADSVKGRFTISRDNAKNSLYLNRSIAPELTALYCALPYINSNTRRGVAADINGGCT 120
Db	61	ABSVKGRFTISRDNSKNTLYLQNNISRAETAVYCARDPILGYBYR---AFNYGGGT 116
Qy	121	MTVSS 126
Db	117	LTVSS 122



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; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 102506
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-102506

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Query Match          80.9%; Score 503; DB 22; Length 118;
Best Local Similarity 82.4%; Pred. No. 1e-42;
Matches 98; Conservative 5; Mismatches 14; Indels 2; Gaps 1;

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QY 2 VOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKRYA 61
   1 VOLVESGGGVQPGKSLRLSCAASGFTFSSYGMMHWROAPGKLEWVAVISYDGSNKRYA 60
DB 1
QY 62 DSVKGRFAISRDNKNTLYLQNMSLTIEDTAVYYCAKDLIESNIAELMGQGLTVTVSS 120
   61 DSVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCAKDW--DSYGYDWGQGLTVTVSS 117
DB 61

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## RESULT 11

```

PCT-US03-05128-18
; Sequence 18, Application PC/TUS0305128
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation, et al
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034W01
; CURRENT APPLICATION NUMBER: PCT/US03/05128
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-05128-18

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Query Match          80.9%; Score 503; DB 1; Length 120;
Best Local Similarity 80.0%; Pred. No. 1e-42;
Matches 96; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

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QY 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKRY 60
   1 QVOLVSGGGVQPGKSLRLSCAASGFTFSSYGMMHWROAPGKLEWVAVISYDGSNKRY 60
DB 1
QY 61 ADVKGRFAISRDNKNTLYLQNMSLTIEDTAVYYCAKDLIESNIAELMGQGLTVTVSS 120
   61 ADVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCADDYGDYALLDYWGQGLTVTVSS 120
DB 61

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## RESULT 12

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US-10-371-942-18
; Sequence 18, Application US/10371942
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Reneus Jacobus Mattheus
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18

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; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-18

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Query Match          80.9%; Score 503; DB 29; Length 120;
Best Local Similarity 80.0%; Pred. No. 1e-42;
Matches 96; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

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QY 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKRY 60
   1 QVOLVSGGGVQPGKSLRLSCAASGFTFSSYGMMHWROAPGKLEWVAVISYDGSNKRY 60
DB 1
QY 61 ADVKGRFAISRDNKNTLYLQNMSLTIEDTAVYYCAKDLIESNIAELMGQGLTVTVSS 120
   61 ADVKGRFTISRDNKNTLYLQNMSLRAEDTAVYYCADDYGDYALLDYWGQGLTVTVSS 120
DB 61

```

## RESULT 13

```

US-09-791-537-19813
; Sequence 19813, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19813
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-19813

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```

Query Match          80.8%; Score 502.5; DB 22; Length 132;
Best Local Similarity 81.7%; Pred. No. 1.3e-42;
Matches 98; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

```

```

QY 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKRY 60
   16 QVOLVSGGGVQPGKSLRLSCAASGFTFSSYGMMHWROAPGKLEWVAVISYDGSNKRY 75
DB 16
QY 61 ADVKGRFAISRDNKNTLYLQNMSLTIEDTAVYYCAKDLIESNIAELMGQGLTVTVSS 120
   76 ADVKGRFTISRDNKNTLYLQNMGLRAEDTAVYYCAKDLF---YFDYWGQGLTVTVSS 132
DB 76

```

## RESULT 14

```

US-09-791-537-31924
; Sequence 31924, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31924
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-31924

```

```

Query Match          80.7%; Score 502; DB 22; Length 118;
Best Local Similarity 80.8%; Pred. No. 1.3e-42;

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US-09-791-106428
; Sequence 106428, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 106428
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-106428

Query Match      81.6%; Score 507.5; DB 22; Length 125;
Best Local Similarity 80.0%; Pred. No. 3.8e-43;
Matches 100; Conservative 7; Mismatches 13; Indels 5; Gaps 1;

Cy 1 EVOLVESGGGLVQPGKSLRLSCQDSGLTFSSYGMMHWRQAPGAGLEWVAVISYDGNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSSYGMMHWRQAPGKLEWVAVISYDGSNKYY 60

Cy 61 ADSVKGRAISRDNKNTLYLQMSLTIEDTAIVYVCADLIENIAEA-----LWGQGLT 115
Db 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAIVYVCADLPKRAIAALPNMFDPMQGLT 120

Cy 116 TVVSS 120
Db 121 TVVSS 125

RESULT 7
US-09-791-537-68722
; Sequence 68722, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 68722
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-68722

Query Match      81.5%; Score 507; DB 22; Length 118;
Best Local Similarity 80.8%; Pred. No. 4e-43;
Matches 97; Conservative 8; Mismatches 13; Indels 2; Gaps 1;

Cy 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWRQAPGAGLEWVAVISYDGNKYY 60
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTFSSYGMMHWRQAPGKLEWVAVISYDGSNKYY 60

Cy 61 ADSVKGRAISRDNKNTLYLQMSLTIEDTAIVYVCADLIENIAEAALWGQGLT 120
Db 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAIVYVCADLERVGVWN--WGQGLTVVSS 118

RESULT 8
US-09-791-537-102505
; Sequence 102505, Application US/09791537
; GENERAL INFORMATION:
```

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; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 102505
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-102505

Query Match      81.4%; Score 506.5; DB 22; Length 119;
Best Local Similarity 83.2%; Pred. No. 4.6e-43;
Matches 99; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

Cy 2 VQLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWRQAPGAGLEWVAVISYDGNKYYA 61
Db 1 VQLVESGGGVQPGKSLRLSCAASGFTFSSYGMMHWRQAPGKLEWVAVISYDGSNKYYA 60

Cy 62 DSVKGRPAISRDNKNTLYLQMSLTIEDTAIVYVCADLIENIAEAALWGQGLTVVSS 120
Db 61 DSVKGRPTISRDNKNTLYLQMSLRAEDTAIVYVCADLQGLWSSD--YWGQGLTVVSS 118

RESULT 9
US-09-791-537-31283
; Sequence 31283, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31283
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-31283

Query Match      81.4%; Score 506; DB 22; Length 125;
Best Local Similarity 81.5%; Pred. No. 5.4e-43;
Matches 101; Conservative 7; Mismatches 12; Indels 4; Gaps 2;

Cy 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMHWRQAPGAGLEWVAVISYDGNKYY 60
Db 1 EVOLVESGGGVQPGKSLRLSCAASGFTFSSYGMMHWRQAPGKLEWVAVISYDGSNKYY 60

Cy 61 ADSVKGRAISRDNKNTLYLQMSLTIEDTAIVYVCAD--LIENIAEAAL--WGQGLTV 116
Db 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAIVYVCADLIYVYSSGYSIDYWGQGLTV 120

Cy 117 TVSS 120
Db 121 TVSS 124

RESULT 10
US-09-791-537-102506
; Sequence 102506, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
```

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGRLSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKXY 60  
DB 1 EVOLVESGGGLVOPGRLSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKXY 60

QY 61 ADVKGRFPAISRDNKNTLYLQNNSLTIETDAVYCAKDLESNIABALMGOTLVTVSS 120  
DB 61 ADVKGRFPAISRDNKNTLYLQNNSLTIETDAVYCAKDLESNIABALMGOTLVTVSS 120

RESULT 2  
US-09-674-752-46  
; Sequence 46; Application US/09674752  
; GENERAL INFORMATION:  
; APPLICANT: Vooorberg, Johannes  
; TITLE OF INVENTION: Method For Diagnosis and Treatment of Haemophilia A Patients With  
; FILE REFERENCE: Sequence Nos 1-59 for 294-86 PCT/US  
; CURRENT APPLICATION NUMBER: US/09/674,752  
; PRIOR FILING DATE: 2000-12-29  
; PRIOR APPLICATION NUMBER: PCT/NL99/00285  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: EP 98201543.0  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 46  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-674-752-46

Query Match 100.0%; Score 622; DB 20; Length 120;  
Best Local Similarity 100.0%; Pred. No. 8.6e-55;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGRLSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKXY 60  
DB 1 EVOLVESGGGLVOPGRLSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKXY 60

QY 61 ADVKGRFPAISRDNKNTLYLQNNSLTIETDAVYCAKDLESNIABALMGOTLVTVSS 120  
DB 61 ADVKGRFPAISRDNKNTLYLQNNSLTIETDAVYCAKDLESNIABALMGOTLVTVSS 120

RESULT 3  
US-09-791-537-87993  
; Sequence 87993; Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; PRIOR FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 87993  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-87993

Query Match 83.3%; Score 518; DB 22; Length 121;  
Best Local Similarity 81.7%; Pred. No. 3.2e-44;  
Matches 98; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGRLSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKXY 60  
DB 1 EVOLVESGGGLVOPGRLSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKXY 60

QY 61 ADVKGRFPAISRDNKNTLYLQNNSLTIETDAVYCAKDLESNIABALMGOTLVTVSS 120  
DB 61 ADVKGRFPAISRDNKNTLYLQNNSLTIETDAVYCAKDLESNIABALMGOTLVTVSS 120

RESULT 4  
US-09-791-537-31853  
; Sequence 31853; Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; PRIOR FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 31853  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-31853

Query Match 81.8%; Score 509; DB 22; Length 121;  
Best Local Similarity 80.8%; Pred. No. 2.6e-43;  
Matches 97; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGRLSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKXY 60  
DB 1 EVOLVESGGGLVOPGRLSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKXY 60

QY 61 ADVKGRFPAISRDNKNTLYLQNNSLTIETDAVYCAKDLESNIABALMGOTLVTVSS 120  
DB 61 ADVKGRFPAISRDNKNTLYLQNNSLTIETDAVYCAKDLESNIABALMGOTLVTVSS 120

RESULT 5  
US-09-791-537-69157  
; Sequence 69157; Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; PRIOR FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 69157  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-69157

Query Match 81.8%; Score 508.5; DB 22; Length 117;  
Best Local Similarity 82.5%; Pred. No. 2.8e-43;  
Matches 99; Conservative 7; Mismatches 11; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVOPGRLSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKXY 60  
DB 1 EVOLVESGGGLVOPGRLSLRLSCVDSGLTFSSYGMMHWROAPGAGLEWVAVISYDGNKXY 60

QY 61 ADVKGRFPAISRDNKNTLYLQNNSLTIETDAVYCAKDLESNIABALMGOTLVTVSS 120  
DB 61 ADVKGRFPAISRDNKNTLYLQNNSLTIETDAVYCAKDLESNIABALMGOTLVTVSS 120

RESULT 6

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: December 30, 2003, 10:54:45 ; Search time 191.162 Seconds  
(without alignments)  
571.193 Million cell updates/sec

Title: US-09-674-752-46

Perfect score: 622  
Sequence: 1 EVQLVESGGGLVQPGKSLRL.....IESNIARALWGQTLVTWSS 120

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Pending Patents AA Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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	622	100.0	120	20	US-09-674-752-46	Sequence 46, Appl 1	518	83.3	121	22	US-09-791-537-87993	Sequence 87993, A	509	81.8	121	22	US-09-791-537-31853	Sequence 31853, A	508.5	81.8	117	22	US-09-791-537-69157	Sequence 69157, A	507.5	81.5	118	22	US-09-791-537-106428	Sequence 106428, A	507	81.6	118	22	US-09-791-537-68722	Sequence 68722, A	506.5	81.4	119	22	US-09-791-537-102505	Sequence 102505, A	506	81.4	125	22	US-09-791-537-31283	Sequence 31283, A	503	80.9	118	22	US-09-791-537-102506	Sequence 102506, A	503	80.9	120	1	PCT-US03-05128-18	Sequence 18, Appl 1	502.5	80.8	113	22	US-09-791-537-119813	Sequence 119813, A	502	80.7	118	22	US-09-791-537-31924	Sequence 31924, A	502	80.7	122	22	US-09-791-537-69145	Sequence 69145, A	502	80.6	128	22	US-09-791-537-63340	Sequence 63340, A	501.5	80.6	119	22	US-09-791-537-80297	Sequence 80297, A	501.5	80.6	120	22	US-09-791-537-63269	Sequence 63269, A	501.5	80.6	121	1	PCT-US03-05128-54	Sequence 54, Appl 1	501.5	80.6	121	1	PCT-US03-05128-62	Sequence 62, Appl 1	501.5	80.6	121	29	US-10-371-942-54	Sequence 54, Appl 1	501.5	80.6	121	29	US-10-371-942-62	Sequence 62, Appl 1	501.5	80.6	121	29	US-10-371-942-62	Sequence 62, Appl 1	501.5	80.6	123	22	US-09-791-537-69270	Sequence 69270, A	501.5	80.6	123	22	US-09-791-537-711-7	Sequence 7, Appl 1	501.5	80.6	123	32	US-09-791-537-11717	Sequence 11, Appl 1	501.5	80.6	123	28	US-09-791-537-69606	Sequence 69606, A	501	80.5	122	1	PCT-US02-36107-114	Sequence 114, App	501	80.5	122	28	US-10-292-088-114	Sequence 114, App	501	80.5	126	22	US-09-791-537-106426	Sequence 106426, A	501	80.5	138	22	US-09-791-537-102461	Sequence 102461, A	501	80.5	227	1	PCT-US02-33556-76	Sequence 76, Appl 1	501	80.5	227	25	US-09-972-656-76	Sequence 76, Appl 1	501	80.5	241	1	PCT-US03-09625-100	Sequence 100, App	500.5	80.5	121	22	US-09-791-537-106429	Sequence 106429, A	500.5	80.5	123	28	US-10-269-711-43	Sequence 43, Appl 1	500.5	80.5	123	32	US-09-791-537-116121	Sequence 116121, A	500.5	80.5	133	22	US-09-791-537-71741	Sequence 71741, A	500	80.4	130	22	US-09-791-537-31907	Sequence 31907, A	500	80.4	130	22	US-09-791-537-116626	Sequence 116626, A	500	80.4	133	22	US-09-791-537-11717	Sequence 11717, App	500	80.4	133	22	US-09-791-537-128053	Sequence 128053, A	499.5	80.3	135	22	US-09-791-537-96305	Sequence 96305, A	499.5	80.3	138	18	US-09-403-107-144	Sequence 144, App

## ALIGNMENTS

RESULT 1  
US-09-674-752-36  
Sequence 36, Application US/09674752  
GENERAL INFORMATION:  
APPLICANT: Vooberg, Johannes  
TITLE OF INVENTION: Method For Diagnosis and Treatment of Haemophilia A Patients With  
FILE REFERENCE: Sequence No 1-59 for 294-86 PCT/US  
CURRENT APPLICATION NUMBER: US/09/674,752  
PRIOR FILING DATE: 2000-12-29  
PRIOR APPLICATION NUMBER: PCT/NI99/00285  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: EP 98201543.0  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 36  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-674-752-36  
Query Match 100.0%; Score 622; DB 20; Length 120;  
Best Local Similarity 100.0%; Pred. No. 8.6e-55;



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QY      1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMHWYRQAPGAGLEWNAVISTGNDKTY 60
      :|||:||||:|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      1 QVQLVDSGGGVQPGRSRLRLSCAASGFTFSSYGMHWYRQAPGKGLEWNAVISTDGSIKYY 60
QY      61 ADSVKGKRFATSRDNNKNTLYLQMNLSLTIEDTAVYYCAKDLIESNIAEALWGCGTLVTYSS 120
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      61 ADSVKGKRFATSRDNNKNTLYLQMNLSLAEDTAVYYCARD--AAVTAEGWGKGLVTYSS 117
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Search completed: December 30, 2003, 11:45:24  
 Job time : 25.7352 secs

;; TITLE OF INVENTION: THEREOF  
;; FILE REFERENCE: ABGENIX.051A  
;; CURRENT APPLICATION NUMBER: US/10/041,860  
;; CURRENT FILING DATE: 2002-01-07  
;; NUMBER OF SEQ ID NOS: 377  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 33  
;; LENGTH: 127  
;; TYPE: PRT  
;; ORGANISM: homo sapiens  
US-10-041-860-33

Query Match 79.3%; Score 493.5; DB 12; Length 127;  
Best Local Similarity 74.8%; Pred. No. 2.8e-40;  
Matches 95; Conservative 8; Mismatches 17; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVQPGSRSLSCVDSGLTFSSYGMHWVQAPAGLEWVAIVSYDNDKRY 60  
DB 1 QVQLVESGGGVQPGSRSLSCASGFTFSYGMHWVQAPGKGLEWVAIIWYDNDKRY 60  
QY 61 ADVKGRFAISRDNKNTLYLQMSLTIEDTAVYYCAK-----DLIESNIAELMGQG 113  
DB 61 ADVKGRFTVSRDNRKNTLYLQMSLRADTAVYYCARGYYDSSDYLYYYGMDVWGQG 120  
QY 114 TLVTVSS 120  
DB 121 TTVTVSS 127

## RESULT 13

US-10-041-860-211  
;; Sequence 211, Application US/10041860  
;; Publication No. US20030157109A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Corvalan, Jose R.F.  
;; APPLICANT: Jia, Xiao-Chi  
;; APPLICANT: Peng, Xiao  
;; APPLICANT: Yang, Xiao-Dong  
;; APPLICANT: Chen, Francine  
;; APPLICANT: Gazit, Gadi  
;; APPLICANT: Weber, Richard  
;; APPLICANT: Bezaheh, Binayam  
;; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USBS  
;; FILE REFERENCE: ABGENIX.051A  
;; CURRENT APPLICATION NUMBER: US/10/041,860  
;; CURRENT FILING DATE: 2002-01-07  
;; NUMBER OF SEQ ID NOS: 377  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 211  
;; LENGTH: 127  
;; TYPE: PRT  
;; ORGANISM: homo sapiens  
US-10-041-860-211

Query Match 79.3%; Score 493.5; DB 12; Length 127;  
Best Local Similarity 74.8%; Pred. No. 2.8e-40;  
Matches 95; Conservative 8; Mismatches 17; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVQPGSRSLSCVDSGLTFSSYGMHWVQAPAGLEWVAIVSYDNDKRY 60  
DB 1 QVQLVESGGGVQPGSRSLSCASGFTFSYGMHWVQAPGKGLEWVAIIWYDNDKRY 60  
QY 61 ADVKGRFAISRDNKNTLYLQMSLTIEDTAVYYCAK-----DLIESNIAELMGQG 113  
DB 61 ADVKGRFTVSRDNRKNTLYLQMSLRADTAVYYCARGYYDSSDYLYYYGMDVWGQG 120  
QY 114 TLVTVSS 120  
DB 121 TTVTVSS 127

## RESULT 14

## US-10-041-860-331

;; Sequence 331, Application US/10041860  
;; Publication No. US20030157109A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Corvalan, Jose R.F.  
;; APPLICANT: Jia, Xiao-Chi  
;; APPLICANT: Peng, Xiao  
;; APPLICANT: Yang, Xiao-Dong  
;; APPLICANT: Chen, Francine  
;; APPLICANT: Gazit, Gadi  
;; APPLICANT: Weber, Richard  
;; APPLICANT: Bezaheh, Binayam  
;; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USBS  
;; FILE REFERENCE: ABGENIX.051A  
;; CURRENT APPLICATION NUMBER: US/10/041,860  
;; CURRENT FILING DATE: 2002-01-07  
;; NUMBER OF SEQ ID NOS: 377  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 331  
;; LENGTH: 127  
;; TYPE: PRT  
;; ORGANISM: homo sapiens  
US-10-041-860-331

Query Match 79.3%; Score 493.5; DB 12; Length 127;  
Best Local Similarity 74.8%; Pred. No. 2.8e-40;  
Matches 95; Conservative 8; Mismatches 17; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVQPGSRSLSCVDSGLTFSSYGMHWVQAPAGLEWVAIVSYDNDKRY 60  
DB 1 QVQLVESGGGVQPGSRSLSCASGFTFSYGMHWVQAPGKGLEWVAIIWYDNDKRY 60  
QY 61 ADVKGRFAISRDNKNTLYLQMSLTIEDTAVYYCAK-----DLIESNIAELMGQG 113  
DB 61 ADVKGRFTVSRDNRKNTLYLQMSLRADTAVYYCARGYYDSSDYLYYYGMDVWGQG 120  
QY 114 TLVTVSS 120  
DB 121 TTVTVSS 127

## RESULT 15

US-09-880-748-1912  
;; Sequence 1912, Application US/09880748  
;; Publication No. US2003005937A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ruben et al.  
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
;; FILE REFERENCE: PF523  
;; CURRENT APPLICATION NUMBER: US/09/880,748  
;; CURRENT FILING DATE: 2001-06-15  
;; PRIOR APPLICATION NUMBER: 60/212,210  
;; PRIOR FILING DATE: 2000-06-15  
;; PRIOR APPLICATION NUMBER: 60/240,816  
;; PRIOR FILING DATE: 2000-10-17  
;; PRIOR APPLICATION NUMBER: 60/276,248  
;; PRIOR FILING DATE: 2001-03-16  
;; PRIOR APPLICATION NUMBER: 60/277,379  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/293,499  
;; PRIOR FILING DATE: 2001-05-25  
;; NUMBER OF SEQ ID NOS: 3239  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 1912  
;; LENGTH: 240  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-880-748-1912

Query Match 79.3%; Score 493.5; DB 11; Length 240;  
Best Local Similarity 79.2%; Pred. No. 5.6e-40;  
Matches 95; Conservative 9; Mismatches 13; Indels 3; Gaps 1;

APPLICANT: Es van, Helmut  
APPLICANT: Havena, Menzo  
APPLICANT: Verlinden, Stefan  
TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID  
TITLE OF INVENTION: TRANSPORTER  
FILE REFERENCE: 2183-4080US  
CURRENT APPLICATION NUMBER: US/10/235,175  
CURRENT FILING DATE: 2002-09-04  
PRIOR APPLICATION NUMBER: US/09/315,926  
PRIOR FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: EP 99201593.3  
PRIOR FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: EP 98201693.3  
PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 80  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Description of Artificial Sequence: phage  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(248)  
OTHER INFORMATION: /note="hCAT1 amino acid sequence"  
US-10-235-175-80

Query Match 79.6%; Score 495; DB 12; Length 248;  
Best Local Similarity 78.3%; Pred. No. 4.2e-40;  
Matches 94; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 1 EVOLVESGGGLVQPGSRSLRLSCVDSGLTFSSYGHWVRQAAGGLEWVAVISYDGNKXY 60  
Db 23 QVQLVDSGGGVQPGSRSLRLSCAASGFTFSYGMHWVRQAAGGLEWVAVISYDGNKXY 82  
Qy 61 ADSVKGRAISRDNKNTLYLQNNSLTIETDAVYVYCAKDLIESNIAEALMGOGTLVTSS 120  
Db 83 ADSVKGRTISRDNKNTLYLQNNSLRAEDTAVYVYCAKGIYTKSRFYWGOGTLVTSS 142

RESULT 10  
US-09-880-748-512  
Sequence 512, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 512  
LENGTH: 249  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-512

Query Match 79.6%; Score 495; DB 11; Length 249;  
Best Local Similarity 77.0%; Pred. No. 4.2e-40;  
Matches 97; Conservative 7; Mismatches 16; Indels 6; Gaps 1;

Qy 1 EVOLVESGGGLVQPGSRSLRLSCVDSGLTFSSYGHWVRQAAGGLEWVAVISYDGNKXY 60  
Db 1 QVQLVDSGGGVQPGSRSLRLSCAASGFTFSYGMHWVRQAAGGLEWVAISYDGNKXY 60  
Qy 61 ADSVKGRAISRDNKNTLYLQNNSLTIETDAVYVYCAKDLIESNIAEALMGOGT 114  
Db 61 ADSVKGRTISRDNKNTLYLQNNSLRAEDTAVYVYCAKGIYTKSRFYWGOGT 120  
Qy 115 LVTYSS 120  
Db 121 MVTYSS 126

RESULT 11  
US-09-880-748-1109  
Sequence 1109, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1109  
LENGTH: 249  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-1109

Query Match 79.4%; Score 494; DB 11; Length 249;  
Best Local Similarity 76.2%; Pred. No. 5.2e-40;  
Matches 96; Conservative 10; Mismatches 14; Indels 6; Gaps 2;

Qy 1 EVOLVESGGGLVQPGSRSLRLSCVDSGLTFSSYGHWVRQAAGGLEWVAVISYDGNKXY 60  
Db 1 QVQLVDSGGGVQPGSRSLRLSCAASGFTFSYGMHWVRQAAGGLEWVAISYDGNKXY 60  
Qy 61 ADSVKGRAISRDNKNTLYLQNNSLTIETDAVYVYCAKDLIESNIAEALMGOGT 114  
Db 61 VDSVKGRTISRDNKNTLYLQNNSLRAEDTAVYVYCAKGIYTKSRFYWGOGT 120  
Qy 115 LVTYSS 120  
Db 121 MVTYSS 126

RESULT 12  
US-10-041-860-33  
Sequence 33, Application US/10041860  
Publication No. US20030157109A1  
GENERAL INFORMATION:  
APPLICANT: Corvalan, Jose R.F.  
APPLICANT: Jia, Xiao-Chi  
APPLICANT: Feng, Xiao  
APPLICANT: Yang, Xiao-Dong  
APPLICANT: Chen, Francine  
APPLICANT: Gazit, Gad  
APPLICANT: Weber, Richard  
APPLICANT: Bezabeh, Binyam  
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES



US-10-325-694-144  
; Sequence 144, Application US/10325694  
; Publication No. US20030148463A1  
; GENERAL INFORMATION:  
; APPLICANT: KUPER, PETER  
; APPLICANT: RAUM, TOBIAS  
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN  
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
; FILE REFERENCE: 38164000  
; CURRENT APPLICATION NUMBER: US/10/325,694  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US/09/403,107  
; PRIOR FILING DATE: 1999-10-14  
; NUMBER OF SEQ ID NOS: 152  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 144  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-10-325-694-144

Query Match 80.3%; Score 499.5; DB 12; Length 138;  
Best Local Similarity 77.2%; Pred. No. 8.1e-41;  
Matches 98; Conservative 7; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60  
DB 1 EVOLVESGGGVOPGSRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60  
QY 61 ADVSKGRFAISRDNKNTLYLQNNSLTIEDTAVYYCAKDLIESN-----IABALWGG 113  
DB 61 ADVSKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAKDWGSGMPPYYGYGMDVWGQ 120  
QY 114 TLVTVSS 120  
DB 121 TTVTVSS 127

## RESULT 3

US-10-269-805-21  
; Sequence 21, Application US/10269805  
; Publication No. US20030124129A1  
; GENERAL INFORMATION:  
; APPLICANT: OLINER, JONATHAN D.  
; TITLE OF INVENTION: ANGIOPEPTIN-2 SPECIFIC BINDING AGENTS  
; FILE REFERENCE: A-722  
; CURRENT APPLICATION NUMBER: US/10/269,805  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 60/328,604  
; PRIOR FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-269-805-21

Query Match 80.1%; Score 498.5; DB 15; Length 123;  
Best Local Similarity 79.7%; Pred. No. 8.9e-41;  
Matches 98; Conservative 6; Mismatches 16; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVOPGSRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60  
DB 1 QVQLQESGGGVOPGSRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60  
QY 61 ADVSKGRFAISRDNKNTLYLQNNSLTIEDTAVYYCAK---DLIESNIAEALWGGTLVT 117  
DB 61 ADVSKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAKGPVDPYGVDAIDVWGQTLVT 120  
QY 118 VSS 120  
DB 121 VSS 123

RESULT 4  
US-09-880-748-1731  
; Sequence 1731, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunoselectively Bind Blyts  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1731  
; LENGTH: 252  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-1731

Query Match 80.1%; Score 498.5; DB 11; Length 252;  
Best Local Similarity 75.2%; Pred. No. 1.9e-40;  
Matches 97; Conservative 9; Mismatches 14; Indels 9; Gaps 1;

QY 1 EVOLVESGGGLVOPGSRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60  
DB 1 QVQLQESGGGVOPGSRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60  
QY 61 ADVSKGRFAISRDNKNTLYLQNNSLTIEDTAVYYCAKDLIE-----SNIAEALW 111  
DB 61 ADVSKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCARLREYDILTGYYYYGMDVWG 120  
QY 112 QGTLTVSS 120  
DB 121 RGTTLTVSS 129

## RESULT 5

US-09-791-153A-63  
; Sequence 63, Application US/09791153A  
; Publication No. US20030103978A1  
; GENERAL INFORMATION:  
; APPLICANT: Deehpande, Rajendra  
; APPLICANT: Hitz, Anna  
; APPLICANT: Boyle, William  
; APPLICANT: Sullivan, John  
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN  
; FILE REFERENCE: A-633A  
; CURRENT APPLICATION NUMBER: US/09/791,153A  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: 09/511,139  
; PRIOR FILING DATE: 2000-02-23  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 63  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-153A-63

Query Match 80.0%; Score 497.5; DB 11; Length 113;  
Best Local Similarity 80.8%; Pred. No. 1e-40;  
Matches 97; Conservative 5; Mismatches 11; Indels 7; Gaps 1;

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OM protein - protein search, using SW model

Run on: December 30, 2003, 11:01:15 ; Search time 25.7352 Seconds  
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927.994 Million cell updates/sec

Title: US-09-674-752-46

Perfect score: 622  
Sequence: 1 EVOLVESGGGLVQPGKSLRL.....IESNIAELMGQGLTVTSS 120

Scoring table:

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Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0  
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Listing first 45 summaries

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Published Applications AA:\*

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- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10C\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	80.5	227	11	US-09-972-656-76 Sequence 76, App1
2	499.5	80.3	138	12	US-10-325-694-144 Sequence 14, App1
3	498.5	80.1	123	15	US-10-269-805-21 Sequence 21, App1
4	498.5	80.1	252	11	US-09-880-748-1731 Sequence 1731, App1
5	497.5	80.0	113	11	US-09-791-1534-63 Sequence 63, App1
6	496.5	79.8	138	12	US-10-325-694-150 Sequence 150, App1
7	495.5	79.7	119	11	US-10-010-729-7 Sequence 7, App1
8	495.5	79.7	252	11	US-09-880-748-1394 Sequence 1394, App1
9	495	79.6	248	12	US-10-235-175-80 Sequence 80, App1
10	495	79.6	249	11	US-09-880-748-512 Sequence 512, App1
11	494	79.4	249	11	US-09-880-748-1109 Sequence 1109, App1
12	493.5	79.3	127	12	US-10-041-860-33 Sequence 33, App1
13	493.5	79.3	127	12	US-10-041-860-211 Sequence 211, App1
14	493.5	79.3	127	12	US-10-041-860-331 Sequence 331, App1
15	493.5	79.3	240	11	US-09-880-748-1912 Sequence 1912, App1

16	493	79.3	248	11	US-09-880-748-1890 Sequence 1890, App1
17	491.5	79.0	109	12	US-10-309-764-1 Sequence 1, App1
18	491.5	79.0	123	15	US-10-269-805-1 Sequence 1, App1
19	491	78.9	122	15	US-10-269-805-39 Sequence 39, App1
20	490.5	78.9	119	12	US-10-120-377-76 Sequence 76, App1
21	490	78.8	241	11	US-09-880-748-1887 Sequence 1887, App1
22	490	78.8	241	11	US-09-880-748-1901 Sequence 1901, App1
23	490	78.8	247	11	US-09-880-748-1330 Sequence 1330, App1
24	490	78.8	249	11	US-09-880-748-1397 Sequence 1397, App1
25	490	78.8	249	11	US-09-880-748-1102 Sequence 1102, App1
26	490	78.8	249	11	US-09-880-748-1115 Sequence 1115, App1
27	489	78.6	249	11	US-09-880-748-1117 Sequence 1117, App1
28	489	78.6	252	11	US-09-880-748-1627 Sequence 1627, App1
29	488.5	78.5	238	11	US-09-880-748-1931 Sequence 1931, App1
30	488.5	78.5	451	15	US-10-153-382-17 Sequence 17, App1
31	488	78.5	118	12	US-10-120-377-78 Sequence 78, App1
32	488	78.5	247	11	US-09-880-748-924 Sequence 924, App1
33	488	78.5	252	11	US-09-880-748-1519 Sequence 1519, App1
34	488	78.5	254	11	US-09-880-748-977 Sequence 977, App1
35	487	78.3	249	11	US-09-880-748-911 Sequence 911, App1
36	487	78.3	249	11	US-09-880-748-1119 Sequence 1119, App1
37	487	78.3	249	11	US-09-880-748-1956 Sequence 1956, App1
38	486	78.1	122	15	US-10-269-805-53 Sequence 53, App1
39	486	78.1	251	11	US-09-880-748-952 Sequence 952, App1
40	486	78.1	251	11	US-09-880-748-982 Sequence 982, App1
41	486	78.1	254	11	US-09-880-748-981 Sequence 981, App1
42	486	78.1	254	11	US-09-880-748-1428 Sequence 1428, App1
43	485.5	78.1	123	15	US-10-243-265-2 Sequence 2, App1
44	485.5	78.1	241	11	US-09-880-748-2055 Sequence 2055, App1
45	485	78.0	122	10	US-09-144-886-68 Sequence 68, App1

#### ALIGNMENTS

RESULT 1  
US-09-972-656-76  
Sequence 76, Application US/09972656  
Publication No. US20030099647A1  
GENERAL INFORMATION:  
APPLICANT: Deshpande, Rajendra  
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
TITLE OF INVENTION: Neutralizing Activity  
FILE REFERENCE: A-799  
CURRENT FILING DATE: 2001-10-05  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 76  
LENGTH: 227  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-972-656-76

Query Match 80.5%; Score 501; DB 11; Length 227;  
Beet Local Similarity 77.4%; Pred. No. 1e-40;  
Matches 96; Conservative 9; Mismatches 15; Indels 4; Gaps 1;

QY	1	EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSGYGMHWQAQAGLEWVAIVSYGNDKRY	60
DB	1	OVOLVETGGVVOGRSLRLSCAASGFTSSYAMHWQAQAGLEWVAIVSYGSKRY	60
QY	61	ADSVKGRPAISRDAKNTLYQNNSLTIEDTAVYYCAKDLI-----ESNIAELMGQGLTV	116
DB	61	ADSVKGRFTISRDKNTLYQNNSLRAEDTAVYYCASDLVLTMTSRRAFDIWGQGTIV	120
QY	117	TVSS 120	
DB	121	TVSS 124	

RESULT 2

PD 01-DEC-1999.  
XX 20-MAY-1999; 99EP-0201593.  
PF 20-MAY-1998; 98EP-0201693.  
PR 20-MAY-1998; 98EP-0201693.  
XX (INTR-) INTROGENE BV.  
PA Van Be H, Verlinden S, Havenga M;  
PI MPI; 2000-025491/03.  
DR N-PSDB; AAZ38921.  
XX  
PT New gene therapy vectors, useful for treating balloon angioplasty  
patients -  
PS Claim 13; Fig 16; 50pp; English.  
XX  
CC The present invention describes a virus-like particle or gene delivery  
CC vehicle (I) provided with a ligand capable of binding to a human amino  
CC acid transporter. (I) is used to deliver genes to human cells or primate  
CC cells that express the hCAT amino acid transporter, such as endothelial,  
CC haematopoietic or smooth muscle cells, as part of a gene therapy regime.  
CC The vectors are especially useful for providing local applications of  
CC adenoviral vector to patients with restenosis following balloon  
CC angioplasty, where smooth muscle cells need to be transduced with cDNAs  
CC cDNA, for example. (I) may also be used to pseudotype recombinant type C  
CC retrovirus including murine leukemia retroviruses and lentiviruses. In  
CC addition (I) may be used in functional genomics where transduction of as  
CC many cell types as possible is required. The new gene delivery vehicles  
CC transduce DNA more efficiently and specifically into tissues that are  
CC hard to transform, such as endothelial cells or smooth muscle cells as  
CC compared to a wildtype adenoviral vector. This increased specificity  
CC results in lower multiplicities of infection which can occur with prior  
CC art vectors, so preventing tissue toxicity. In addition the new vectors  
CC allow DNA to be transduced into cells that are in low abundance in cell  
CC mixtures and tissues, which increases their efficiency for use as gene  
CC therapy vehicles. The alteration of the ligand on the viral envelope  
CC increases the potential host cell range of these vehicles. The present  
CC sequence represents a hCAT1 binding human antibody molecule from the  
CC present invention.  
SQ Sequence 490 AA;  
Query Match 79.6%; Score 495; DB 21; Length 490;  
Best Local Similarity 78.3%; Pred. No. 6e-39;  
Matches 94; Conservative 9; Mismatches 17; Indels 0; Gaps 0;  
QY 1 EVOLVESSGGLVOPGRSLRLSCVDSGLTFSSYGMAWRQAPGAGLEWVAVISYDGNKYY 60  
DB :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 318  
259 QVOLVQSGGVQVQPSRLSLSCASGFTFSSYAMHWROAPGKLEWVAVISYDGSNKYY 318  
QY 61 ADSVKGRAIISRDNAKNTLYIQMNSLTEDPAVYYCAKDLIESNTAEALMGCGTLVTYSS 120  
DB :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 378  
319 ADSVKGRTISRDNKNTLYIQMNSLRAEDTAVYYCARGITVTKSRFDYWGCGTLVTYSS 378

Search completed: December 30, 2003, 10:54:35  
Job time : 38.6861 secs

XX WO200202641-A1.  
 XX 10-JAN-2002.  
 XX 15-JUN-2001; 2001WO-US19110.  
 XX 16-JUN-2000; 2000US-212210P.  
 XX 17-OCT-2000; 2000US-240816P.  
 XX 16-MAR-2001; 2001US-276248P.  
 XX 21-MAR-2001; 2001US-277379P.  
 XX 25-MAY-2001; 2001US-293499P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX WPI; 2002-114799/15.  
 XX Antibodies against B lymphocyte Stimulating polypeptides, useful for  
 XX the diagnosis and treatment of cancers and immune disorders -  
 XX Claim 1; Page 1014-1015; 3148pp; English.  
 XX This invention describes novel antibodies that immunospecifically bind to  
 XX B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 XX tumour necrosis factor (TNF) super family and induces B cell  
 XX proliferation and differentiation. The antibodies of the invention have  
 XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 XX antirheumatic and antiAIDS activity and can be used in vaccines to  
 XX inhibit the expression and activity of Blys. The antibodies bind to Blys  
 XX and so may be used to detect and quantitate the presence of Blys in  
 XX biological samples and may be used in this way to diagnose disease  
 XX associated with aberrant expression of Blys. They may also be  
 XX administered to treat diseases associated with aberrant Blys expression  
 XX and activity such as cancer, immune, and autoimmune disorders and  
 XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 XX the antibodies and fragments of the antibodies described in the method  
 XX of the invention.  
 XX Sequence 249 AA;  
 XX  
 XX Query Match 79.6%; Score 495; DB 23; Length 249;  
 XX Best Local Similarity 77.0%; Pred. No. 2.8e-39;  
 XX Matches 97; Conservative 7; Mismatches 16; Indels 6; Gaps 1;  
 XX  
 XX QY 1 EVQLVESGGGLVQPGSRSLRLSCVDSGTLFPSSYGMHWVRQAPGAGLEWVAIVISDGNDRYY 60  
 XX DB 1 QVQLVSGGGGVVQPGSRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAIVISDGSNKYY 60  
 XX QY 61 ADSVKGKFAISRDNNAKNTLYLQMNLSLTIEDTAVYYCAKD-----LIESNIAELWGQGT 114  
 XX DB 61 ADSVKGKFRITSRDNRNNTLYLQMNLSLRADTAVYYCAKQGYDYLIGYSYGGMDVWGQGT 120  
 XX QY 115 LVTVSS 120  
 XX DB 121 MVTVSS 126  
 XX  
 XX RESULT 14  
 XX AAY56287  
 XX ID AAY56287 standard; Protein; 254 AA.  
 XX AC AAY56287;  
 XX XX  
 XX DT 08-FEB-2000 (first entry)  
 XX XX  
 XX DE HCAT1 clone 25 antibody variable heavy chain protein sequence.  
 XX XX  
 XX KM Human cationic amino acid transporter; hCAT1; targeted delivery;

KW gene delivery; virus-like particle; retroviral envelope molecule;  
 KW infection; gene therapy; restenosis; balloon angioplasty;  
 KW smooth muscle cell; transduction.  
 XX  
 XX OS Synthetic.  
 XX OS Homo sapiens.  
 XX XX  
 XX EP959136-A1.  
 XX 24-NOV-1999.  
 XX PD 20-MAY-1998; 98EP-0201693.  
 XX PF 20-MAY-1998; 98EP-0201693.  
 XX PR 20-MAY-1998; 98EP-0201693.  
 XX (INTR-) INTROGENE BV.  
 XX WPI; 2000-001283/01.  
 XX DR N-PSDB; AA238770.  
 XX New virus-like particle or gene delivery vehicle, useful for gene  
 XX therapy -  
 XX Claim 13; Fig 16; 66pp; English.  
 XX  
 XX The present invention describes a virus-like particle or gene delivery  
 XX vehicle comprising a ligand capable of binding to a human amino acid  
 XX transporter. The method is useful for the target delivery of substances  
 XX to cells e.g. gene therapy. A human cationic amino acid transporter  
 XX (hCAT1) targeted adenovirus is useful for local applications of  
 XX adenoviral vector e.g. in patients with restenosis following balloon  
 XX angioplasty where smooth muscle cells need to be transduced with an  
 XX adenoviral vector carrying the cMOS cDNA. More efficient transduction  
 XX of tissues can be carried out therefore resulting in lower  
 XX multiplicity's of infections that can be used and therefore less vector  
 XX associated toxicity to the tissues surrounding the target cells. AA238737  
 XX to AA238770, and AAY56264 to AAY56287 represent sequences used in the  
 XX exemplification of the present invention.  
 XX Sequence 254 AA;  
 XX  
 XX Query Match 79.6%; Score 495; DB 21; Length 254;  
 XX Best Local Similarity 78.3%; Pred. No. 2.8e-39;  
 XX Matches 94; Conservative 9; Mismatches 17; Indels 0; Gaps 0;  
 XX  
 XX QY 1 EVQLVESGGGLVQPGSRSLRLSCVDSGTLFPSSYGMHWVRQAPGAGLEWVAIVISDGNDRYY 60  
 XX DB 23 QVQLVSGGGGVVQPGSRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAIVISDGSNKYY 82  
 XX QY 61 ADSVKGKFAISRDNNAKNTLYLQMNLSLTIEDTAVYYCAKDLISNIAELWGQGT LVTVSS 120  
 XX DB 83 ADSVKGKFRITSRDNRNNTLYLQMNLSLRADTAVYYCARIGITVTKSRFDVWGQGT LVTVSS 142  
 XX  
 XX RESULT 15  
 XX AAY56637  
 XX ID AAY56637 standard; Protein; 490 AA.  
 XX AC AAY56637;  
 XX XX  
 XX DT 22-FEB-2000 (first entry)  
 XX XX  
 XX DE hCAT1 binding human antibody molecule protein sequence.  
 XX XX  
 XX KM Virus-like particle; ligand; gene delivery; envelope protein; hCAT1;  
 XX KM human cationic amino acid transporter 1; retrovirus; adenovirus;  
 XX KM targeted delivery; gene therapy; balloon angioplasty.  
 XX XX  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX XX  
 XX PN EP960942-A2.





CC different (poly)peptides lack an intrinsic affinity for one another and  
 CC are linked via the constant domains. The heteromimibodies have  
 CC cytotoxic, immunostimulatory, antileukemia and antiproliferative  
 CC activities. These compounds can be used for diagnosing, preventing and  
 CC treating malignant cell growth related to malignancies of haematopoietic  
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,  
 CC melanomas and sarcomas.  
 CC The present sequence is the left chain of a heteromimibody  
 CC comprising HD70 single-chain Fv (scFv) fragment N-terminally linked to  
 CC human CD1 domain which bears at its C-terminus the human inflammatory  
 CC cytokine granulocyte/macrophage colony stimulating factor (GM-CSF), plus  
 CC a heparin-binding sequence for ease of purification. HD70 scFv  
 CC specifically recognises the human epithelial cell adhesion molecule  
 CC (EPCAM) also called 17-1A antigen.  
 CC  
 SO Sequence 523 AA;  
 Query Match 79.8%; Score 496.5; DB 21; Length 523;  
 Best Local Similarity 76.4%; Pred. No. 4.7e-39;  
 Matches 97; Conservative 8; Mismatches 15; Indels 7; Gaps 1;  
 QY 1 EVQLVSGGGLVQPGKSLRLSCYDSGTFSSYGMHWVRQAPGKGLKRVAVISYDGSNKKY 60  
 DB 142 EVQLVSGGGLVQPGKSLRLSCYDSGTFSSYGMHWVRQAPGKGLKRVAVISYDGSNKKY 201  
 QY 61 ADSVKGKPAISRDNKATLYLQNNSLTIETDAVYYCAKDILISN-----IAEALMGOG 113  
 DB 202 ADSVKGKFTISRDNKATLYLQNNSLRAEDTAVYYCAKDIMGSGKRPYYTYGMDVWGOG 261  
 QY 114 TLVTVSS 120  
 DB 262 TLVTVSS 268  
 RESULT 10  
 ID AAY44995 standard; Protein; 524 AA.  
 AC AAY44995;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE HD70scFv-CK-interleukin 2.  
 XX  
 KM HD70; single-chain Fv fragment; scFv; antibody; 17-1A antigen; human;  
 KM BPCAM; epithelial cell adhesion molecule; inflammatory cytokine;  
 KM IL-2; interleukin-2; CK-domain; kappa light chain constant domain;  
 KM heteromimibody; multifunctional compound; immunoglobulin;  
 KM cytotoxic; immunostimulatory; antileukemia; diagnosis; prevention;  
 KM antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;  
 KM leukaemia; solid tumour; carcinoma; melanoma; sarcoma.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200006605-A2.  
 XX  
 PD 10-FEB-2000.  
 XX  
 PF 28-JUL-1999; 99WO-EP05416.  
 XX  
 PR 28-JUL-1998; 98EP-0114082.  
 XX  
 PA (MICR-) MICROMET GBS BIOMEDIZINISCH FÖRSCHUNG.  
 XX  
 PI Kufer P, Dreier T, Baerle PA, Borschert K, Zettl F;  
 XX  
 DR WPI; 2000-195265/17.  
 XX  
 DR N-PSDB; AA250588.  
 XX  
 PT New multifunctional compounds useful for preventing and/or treating  
 XX malignant cell growth and for detection and diagnosis  
 XX Example 10; Fig 55B; 16pp; English.

XX  
 CC The patent discloses heteromimibodies which are multifunctional compounds  
 CC producible in a mammalian host cell as a secretable and fully functional  
 CC heterodimer of two polypeptide chains, where one of the polypeptide  
 CC chains comprises, a CH1 domain (constant domain of an immunoglobulin  
 CC heavy chain) and the other chain comprises CD domain (constant domain of  
 CC an immunoglobulin light chain). The polypeptide chains further comprise,  
 CC fused to the constant domains at least two (poly)peptides having  
 CC different receptor or ligand functions, where further at least two of the  
 CC different (poly)peptides lack an intrinsic affinity for one another and  
 CC are linked via the constant domains. The heteromimibodies have  
 CC cytotoxic, immunostimulatory, antileukemia and antiproliferative  
 CC activities. These compounds can be used for diagnosing, preventing and  
 CC treating malignant cell growth related to malignancies of haematopoietic  
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,  
 CC melanomas and sarcomas.  
 CC The present sequence is the right chain of a heteromimibody  
 CC comprising HD70 single-chain Fv (scFv) fragment N-terminally linked to  
 CC human CK domain (constant domain of immunoglobulin-kappa light chain)  
 CC which bears at its C-terminus the human inflammatory cytokine  
 CC interleukin-2 (IL-2). HD70 scFv specifically recognises the human  
 CC epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen.  
 CC  
 SO Sequence 524 AA;  
 Query Match 79.8%; Score 496.5; DB 21; Length 524;  
 Best Local Similarity 76.4%; Pred. No. 4.7e-39;  
 Matches 97; Conservative 8; Mismatches 15; Indels 7; Gaps 1;  
 QY 1 EVQLVSGGGLVQPGKSLRLSCYDSGTFSSYGMHWVRQAPGKGLKRVAVISYDGSNKKY 60  
 DB 142 EVQLVSGGGLVQPGKSLRLSCYDSGTFSSYGMHWVRQAPGKGLKRVAVISYDGSNKKY 201  
 QY 61 ADSVKGKPAISRDNKATLYLQNNSLTIETDAVYYCAKDILISN-----IAEALMGOG 113  
 DB 202 ADSVKGKFTISRDNKATLYLQNNSLRAEDTAVYYCAKDIMGSGKRPYYTYGMDVWGOG 261  
 QY 114 TLVTVSS 120  
 DB 262 TLVTVSS 268  
 RESULT 11  
 ID ABB07169 standard; Protein; 119 AA.  
 AC ABB07169;  
 XX  
 DT 13-MAR-2002 (first entry)  
 XX  
 DE shlgM22 heavy chain variable region clone A sequence.  
 XX  
 KM Neuromodulatory; central nervous system; CNS; shlgM22; LYM 22; AKR4;  
 KM eBVH1GM M6119D10; eBV H1GM CB2B68; CB21B12; MS119B5; vlnuclde;  
 KM antiParkinsonian; neuroprotective; nootropic; vulnerary.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200185797-A1.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-MAY-2000; 2000MO-US14902.  
 XX  
 PR 10-MAY-2000; 2000US-0568351.  
 XX  
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.  
 XX  
 PI Rodriguez M, Miller DJ, Pease LR;  
 XX  
 DR WPI; 2002-066596/09.  
 XX  
 DR N-PSDB; ABA94216.  
 XX

CC protein comprises an additional domain positioned N-terminal of the BSD  
 CC and an amino acid sequence that mediates anchoring of the fusion protein  
 CC to the surface of the display system; and (b) identifying a BSD that  
 CC binds to the predetermined epitope. The method is useful to identify bi-  
 CC or multivalent polypeptides that comprise antibody binding sites capable  
 CC of efficiently binding to the corresponding antigen. The polypeptides or  
 CC antibodies identified by the method are useful therapeutically and  
 CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody  
 CC fragments that bind independently of their position within bifunctional  
 CC single-chain fusion proteins can be isolated from combinatorial antibody  
 CC libraries using the new in vitro method.

XX Sequence 127 AA;

Query Match 79.8%; Score 496.5; DB 20; Length 127;  
 Best Local Similarity 76.4%; Pred. No. 9.3e-40;  
 Matches 97; Conservative 8; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGVQVOPGRSRISLSCVDSGLTFSSYGMMHWQAPGAGLEWVAVISYDGNKRY 60

DB 1 EVQLVESGGGVQVOPGRSRISLSCVDSGLTFSSYGMMHWQAPGAGLEWVAVISYDGNKRY 60

QY 61 ADSVKGRAISRDNNAKNTLYIQMNSLTIEDPAVYYCAKDLIESN-----IAEALMGCG 113

DB 61 ADSVKGRTISRDNNAKNTLYIQMNSLTIEDPAVYYCAKDMGSGMRPRYYTGMDVWGCG 120

QY 114 TLVTYSS 120

DB 121 TTVTVSS 127

RESULT 8

AAW80815  
 ID AAW80815 standard; Protein; 138 AA.

XX AAW80815;

XX 16-FEB-1999 (first entry)

XX Amino acid sequence of human D4.5 heavy chain variable region.

XX Human; D4.5 heavy chain variable region; receptor; antigen;

XX tumour; auto-immune disease; graft rejection; allergy; inflammatory disease; endocrine disease; degenerative disease.

XX Homo sapiens.

XX MO9846645-A2.

XX 22-OCT-1998.

XX 14-APR-1998; 98WO-EP02180.

XX 14-APR-1997; 97EP-0106109.

XX (KUFE/) KUFER P.

XX (RAUM/) RAUM T.

XX Kufer P, Raum T;

XX WPI; 1998-594564/50.

XX N-PSDB; AA68537.

XX Claim 9; Fig 7; 84pp; English.

CC This is the amino acid sequence of the human D4.5 heavy chain  
 CC variable region, used in the method of the invention, for providing  
 CC receptors that can be used for targeting antigens in humans without  
 CC being immunogenic themselves. Such receptors can be used for treating

CC diseases such as tumours or auto-immune diseases, graft rejection  
 CC after transplantation, infectious diseases by targeting cellular  
 CC receptors as well as allergic, inflammatory, endocrine and  
 CC degenerative diseases by targeting key molecules involved in the  
 CC pathological process.

XX Sequence 138 AA;

Query Match 79.8%; Score 496.5; DB 19; Length 138;  
 Best Local Similarity 76.4%; Pred. No. 1e-39;  
 Matches 97; Conservative 8; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLVESGGGVQVOPGRSRISLSCVDSGLTFSSYGMMHWQAPGAGLEWVAVISYDGNKRY 60

DB 1 EVQLVESGGGVQVOPGRSRISLSCVDSGLTFSSYGMMHWQAPGAGLEWVAVISYDGNKRY 60

QY 61 ADSVKGRAISRDNNAKNTLYIQMNSLTIEDPAVYYCAKDLIESN-----IAEALMGCG 113

DB 61 ADSVKGRTISRDNNAKNTLYIQMNSLTIEDPAVYYCAKDMGSGMRPRYYTGMDVWGCG 120

QY 114 TLVTYSS 120

DB 121 TTVTVSS 127

RESULT 9

AA44994  
 ID AA44994 standard; Protein; 523 AA.

XX AA44994;

XX 23-MAY-2000 (first entry)

XX HD70scFv-CH1-GM-CSF chain.

XX HD70; single-chain variable fragment; scFv; 17-1A antigen; human;

XX BpCM; epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;

XX granulocyte/macrophage colony stimulating factor; heteroninbody;

XX CH1-domain; multifunctional compound; heavy chain constant domain;

XX immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis;

XX antiproliferative; prevention; treatment; malignant; haematopoietic cell;

XX lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.

XX Homo sapiens.

XX MO200006605-A2.

XX 10-FEB-2000.

XX 28-JUL-1999; 99WO-EP05416.

XX 28-JUL-1998; 98EP-0114082.

XX (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.

XX Kufer P, Dreier T, Baerle PA, Borsche K, Zetcl F;

XX WPI; 2000-195265/17.

XX N-PSDB; AA250587.

CC New multifunctional compounds useful for preventing and/or treating  
 CC malignant cell growth and for detection and diagnosis -  
 CC Example 10; Fig 55A; 16pp; English.

CC The patent discloses heteroninbodies which are multifunctional compounds  
 CC producible in a mammalian host cell as a secretable and fully functional  
 CC heterodimer of two polypeptide chains, where one of the polypeptide  
 CC chains comprises, a CH1-domain (constant domain of an immunoglobulin  
 CC heavy chain) and the other chain comprises CL-domain (constant domain of  
 CC an immunoglobulin light chain). The polypeptide chains further comprise,  
 CC fused to the constant domains at least two (polypeptides having  
 CC different receptor or ligand functions, where further at least two of the

[illegible]

CC	gene (AAI60369) obtained by panning a phage antibody library produced
CC	from cloned germ-line V genes and synthetic CDRs. The antigen-
CC	-binding domains of human antibodies (see AAI5522-40) to TGF beta-1
CC	and/or beta-2 can be used to counter the adverse effects of TGF
CC	beta, such as (i) promotion of fibrosis (in dermal, ocular or
CC	retinopathy, lung fibrosis, arterial injury, proliferative
CC	syndrome, liver cirrhosis, post myocardial infarction, post-
CC	angioplasty restenosis, scleroderma, vascular disorders, cataract,
CC	glaucoma, or esp. neural scattering and glomerulonephritis, also
CC	(not claimed) osteoporosis), or (ii) immune and inflammatory
CC	diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases
CC	or macrophage pathogen infection). Nucleic acids encoding human
CC	antibody VH and VL can be used for prodn. of recombinant antigen-
CC	-binding domains. These are highly specific, have low dissociation
CC	constants (pref. less than 5 nM) and low IC50s for neutralisation.
CC	xx
SQ	Sequence 115 AA;
Query Match	79.8%; Score 496.5; DB 18; Length 115;
Best Local Similarity	80.8%; Pred. No. 8.3e-40;
Matches 97; Conservative	6; Mismatches 12; Indels 5; Gaps 1
Dc	1 EVOLVEGGGGLVPGGRSLRLSCVDSSGLTFFSSYGMHWYQAQGAGLEWAVISYDGNDRXY 60
Dc	1 EVQLVESGGGVGVGGRSIRLSCAASGFRFSSYGHWVRQAQKGLEWAVIMYDSNKKY 60
Dc	61 ADVSKGRPAISRDNNAKTLYLNKNSLTIEDTAIVYYCAKDILIESNIABLMKGCTLVTVSS 120
Dc	61 ADVSKGRFTISRDNKNTLYLNKMSLRADPTAVYVYCGRTLESS-----LMCGITLVTVSS 115
RESULT 7	
ID	AAI17954 standard; Protein; 127 AA.
XX	AAI17954;
AC	AAI17954;
XX	
DT	04-AUG-1999 (first entry)
DE	Human D4.5 heavy chain variable region.
XX	
KX	Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW	autoimmune disease; scFv-antibody; single-chain Fv.
OS	Homo sapiens.
PV	MO9925618-Al.
PD	27-MAY-1999.
PF	16-NOV-1998; 98WO-EP07313.
PR	17-NOV-1997; 97EP-0120096.
PA	(KUFE/) KUPER P.
PI	Borchert K, Kufer P, Luttreue R, Raum T, Zeitl F;
DR	WI, 1999-338004/28.
N-PSDB;	AAK77236.
PT	Phage display system for identification of binding site domains
XX	retaining capacity to bind an epitope
XX	
PS	Disclosure; Fig 3.1; 15zpp; English.
CC	The invention relates to a method of identifying binding site domains
CC	(BSD) that retain the capacity of binding to a predetermined epitope when
CC	positioned C-terminal of at least one further domain in a recombinant bi-
CC	multivalent polypeptide. The method comprises (a) testing a panel of
CC	BSD displayed on the surface of a biological display system as part of a
CC	fusion protein for binding to a predetermined epitope, where the fusion

ID ABB45720 standard; Protein; 252 AA.  
 AC ABB45720;  
 DT 19-AUG-2002 (first entry)  
 DE Human Blys binding scFv SEQ ID 1731.  
 XX  
 XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KM immunosuppressive; immunostimulant; immunomodulatory; antineumatic;  
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KM systemic lupus erythematosus; rheumatoid arthritis; CYID; AIDS;  
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
 OS Homo sapiens.  
 XX  
 XX MO200202641-A1.  
 PN  
 XX 10-JAN-2002.  
 PD  
 XX 15-JUN-2001; 2001WO-US19110.  
 PE  
 XX 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX  
 DR WPI; 2002-114799/15.  
 XX  
 PT Antibodies against B lymphocyte stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 XX  
 PS Claim 1; Page 2468-2469; 3148pp; English.  
 XX  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antineumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABB43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX  
 SO Sequence 252 AA;  
 Query Match 80.1%; Score 498.5; DB 23; Length 252;  
 Best Local Similarity 75.2%; Pred. No. 1.3e-39;  
 Matches 97; Conservative 9; Mismatches 14; Indels 9; Gaps 1;  
 Oy 1 EVQLVESGGGLVQPRGRLRSCTVDGSLTPSSSGMGWVRQAPRAGLGVAVSYDNDKRY 60  
 Db 1 QVQLVESGGGVQPRSLRLSCAASGFTPSYGMHWVRQAPKGLAVAVSYDSNRY 60  
 Oy 61 ADSVGRFAISRDNANTLYLQMSLTIEDTAVVYCAKDLIE-----SNIAELWG 111  
 Db 61 ADSVGRFTISRDNKNTLYLQMSLRADTAVVYCAKDRLEYDILGYYTYTYGMDYWG 120

Oy 112 QGLTVTVSS 120  
 :|||||  
 Db 121 RGLTVTVSS 129  
 RESULT 5  
 ID ABB07186 standard; Protein; 119 AA.  
 AB07186  
 AC ABB07186;  
 DT 13-MAR-2002 (first entry)  
 DE bHlgM22 heavy chain variable region clone B sequence.  
 XX  
 XX Neuromodulatory; central nervous system; CNS; bHlgM22; LYM 22; AKR4;  
 KM ebvHlgM M6119D10; ebv HlgM CB2bG8; CB21E12; CB21E7; MS119E5; vltucide;  
 KM antiparkinsonian; neuroprotective; nootropic; vulnery.  
 XX  
 OS Homo sapiens.  
 XX  
 XX MO200185797-A1.  
 PN  
 XX 15-NOV-2001.  
 PD  
 XX 30-MAY-2000; 2000WO-US14902.  
 PF  
 XX 10-MAY-2000; 2000US-0568351.  
 PR  
 XX (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.  
 PI Rodriguez M, Miller DJ, Pease LR;  
 XX  
 DR WPI; 2002-066596/09.  
 DR N-PSDB; ABA94243.  
 XX  
 PT Novel neuromodulatory agent (a human Igm monoclonal antibody),  
 PT promoting neurite outgrowth, regeneration, remyelination and  
 PT neuroprotection in central nervous system, useful to treat  
 PT post-infectious encephalomyelitis -  
 XX  
 PS Claim 23; Fig 17; 219pp; English.  
 XX  
 CC The invention provides a neuromodulatory agent (I) capable of promoting  
 CC neurite outgrowth, regeneration, remyelination and neuroprotection in  
 CC central nervous system (CNS). (I) is capable of inducing remyelination,  
 CC promoting cellular proliferation of glial cells, and promoting Ca2+  
 CC signaling with oligodendrocytes. An humanised antibody to (I) can be  
 CC selected from antibody bHlgM22 (LYM 22), ebvHlgM M6119D10, ebv HlgM  
 CC CB2bG8, AKR4, CB21E12, CB21E7 or MS119E5. (I) is useful for stimulating  
 CC remyelination of CNS axons, stimulating proliferation of glial cells in  
 CC CNS axons, or treating demyelinating disease of CNS in a mammal in need  
 CC of such therapy. (I) is capable of binding to structures and cells within  
 CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS  
 CC or a mouse infected with Strain DA of Theiler's murine encephalomyelitis  
 CC (THEV) or for treating a human being having multiple sclerosis, or a  
 CC human or domestic animal with a viral demyelinating disease, or a post-  
 CC neural disease of CNS. (I) is also useful for an in vitro method of  
 CC stimulating the proliferation of glial cells from mixed cell culture.  
 CC (I) is also useful for stimulating remyelination of CNS axons. The  
 CC antibodies are useful for preventing infection by a bacterium, virus or  
 CC like pathogen that causes demyelination or other neurodegenerative  
 CC condition in a subject. Methods where (I) is administered to a patient  
 CC are useful for treating multiple sclerosis, Parkinson's disease,  
 CC Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral  
 CC demyelinating disease, CNS diseases, and other conditions in the CNS  
 CC where nerves are damaged as by trauma. The present sequence represents  
 CC the bHlgM22 heavy chain variable region clone B amino acid sequence.  
 XX  
 SO Sequence 119 AA;  
 Query Match 80.0%; Score 497.5; DB 23; Length 119;  
 Best Local Similarity 80.8%; Pred. No. 6.9e-40;

XX Example 8; Fig 9A; 61pp; English.

CC This invention describes a novel polynucleotide (I) (a  
CC hybridizable polynucleotide) comprising a contiguous  
CC coding for a human antibody with factor VIII specific;  
CC hemostatic activity. (I) is useful as a primer or probe  
CC presence of inhibitory antibodies directed against fac  
CC polypeptides of the invention and the antibodies gene  
CC are useful in compositions for neutralizing factor VII  
CC antibodies in hemophilia A patients. This sequence rei  
CC factor VIII antibody A3-C1 specific scFv protein B35 w  
CC in the method of the invention.

SO Sequence 120 AA;

Query Match 100.0%; Score 622; DB 21; Leng 20;  
Best Local Similarity 100.0%; Pred. No. 9,5e-52;  
Matches 120; Conservative 0; Mismatches 0; Indels 0;

QY 1 EVOLVESGGGLVPGPGRSLRLSCVDSGTLTFSYGMHWROAPGAGI VISYDGNKYY 60  
DB 1 EVOLVESGGGLVPGPGRSLRLSCVDSGTLTFSYGMHWROAPGAGI VISYDGNKYY 60  
QY 61 ADSVKGFAISRDNKNTLYLQMNSLTIEDTAVYYCAKDLIESN MGQGLTVTVSS 120  
DB 61 ADSVKGFAISRDNKNTLYLQMNSLTIEDTAVYYCAKDLIESN MGQGLTVTVSS 120

# RESULT 2

AAV50968 standard; Protein; 120 AA.

AAV50968;

23-MAR-2000 (first entry)

Human FVIII antibody heavy chain variable region B35 I

Human; heavy chain; antibody; factor VIII; hemostatic;

hemophilia A.

Homo sapiens.

MO9958680-A2.

18-NOV-1999.

07-MAY-1999; 99WO-NL00285.

08-MAY-1998; 98EP-0201543.

(SANO-) STICHTING SANQUIN BLOEDVOORZIENING.

Voorberg JJ, Van Den Brink EM, Turenhout EAM;

WPI; 2000-053102/04.

N-PSDB; AAZ43865.

New polynucleotide, polypeptide and antibody useful f

presence of neutralizing antibodies against factor VII

treatment of hemophilia A patients with these antibod

Example 8; Fig 9D; 61pp; English.

CC This invention describes a novel polynucleotide (I) (a  
CC hybridizable polynucleotide) comprising a contiguous  
CC coding for a human antibody with factor VIII specific;  
CC hemostatic activity. (I) is useful as a primer or probe  
CC presence of inhibitory antibodies directed against fa  
CC polypeptides of the invention and the antibodies gene  
CC are useful in compositions for neutralizing factor VII  
CC antibodies in hemophilia A patients. This sequence rei

CC of the human factor VIII antibody heavy chain variable region protein B35  
CC which is used in the method of the invention.

SO Sequence 120 AA;

Query Match 100.0%; Score 622; DB 21; Length 120;  
Best Local Similarity 100.0%; Pred. No. 9,5e-52;  
Matches 120; Conservative 0; Mismatches 0; Indels 0;

QY 1 EVOLVESGGGLVPGPGRSLRLSCVDSGTLTFSYGMHWROAPGAGLEWAVISYDGNKYY 60  
DB 1 EVOLVESGGGLVPGPGRSLRLSCVDSGTLTFSYGMHWROAPGAGLEWAVISYDGNKYY 60  
QY 61 ADSVKGFAISRDNKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALMGQGLTVTVSS 120  
DB 61 ADSVKGFAISRDNKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALMGQGLTVTVSS 120

# RESULT 3

AAV08598 standard; Protein; 223 AA.

AAV08598;

05-AUG-1999 (first entry)

Anti-human TNF-alpha monoclonal antibody H-chain protein.

Monoclonal antibody; H chain; heavy chain; anti-human; TNF-alpha;

tumour necrosis factor; light chain; L chain.

Homo sapiens.

JP11127855-A.

18-MAY-1999.

27-OCT-1997; 97JP-0293994.

27-OCT-1997; 97JP-0293994.

(NIHA) JAPAN ENERGY CORP.

WPI; 1999-350318/30.

N-PSDB; AAX77407.

Recombinant anti-human TNF-alpha human monoclonal antibody -

produced stably with a high purity, and in large amounts

Claim 3; Page 12-13; 22pp; Japanese.

This invention describes novel recombinant anti-human TNF-alpha human

monoclonal antibody consisting of a heavy (H) chain and a light (L)

chain. The recombinant anti-human TNF-alpha human monoclonal antibody

can be produced stably in a high purity and in a large amount.

SO Sequence 223 AA;

Query Match 82.6%; Score 514; DB 20; Length 223;  
Best Local Similarity 81.7%; Pred. No. 3,8e-41;  
Matches 98; Conservative 9; Mismatches 11; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVPGPGRSLRLSCVDSGTLTFSYGMHWROAPGAGLEWAVISYDGNKYY 60  
DB 1 EVOLVESGGGLVPGPGRSLRLSCVDSGTLTFSYGMHWROAPGAGLEWAVISYDGNKYY 60  
QY 61 ADSVKGFAISRDNKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALMGQGLTVTVSS 120  
DB 61 ADSVKGFAISRDNKNTLYLQMNSLTIEDTAVYYCAKDLIESNIAEALMGQGLTVTVSS 118

# RESULT 4

ABP45720

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 : Search time 318 Seconds  
(without alignment)  
493.415 Million c

Title: US-09-674-752-46

Perfect score: 622  
Sequence: 1 EVOLVESGGGLVPGFSLRL.....IESNIAELALMGC /TVSS 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2	.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA3	.DAT:*
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7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA7	.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA8	.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA9	.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA10	.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA11	.DAT:*
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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA24	.DAT:*

Pred. No. is the number of results predicted by chance score greater than or equal to the score of the result and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Option
1	622	100.0	120	21	AAV50963
2	622	100.0	120	21	AAV50968
3	514	82.6	223	20	AAV08598
4	498.5	80.1	252	23	ABP45720
5	497.5	80.0	119	23	ABP45720
6	496.5	79.8	115	18	AAW15522
7	496.5	79.8	127	20	AAW17954
8	496.5	79.8	138	19	AAW80815
9	496.5	79.8	523	21	AAV44994

10	496.5	79.8	524	21	AAV44995	HD08CFV-CK-interf
11	495.5	79.7	119	23	ABP45715	SH1G22 heavy chain
12	495.5	79.7	252	23	ABP45383	Human Blys binding
13	495	79.6	249	23	ABP44501	Human Blys binding
14	495	79.6	254	21	AAV56287	HCAT1 clone 25 ant
15	495	79.6	490	21	AAV56637	HCAT1 binding huma
16	494	79.4	113	22	AAU02537	Anti-adipocyte mon
17	494	79.4	120	22	AAU02501	Anti-adipocyte mon
18	494	79.4	249	23	ABP45098	Human Blys binding
19	493.5	79.3	117	18	AAW15523	Anti-TGF beta-2 sc
20	493.5	79.3	240	23	ABP45901	Human Blys binding
21	493	79.3	113	22	AAU02538	Anti-adipocyte mon
22	493	79.3	248	23	ABP45879	Human Blys binding
23	492.5	79.2	519	22	AAU01993	Human secreted pro
24	491.5	79.0	119	22	AAU02515	Anti-adipocyte mon
25	491	78.9	118	23	ABG30463	Human anti-CD40 mo
26	490.5	78.9	119	24	AAE32095	Human VEGF-2 hybr
27	490.5	78.9	120	15	AAE32064	Heavy chain variab
28	490	78.8	241	23	ABP45876	Human Blys binding
29	490	78.8	241	23	ABP45890	Human Blys binding
30	490	78.8	247	23	ABP45319	Human Blys binding
31	490	78.8	249	23	ABP44386	Human Blys binding
32	490	78.8	249	23	ABP45091	Human Blys binding
33	490	78.8	249	23	ABP45104	Human Blys binding
34	489.5	78.7	123	18	AAW15534	Anti-TGF beta-1 sc
35	489.5	78.7	192	14	AAE38161	Sequence of the he
36	489	78.6	249	23	ABP45106	Human Blys binding
37	489	78.6	252	23	ABP45616	Human Blys binding
38	488.5	78.5	125	23	AAO18437	Anti-CD2 antibody
39	488.5	78.5	238	23	ABP45920	Human Blys binding
40	488.5	78.5	451	21	AAV37734	The heavy chain of
41	488	78.5	118	24	AAE32097	Human VEGF-2 hybr
42	488	78.5	247	23	ABP44913	Human Blys binding
43	488	78.5	252	23	ABP45508	Human Blys binding
44	488	78.5	254	23	ABP44966	Human Blys binding
45	487	78.3	249	23	ABP44900	Human Blys binding

## ALIGNMENTS

RESULT 1  
AAV50963  
ID AAV50963 standard; Protein: 120 AA.  
XX  
AC AAV50963;  
XX  
DT 23-MAR-2000 (first entry)  
XX  
DB Human FVIII antibody A3-C1 scFv heavy chain protein B35.  
XX  
KW Human; heavy chain; antibody; factor VIII; hemostatic;  
XX hemophilia A; scFv; A3-C1.  
XX  
OS Homo sapiens.  
XX  
PN WO958680-A2.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-NL00285.  
XX  
PR 08-MAY-1998; 98EP-0201543.  
XX  
PA (SANO-) STRICHTING SANQUIN BLOEDVOORZIENING.  
XX Voorberg JJ, Van Den Brink EM, Turenhout EAM;  
XX WPI; 2000-053102/04.  
XX  
PT New polyclonal, polypeptide and antibody useful for diagnosing the  
PT presence of neutralizing antibodies against factor VIII and for  
PT treatment of hemophilia A patients with these antibodies -

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ database  
 DR EMBL; AF307937; AAL09421.1; -  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON TER 1  
 FT NON TER 119  
 SQ SEQUENCE 119 AA; 13025 MW; F6E90404381CA7C CRC64;

Query Match 66.8%; Score 415.5; DB 11; Len 119;  
 Best Local Similarity 70.0%; Pred. No. 4.5e-36;  
 Matches 84; Conservative 10; Mismatches 25; Indel 1; Gaps 1;

QY 1 EVOLVSGGGLVQPGSLRLSCVDSGLTFSSYGMHWVQAPGAGL VVISYDGNKYY 60  
 DB 1 EVOLVSGGGLVQPGSLRLSCVDSGLTFSSYGMHWVQAPGAGL VVISYDGNKYY 60  
 QY 61 ADSVKGFAISRDNKNTLYLQMSLTIETDAVYCAKDLIESNI LMGQGLVTVSS 120  
 DB 61 PDSVKGFTISRDNKNTLYLQMSLTKSEDTAVYCARH-GDYDV LMGQGLVTVSS 119

## RESULT 15

08NCL6 PRELIMINARY; PRT; 493 AA.

AC 08NCL6;  
 DT 01-OCT-2002 (TRENBLrel. 22, Created)  
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE Hypothetical protein FLJ90170.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; H  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Isogai T., Ota T., Nishikawa T., Hayaehi K., Otsuki T.,  
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y.,  
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nag  
 RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S.,  
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.,  
 RT "NEDO human cDNA sequencing project";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ database  
 DR EMBL; AK074651; BAC1114.1; -  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00409; IG; 4.  
 DR SMART; SM00407; IGL; 2.  
 DR SMART; SM00406; IGL; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 493 AA; 53224 MW; 12ECD7E09477101 CRC64;

Query Match 66.8%; Score 414.5; DB 4; Len 193;  
 Best Local Similarity 66.7%; Pred. No. 3.7e-35;  
 Matches 82; Conservative 10; Mismatches 26; Indel 5; Gaps 2;

QY 1 EVOLVSGGGLVQPGSLRLSCVDSGLTFSSYGMHWVQAPGAGL VVISYDGNKYY 60  
 DB 20 QVOLVSGGGLVQPGSLRLSCVDSGLTFSSYGMHWVQAPGAGL VVISYDGNKYY 79  
 QY 61 ADSVKGFAISRDNKNTLYLQMSLTIETDAVYCAKDLIESNI LMGQGLVTVSS 117  
 DB 80 SDSVKGFTISRDNKNTLYLQMSLTKSEDTAVYCARH-GDYDV LMGQGLVTVSS 137

QY 118 VSS 120  
 DB 138 VSS 140

Search completed: December 30, 2003, 11:01:08  
 Job time : 29.2445 secs



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DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
RN NCB1_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strauberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases;
DR EMBL: BC021276; AAH21276.1; -
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; 2.
KM Hypothetical protein.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 70.1%; Score 436; DB 4; Length
Best Local Similarity 71.8%; Pred. No. 2, 4e-37;
Matches 89; Conservative 6; Mismatches 25; Indels 4; Gaps 1;

OY 1 EVQLVESGGGLVQPGSRSLRLSCVDSGTLTFSSYGMMWVQAQAGLE
DB 20 EVQLVESGGGLVQPGSRSLRLSCAASGFTPDYAMHWVRAQPKGLE
OY 61 ADSVKGRAISRDNKNTLYLQMSLTIEDTAVVYCAQDLISNT-
DB 80 ADSVKGRTISRDNKNTLYLQMSLTIEDTAVVYCAQDLISNT-
OY 117 TVSS 120
DB 140 TVSS 143

RESULT 12
O9UL72 PRELIMINARY; PRT; 118 AA.
AC O9UL72;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable res
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
RN NCB1_TaxID=9606;
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis a
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL: AF035042; AAD56278.1; -.
DR HSP: P01772; 2F84.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
FT NON_TER 1
FT 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 67.2%; Score 418; DB 4; Length
Best Local Similarity 72.5%; Pred. No. 2, 4e-36;

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Matches 87; Conservative 7; Mismatches 24; Indels 2; Gaps 2;

OY 1 EVQLVESGGGLVQPGSRSLRLSCVDSGTLTFSSYGMMWVQAQAGLEWVAISYDNDKYY 60
DB 1 EVQLVESGGGLVQPGSRSLRLSCAASGFTVSSNYMMWVQAQPKGLESVV-TYSGGSSYY 59
OY 61 ADSVKGRAISRDNKNTLYLQMSLTIEDTAVVYCAQDLISNTAEALMGCGTLVTVSS 120
DB 60 ADSVKGRTISRDNKNTLYLQMSLTIEDTAVVYCAQDLISNTAEALMGCGTLVTVSS 118

RESULT 13
O91205 PRELIMINARY; PRT; 473 AA.
AC O91205;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCB1_TaxID=10090;
RP SEQUENCE FROM N.A.
RC Strauberg R.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC010327; AAH01327.1; -.
DR MGD: MGI:2144967; AU044919.
DR InterPro: IPR00345; CytC_heme_bind.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00190; CYTOCHROME_C; 1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
KM Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 66.9%; Score 416; DB 11; Length 473;
Best Local Similarity 69.2%; Pred. No. 2, 4e-35;
Matches 83; Conservative 9; Mismatches 26; Indels 2; Gaps 1;

OY 1 EVQLVESGGGLVQPGSRSLRLSCVDSGTLTFSSYGMMWVQAQAGLEWVAISYDNDKYY 60
DB 20 EVQLVESGGGLVQPGSRSLRLSCAASGFTPDYAMHWVRAQPKGLEWVAISYDNDKYY 79
OY 61 ADSVKGRAISRDNKNTLYLQMSLTIEDTAVVYCAQDLISNTAEALMGCGTLVTVSS 120
DB 80 ADSVKGRTISRDNKNTLYLQMSLTIEDTAVVYCAQDLISNTAEALMGCGTLVTVSS 137

RESULT 14
O920E7 PRELIMINARY; PRT; 119 AA.
AC O920E7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCB1_TaxID=10090;
RP SEQUENCE FROM N.A.
RC Atkin J.D., Iape A., Jennings I.G., Horatits O., Cotton R.G.H.;
RA "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells.";

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DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DR Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; H
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Spleen;
RA Strauberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ database;
DR EMBL; BC024289; AAH24289.1; -
DR InterPro; IPR003006; IG_1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 71.1%; Score 442; DB 4; Length 1;
Best Local Similarity 73.8%; Pred. No. 4, 4e-38;
Matches 90; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVPGPGRSLRLSCVDSGLTFSSYGMHWYRQAPGAGL AVISYDGNKYY 60
DB 20 EVOLVESGGGLVPGGSLRLSCAASGFTFSYNNWVROAPGKGLI SSMSSSSSYIYY 79
QY 61 ADVKGRFAISRNKNTLYLQNNSLTIEPTAVYYCAKDLSNIAEAL--WCGTLVTV 118
DB 80 ADVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCARDLRLQVLS FDLWGRGTLVTV 139
QY 119 SS 120
DB 140 SS 141

RESULT 9
Q9UL91 PRELIMINARY; PRT; 118 AA.
ID Q9UL91;
AC Q9UL91;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable re
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; H
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

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Query Match 70.4%; Score 438; DB 4; Length 118;
Best Local Similarity 74.8%; Pred. No. 1, 9e-38;
Matches 89; Conservative 8; Mismatches 20; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVPGPGRSLRLSCVDSGLTFSSYGMHWYRQAPGAGL AVISYDGNKYY 60
DB 1 EVOLVESGGGLVPGGSLRLSCAASGFTFSYNNWVROAPGKGLI SSMSSSSSYIYY 79
QY 61 ADVKGRFAISRNKNTLYLQNNSLTIEPTAVYYCAKDLSNIAEAL--WCGTLVTV 119
DB 61 ADVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCARC--DSSRAFDIWGCGTLVTVS 117

RESULT 10
Q96K68 PRELIMINARY; PRT; 494 AA.
ID Q96K68;
AC Q96K68;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FlJ14473.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Mammary gland;
RA Isegai T., Ota T., Hayaashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shitatori A., Sudo H.,
RA Watanabe M., Hosokiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakami K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saio K.,
RA Yamamoto J., Nakamatsu A., Nakamura Y., Nagahara K., Masuno Y.,
RA Minomiya K., Iwayanagi T.;
RT "NEBO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ database.
DR EMBL; AK027379; BAB55072.1; -
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AB5AE4C0E CRC64;

Query Match 70.1%; Score 436; DB 4; Length 494;
Best Local Similarity 71.3%; Pred. No. 2e-37;
Matches 87; Conservative 10; Mismatches 23; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVPGPGRSLRLSCVDSGLTFSSYGMHWYRQAPGAGL AVISYDGNKYY 60
DB 20 EVOLVESGGGLVPGGSLRLSCAASGFTFSYNNWVROAPGKGLI SSMSSSSSYIYY 79
QY 61 ADVKGRFAISRNKNTLYLQNNSLTIEPTAVYYCAKDLSNIAEAL--WCGTLVTV 118
DB 80 RDSVKGFTISRDNKNSLYLQNNSLRAEDTAVYYCARDCNCAICIGSPKCGTLVTV 139
QY 119 SS 120
DB 140 SS 141

RESULT 11
Q8WU38 PRELIMINARY; PRT; 573 AA.
ID Q8WU38;
AC Q8WU38;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

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AC Q9UL84:
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable reg
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Ho
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis a
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D4136545B8 CRC64;

Query Match 72.7%; Score 452; DB 4; Length
Best Local Similarity 73.4%; Pred. No. 6.5e-40;
Matches 91; Conservative 9; Mismatches 18; Indels

QY 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMMWRQAPGAGLE
DB 1 EVOLVESGGGVOPGRSLRLSCAASGFTFSNYSMMWRQAPGKGLIE
QY 61 ADSVKGRAISRDNKNTLYLQMSLTIEDTAVVYCAKD---LIE
DB 61 ADSVKGRTTIFRDNKSNMMDLQMSLRADDTAVVYCAKDERGLVIG
QY 117 TVSS 120
DB 119 TVSS 122

RESULT 6
ID Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71:
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable reg
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Ho
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis a
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.

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DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13154 MW; 2F04SCFA5D50736 CRC64;

Query Match 71.5%; Score 444.5; DB 4; Length 121;
Best Local Similarity 71.3%; Pred. No. 4e-39;
Matches 87; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

QY 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMMWRQAPGAGLEAVISYDNDKYY 60
DB 1 EVOLVESGGGVOPGRSLRLSCAASGFTFDGYAMHWYQAPGKGLVWVSLISGDGSTYY 60
QY 61 ADSVKGRAISRDNKNTLYLQMSLTIEDTAVVYCAKDLIESNIAEA--LWGQSTLVTV 118
DB 61 ADSVKGRTTISRDNKSNLSLQMSLRADDTAVVYCAKGRV-TTIDRFDIWGQSTMTV 119
QY 119 SS 120
DB 120 SS 121

RESULT 7
ID Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9:
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Struhsberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAH15760.1; -.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 71.2%; Score 444.5; DB 4; Length 597;
Best Local Similarity 71.2%; Pred. No. 3.3e-38;
Matches 89; Conservative 8; Mismatches 23; Indels 5; Gaps 1;

QY 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMMWRQAPGAGLEAVISYDNDKYY 60
DB 20 EVOLVESGGGLVOPGRSLRLSCAASGFTFSYAMHWYQAPGKGLVWVSLISGSGSTYY 79
QY 61 ADSVKGRAISRDNKNTLYLQMSLTIEDTAVVYCAKD-----LIESNIAEALWGQSTL 115
DB 80 ADSVKGRTTISRDNKNTLYLQMSLRADDTAVVYCAKDPGYSASGVYTRIEDYWGQSTL 139
QY 116 TVSS 120
DB 140 TVSS 144

RESULT 8
ID Q8TC77 PRELIMINARY; PRT; 471 AA.
AC Q8TC77:

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RESULT 2
09UL90          PRELIMINARY;      PRT;      113 AA.
AC 09UL90;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable re
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; H
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57EDD19086D07F CRC64;

Query Match 79.8%; Score 496.5; DB 4; Leng 113;
Best Local Similarity 80.8%; Pred. No. 1.2e-44;
Matches 97; Conservative 4; Mismatches 12; Inde 7; Gaps 1;

QY 1 EVOLVESGGGLVOPGSRSLRSCVDSGLTFSSYGHWVRQAPGAGL
DB 1 EVOLVESGGGVOPGSGSLRSLSCAASGTFSSYGHWVRQAPGAGL
61 ADVYGRFAISRDNAXKTLTYLQNNSLTIEDTAVYYCAKDLESNI/
61 ADVYGRFTISRDNKSTLYLQNNSLRAEDTAVYYCAKDL-----
YMGQGLTVTVSS 120
YMGQGLTVTVSS 113

RESULT 3
09UL93          PRELIMINARY;      PRT;      116 AA.
AC 09UL93;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable re
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; H
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 77.9%; Score 484.5; DB 4; Length 116;
Best Local Similarity 79.0%; Pred. No. 2.3e-43;
Matches 94; Conservative 6; Mismatches 16; Inde 3; Gaps 1;

QY 2 VOLVESGGGLVOPGSRSLRSCVDSGLTFSSYGHWVRQAPGAGLEAVAVISYDGNKRYA 61
DB 1 VOLVESGGGVOPGSGSLRSLSCAASGTFSSYGHWVRQAPGAGLEAVAVISYDGNKRYA 60
61 ADVYGRFAISRDNAXKTLTYLQNNSLTIEDTAVYYCAKDLESNI/
61 ADVYGRFTISRDNKSTLYLQNNSLRAEDTAVYYCAKDL-----
YMGQGLTVTVSS 120
YMGQGLTVTVSS 116

RESULT 4
09Y509          PRELIMINARY;      PRT;      147 AA.
AC 09Y509;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Vh3 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCMAA7BC925C CRC64;

Query Match 74.1%; Score 461; DB 4; Length 147;
Best Local Similarity 69.8%; Pred. No. 9.4e-41;
Matches 90; Conservative 13; Mismatches 14; Inde 12; Gaps 2;

QY 1 EVOLVESGGGLVOPGSRSLRSCVDSGLTFSSYGHWVRQAPGAGLEAVAVISYDGNKRY 60
DB 1 QVHLVESGGGVOPGSGSLRSLSCAASGTFSTYGMHWVRQAPGAGLDVVALISIDSGTQY 60
61 ADVYGRFAISRDNAXKTLTYLQNNSLTIEDTAVYYCAKDLESNI/
61 ADVYGRFTISRDNKSTLYLQNNSLRAEDTAVYYCAKDL-----
YMGQGLTVTVSS 120
YMGQGLTVTVSS 112

RESULT 5
09UL84          PRELIMINARY;      PRT;      122 AA.
AC 09UL84;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable re
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; H
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 77.9%; Score 484.5; DB 4; Length 116;
Best Local Similarity 79.0%; Pred. No. 2.3e-43;
Matches 94; Conservative 6; Mismatches 16; Inde 3; Gaps 1;

QY 2 VOLVESGGGLVOPGSRSLRSCVDSGLTFSSYGHWVRQAPGAGLEAVAVISYDGNKRYA 61
DB 1 VOLVESGGGVOPGSGSLRSLSCAASGTFSSYGHWVRQAPGAGLEAVAVISYDGNKRYA 60
61 ADVYGRFAISRDNAXKTLTYLQNNSLTIEDTAVYYCAKDLESNI/
61 ADVYGRFTISRDNKSTLYLQNNSLRAEDTAVYYCAKDL-----
YMGQGLTVTVSS 120
YMGQGLTVTVSS 112

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

```
Run on:      December 30, 2003, 10:46:19 ; Search time 29.45 Seconds
              (without alignment)
              1058.876 Million ; 1 updates/sec
```

Title: US-09-674-752-46

Sequence: 1 EVQLVESGGGLVQPGKSLRL...IESNIAEALWGQ...VTVSS 120

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 8305

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Database : SPTREMBL\_23:\*

- ```

1: 1:  sp_archaea:*
2: 2:  sp_bacteria:*
3: 3:  sp_fungi:*
4: 4:  sp_human:*
5: 5:  sp_invertebrate:*
6: 6:  sp_mammal:*
7: 7:  sp_mhc:*
8: 8:  sp_organelle:*
9: 9:  sp_plage:*
10: 10: sp_plant:*
11: 11: sp_rodent:*
12: 12: sp_virus:*
13: 13: sp_vertebrate:*
14: 14: sp_unclassified:*
15: 15: sp_virus:*
16: 16: sp_bacteriap:*
17: 17: sp_archaeap:*

```

Pred. No. is the number of results predicted by chance. The score greater than or equal to the score of the result and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length DB | ID     | Description         |
|------------|-------|-------------|-----------|--------|---------------------|
| 1          | 513   | 82.5        | 613       | Q8WUX1 | Q1 k1 homo sapien   |
| 2          | 486.5 | 79.8        | 113       | Q9UJ90 | Q2 .93 homo sapien  |
| 3          | 484.5 | 77.9        | 116       | Q9UJ93 | Q3 .93 homo sapien  |
| 4          | 461   | 74.1        | 147       | Q9Y509 | Q4 .09 homo sapien  |
| 5          | 452   | 72.7        | 122       | Q9UJ84 | Q5 84 homo sapien   |
| 6          | 444.5 | 71.5        | 121       | Q9UJ71 | Q6 71 homo sapien   |
| 7          | 444.5 | 71.5        | 597       | Q96B89 | Q7 .09 homo sapien  |
| 8          | 442   | 71.1        | 471       | Q8TC77 | Q8 .77 homo sapien  |
| 9          | 438   | 70.4        | 118       | Q9UJ91 | Q9 .91 homo sapien  |
| 10         | 436   | 70.1        | 494       | Q96K68 | Q10 68 homo sapien  |
| 11         | 436   | 70.1        | 573       | Q8WJ38 | Q11 38 homo sapien  |
| 12         | 418   | 67.2        | 118       | Q9UJ72 | Q12 .72 homo sapien |
| 13         | 416   | 66.9        | 473       | Q91Z05 | Q13 .05 mus muscul  |
| 14         | 415.5 | 66.8        | 119       | Q9Z0E7 | Q14 .07 mus muscul  |
| 15         | 414.5 | 66.6        | 493       | Q8NCL6 | Q15 .16 homo sapien |
| 16         | 412   | 66.2        | 112       | Q9HCC1 | Q16 .01 homo sapien |

|    |       |      |     |    |        |                     |
|----|-------|------|-----|----|--------|---------------------|
| 17 | 409.5 | 65.8 | 499 | 4  | Q8N5K4 | Q8N5K4 homo sapien  |
| 18 | 398   | 64.0 | 995 | 4  | Q9UTB6 | Q9UTB6 homo sapien  |
| 19 | 396   | 63.7 | 487 | 11 | Q9XRK4 | Q9XRK4 mus musculus |
| 20 | 385.5 | 62.0 | 479 | 11 | Q91WP5 | Q91WP5 mus musculus |
| 21 | 372.5 | 59.9 | 486 | 11 | Q91Z07 | Q91Z07 mus musculus |
| 22 | 370.5 | 59.6 | 131 | 4  | Q9UTB8 | Q9UTB8 homo sapien  |
| 23 | 365   | 58.7 | 469 | 11 | Q8R3V9 | Q8R3V9 mus musculus |
| 24 | 354   | 56.9 | 298 | 11 | Q9QYF0 | Q9QYF0 mus musculus |
| 25 | 348.5 | 56.0 | 480 | 11 | Q91XEL | Q91XEL mus musculus |
| 26 | 348   | 55.9 | 484 | 11 | Q8VEA0 | Q8VEA0 mus musculus |
| 27 | 341   | 55.8 | 124 | 6  | Q9N0M4 | Q9N0M4 Oryctolagus  |
| 28 | 341   | 55.8 | 437 | 11 | Q9RIA4 | Q9RIA4 mus musculus |
| 29 | 338   | 54.3 | 124 | 6  | Q9N0M6 | Q9N0M6 Oryctolagus  |
| 30 | 337   | 54.2 | 124 | 4  | Q9UTL2 | Q9UTL2 homo sapien  |
| 31 | 336.5 | 54.1 | 521 | 4  | Q8N4Y9 | Q8N4Y9 homo sapien  |
| 32 | 331.5 | 53.3 | 104 | 4  | Q9UTL7 | Q9UTL7 homo sapien  |
| 33 | 321   | 51.6 | 121 | 11 | Q99NG4 | Q99NG4 mus musculus |
| 34 | 319.5 | 51.4 | 125 | 4  | Q9UTL5 | Q9UTL5 homo sapien  |
| 35 | 318.5 | 51.2 | 484 | 11 | Q99LA6 | Q99LA6 mus musculus |
| 36 | 315.5 | 50.7 | 112 | 4  | Q9UGF3 | Q9UGF3 homo sapien  |
| 37 | 313   | 50.3 | 145 | 11 | Q924Q9 | Q924Q9 mus musculus |
| 38 | 312   | 50.2 | 139 | 11 | Q924R5 | Q924R5 mus musculus |
| 39 | 305   | 49.0 | 145 | 11 | Q924O6 | Q924O6 mus musculus |
| 40 | 305   | 49.0 | 145 | 11 | Q924R3 | Q924R3 mus musculus |
| 41 | 305   | 49.0 | 463 | 11 | Q99LC4 | Q99LC4 mus musculus |
| 42 | 303   | 48.7 | 145 | 11 | Q924R4 | Q924R4 mus musculus |
| 43 | 302.5 | 48.6 | 146 | 11 | Q924Q3 | Q924Q3 mus musculus |
| 44 | 302   | 48.6 | 159 | 4  | Q96QSO | Q96QSO homo sapien  |
| 45 | 301   | 48.4 | 141 | 11 | Q924Q4 | Q924Q4 mus musculus |

## ALIGNMENTS

## RESULT 1

| ID                    | ORGANISM                                                          | PRELIMINARY   | PRT        | 613 AA  |
|-----------------------|-------------------------------------------------------------------|---------------|------------|---------|
| AC                    | Q8WUK1                                                            |               |            |         |
| DT                    | 01-MAR-2002 (TrEMBLrel. 20, Created)                              |               |            |         |
| DT                    | 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)                 |               |            |         |
| DT                    | 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)               |               |            |         |
| DE                    | Hypothetical protein.                                             |               |            |         |
| OS                    | Homo sapiens (Human).                                             |               |            |         |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |               |            |         |
| OC                    | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.       |               |            |         |
| OX                    | NCBI_TaxId=9606;                                                  |               |            |         |
| RN                    | [1]                                                               |               |            |         |
| RP                    | SEQUENCE FROM N.A.                                                |               |            |         |
| RC                    | TISSUE=Testis;                                                    |               |            |         |
| RA                    | Strausberg R.;                                                    |               |            |         |
| RL                    | Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.           |               |            |         |
| DR                    | EMBL; BC020240; AA020240.1; -                                     |               |            |         |
| DR                    | InterPro; IPR007110; IG-like.                                     |               |            |         |
| DR                    | InterPro; IPR003006; IG_MHC.                                      |               |            |         |
| DR                    | InterPro; IPR003596; IG_v.                                        |               |            |         |
| DR                    | Pfam; PF00047; IG 5.                                              |               |            |         |
| DR                    | SMART; SM00406; IGV 1.                                            |               |            |         |
| DR                    | PROSITE; PS00835; IG LIKE; 5.                                     |               |            |         |
| KM                    | PROSITE; PS00290; IG_MHC; 3.                                      |               |            |         |
| DR                    | Hypothetical protein                                              |               |            |         |
| SC                    | SEQUENCE 613 AA; 67236 MW; 60CF7F950671EB35 CRC64;                |               |            |         |
| Query Match           | 82.5%; Score 513; DB 4; Length 613;                               |               |            |         |
| Best local similarity | 81.7%; Pred. NO. 2e-45;                                           |               |            |         |
| Matches               | 98; Conservative                                                  | 7; Mismatches | 15; Indels | 0; Gaps |
| QY                    | 1 EVQLVESGGGLVQPGKSLRLSCTVDSGLTPSSYGMHWVROAFLGRVAVVISTGDKNTYY 60  |               |            |         |
| Db                    | 20 QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVROAFLGRVAVVISTGDKNTYY 79  |               |            |         |
| QY                    | 61 ASQVSRKFAISDNNKNTLYIQMNSLTETPRNAVYCAKDLIESIAALNCGQGLVTVSS 120  |               |            |         |
| Db                    | 80 ASQVSRKFTISDNNKNTLYIQMNSLTREDTNAVYCAADNSGVEFTDINCGQGMVTVSS 139 |               |            |         |

```

AC P01774;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Ho
OC NCBI_TaxId=9606;
RN [1]
RP MEDLINE=75046755; PubMed=4139708;
RA Capra J.D., Kehoe J.M.;
RT "Structure of antibodies with shared idiotypy: the comp
RT of the heavy chain variable regions of two immunoglobul
RT anti-gamma globulins."
RL Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH
CC GLOBULIN ACTIVITY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR Immunoglobulin V region.
KM DOMAIN 1 112 IG-LIKE.
FT VARIANT 54 54 N -> D (PROBABLY DUE TO DE
FT DURING ISOLATION).
FT /FTID=VAR_003966.
FT NON TER 119 119
SQ SEQUENCE 119 AA; 12953 MW; 2E018AF4DCB2610 CRC64;

```

```

Query Match 63.7%; Score 396; DB 1; Length 119;
Best Local Similarity 68.1%; Pred. No. 7,1e-35;
Matches 81; Conservative 11; Mismatches 25; Indels 2; Gaps 1;

```

```

QY 1 EVQLVESGGGLVQPGSRSLRLSCVDSGTLFSSYGMHWVRQAPGAGLE
DB 1 EVQLVESGGGLVQPGSRSLRLSCVDSGTLFSSYGMHWVRQAPGAGLE
QY 61 ADSVNGRFAISRDNKNTLYLQMSLTIEDTAIVYCAKDL--IESN
DB 61 ADSVNGRFTISRNDKNTLYLQMSLTIEDTAIVYCAKDPYVSP

```

## RESULT 15

```

HY3N_HUMAN
ID HY3N_HUMAN STANDARD; PRT; 119 AA.
AC P01775;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region IAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Ho
OC NCBI_TaxId=9606;
RN [1]
RP MEDLINE=75046755; PubMed=4139708;
RA Capra J.D., Kehoe J.M.;
RT "Structure of antibodies with shared idiotypy: the comp
RT of the heavy chain variable regions of two immunoglobul
RT anti-gamma globulins."
RL Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH
CC ANTI-GAMMA

```

```

CC GLOBULIN ACTIVITY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR Immunoglobulin V region.
KM DOMAIN 1 112 IG-LIKE.
FT NON TER 119 119
SQ SEQUENCE 119 AA; 12858 MW; D6338098794DCF5E CRC64;

```

```

Query Match 62.9%; Score 391; DB 1; Length 119;
Best Local Similarity 66.9%; Pred. No. 2.4e-34;
Matches 79; Conservative 11; Mismatches 26; Indels 2; Gaps 1;

```

```

QY 2 VQLVESGGGLVQPGSRSLRLSCVDSGTLFSSYGMHWVRQAPGAGLEWVAVISYDGNDRYYA 61
DB 2 VQLVESGGGLVQPGSRSLRLSCVDSGTLFSSYGMHWVRQAPGAGLEWVAWKYENGNDKRYA 61
QY 62 DSVNGRFAISRDNKNTLYLQMSLTIEDTAIVYCAKDL--IESNIAEALWGQGLT 117
DB 62 DSVNGRFTISRNDKNTLYLQMSLTIEDTAIVYCAKDPYVSPFAHNGQGLT 119

```

```

Search completed: December 30, 2003, 10:55:53
Job time : 6.43379 secs

```



|                |                                                                              |
|----------------|------------------------------------------------------------------------------|
| DE             | Ig heavy chain V-II region V#26 precursor.                                   |
| OS             | Homo sapiens (Human).                                                        |
| OC             | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute-                    |
| CC             | Mammalia; Eutheria; Primates; Catarrhini; Homidae; Ho-                       |
| XX             | NCBI_TaxID=9606;                                                             |
| RN             | [1]                                                                          |
| RP             | SEQUENCE FROM N.A.                                                           |
| RX             | MEDLINE=81101090; PubMed=6450418;                                            |
| RA             | Mathysse G., Rabbits T.H.;                                                   |
| RT             | "Structure and multiplicity of genes for the human immu-                     |
| RL             | heavy chain variable region.";                                               |
| RU             | Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).                            |
| CC             | -1- SIMILARITY: Contains 1 immunoglobulin-like domain.                       |
| CC             | -----                                                                        |
| CC             | This SWISS-PROT entry is copyright. It is produced thro-                     |
| CC             | ugh the Swiss Institute of Bioinformatics and the                            |
| CC             | European Bioinformatics Institute. There are no r-                           |
| CC             | use by non-profit institutions as long as its con-                           |
| CC             | tent is modified and this statement is not removed. Usage c-                 |
| CC             | ontains requires a license agreement (see http://www.i-                      |
| CC             | or send an email to licenses@db-bd.ch).                                      |
| CC             | -----                                                                        |
| DR             | EMBL; J00236; AAA53516.1; -                                                  |
| DR             | EMBL; M35415; AAA58735.1; -                                                  |
| DR             | PIR; A02047; H3H26.                                                          |
| DR             | PDB; 1HOU; 23-DEC-99.                                                        |
| DR             | GeneW; HGNC:5545; IGHV0.                                                     |
| DR             | GO; GO:0005576; C:extracellular; NAS.                                        |
| DR             | GO; GO:0003823; F:antigen binding activity; NAS.                             |
| DR             | GO; GO:0006955; P:immune response; NAS.                                      |
| DR             | InterPro; IPRO07110; Ig-Like.                                                |
| DR             | InterPro; IPRO03006; Ig_MHC.                                                 |
| DR             | InterPro; IPRO03596; Ig_V.                                                   |
| DR             | Pfam; PF00047; Ig_1.                                                         |
| DR             | SMART; SMO0406; IGV; 1.                                                      |
| DR             | PROSITE; PS50835; IG_LIKE; 1.                                                |
| KW             | Immunoglobulin V region; Signal; 3D-structure.                               |
| FT             | SIGNAL 1 19                                                                  |
| FT             | CHAIN 20 117 IG HEAVY CHAIN V-II REGION /H26.                                |
| FT             | DOMAIN 20 >117 IG-LIKE.                                                      |
| FT             | NON_TER 117                                                                  |
| SO             | SEQUENCE 117 AA; 12562 MW; E826733P1A3CB0F1 CRC64;                           |
| OY             | Query Match 65.1%; Score 405; DB 1; Length 17;                               |
|                | Best Local Similarity 79.6%; Pred. No. 7.8e-36;                              |
|                | Matches 78; Conservative 3; Mismatches 17; Indels 0; Gaps 0;                 |
| DQ             | 1 EVOLVESGGGIIVOPRSRLISCVDSGLTFSSYGMMHWQAAPAGLE <sup>a</sup> AVSYGNDKXY 60   |
|                |                                                                              |
| DQ             | 20 EVQLLESQGGIIVPGSGIRLSCANASGFPSYSMSWVAQAPKGDEL <sup>b</sup> SAISGSGSTYY 79 |
|                |                                                                              |
| OY             | 61 ADSVKGRFAISRDNAKNTLYLOMNSLTIEDPAVVYCAK 98                                 |
|                |                                                                              |
| DQ             | 80 GDSVKGRFTISRDNASKNTLYLOMNSLRADPAVVYCAK 117                                |
|                |                                                                              |
| RESULT 10      |                                                                              |
| HVI6_MOUSE     |                                                                              |
| ID_HVI6_MOUSE  | STANDARD; PRT; 136 AA.                                                       |
| AC_P01783      |                                                                              |
| DT_21-JUL-1986 | (Rel. 01, Created)                                                           |
| DT_21-JUL-1986 | (Rel. 01, Last sequence update)                                              |
| DT_15-SEP-2003 | (Rel. 42, Last annotation update)                                            |
| DE             | Ig heavy chain V region MOPC 21 precursor (Fragment).                        |
| OS             | Mus musculus (Mouse)                                                         |
| OC             | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute-                    |
| CC             | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus-                    |
| OX             | NCBI_TaxID=10090;                                                            |
| RN             | [1]                                                                          |
| RP             | SEQUENCE FROM N.A.                                                           |
| RX             | MEDLINE=81234548; PubMed=6788376;                                            |
| RA             | Bothwell A.L.M., Paekkind M., Reith M., Imamihi-Kari T.,                     |
| RA             | Baltimore D.;                                                                |

```

RT      "Heavy chain variable region contribution to the NPb family of
RN      antibodies: somatic mutation evident in a gamma 2a variable region.";
RL      Cell 24:625-637(1981).
[2]
RN      SEQUENCE OF 17-136.
RX      MEDLINE=7100368; PubMed=401950;
RA      Adetubo K., Milstein C., Secher D.S.;
RT      "Molecular analysis of spontaneous somatic mutants."
RL      Nature 265:299-304(1977).
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license@isb-gib.ch.
CC      or send an email to license@isb-gib.ch.
DR      EMBL; J00522; AAD15290.1; -.
DR      PIR; B90809; GIMS21.
DR      PDB; 1IGC; 03-JUN-95.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; Ig_1.
DR      SMART; SMO0406; IGV_1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Immunoglobulin V region; Signal; 3D-structure.
FT      NON TER                     1
FT      SIGNAL                      16
FT      CHAIN                       17   136       IG HEAVY CHAIN V REGION MOPC 21.
FT      DOMAIN                     115   119       D SEGMENT.
FT      DOMAIN                     120   136       H4 SEGMENT.
FT      DISULFID                    38   112
FT      CONFLICT                   75   78         HYAD -> DYAH (IN REF. 2) .
FT      CONFLICT                   89   90         DN -> ND (IN REF. 2) .
FT      CONFLICT                   115  115        W -> H (IN REF. 2) .
FT      CONFLICT                   120  120        Y -> W (IN REF. 2) .
FT      NON TER                     136
SQ      SEQUENCE                  136 AA; 15071 MW; 2276A9BDBDF7016 CRC64;
Query Match          65.1%; Score 405; DB 1; Length 136;
Beet Local Similarity 68.1%; Pred. No. 9.4e-35;
Matches    82; Conservative 9; Mismatches 29; Indels 0; Gaps 0;
Qy      1 EVQLVESGGGLVPGSRSLRSCVDSSGLTFSSYGMRWRAFGAGLEWNAVISYDGNDKRY 60
Db      17 DVQLVEGSGGLVGPGSRSLRSCVAASGTFFSPGHMWRAQPKGLEWNAVISSSSTLYH 76
Qy      61 ADSVKGFPAISRDAKNTLVYQNNSLTIEDTAIVYYCAKDILIESNIAEALMGCGTLTVSS 120
Db      77 ADYKGFPTISRDNPNTLFQMTSLRSSEDTAMYYCARMCNGNYPYRAMDYWGCGTSVTSS 136
RESULT 11
HV3B_HUMAN STANDARD; PRT; 114 AA.
AC PO1763;
DT 21-JUL-1986 (Rel. 01, Last created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II1 region WEA.
OS Homo sapiens (Human).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
KN [1]
SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Gonl F., Frangione B.;
RT "Antino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33."

```





DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin V region; Pyridone carboxylic acid.  
 FT DOMAIN 1 112  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT NON\_TER 122 122  
 SQ SEQUENCE 122 AA; 13166 MW; 745B6959E84100A CRC64;  
 Query Match 70.9%; Score 441; DB 1; Length 172;  
 Best Local Similarity 63.1%; Pred. No. 1.3e-39;  
 Matches 77; Conservative 24; Mismatches 19; Indels 2; Gaps 1;  
 QY 1 EVOLVESGGGLVQPGSRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYGNDKRY 60  
 DB 1 QVQLVVSQGGAVZPQSRSLRLSCAASGFSFSTYAMHWVRQAPGKGLZWI:SVISYGBBZYY 60  
 QY 61 ADSVKGRAISRDAKNTLYIQMNSLTIEDTAVVYCAKD-----LIESNI/EAALMGQTLVTV 118  
 DB 61 AASVKGRTISRBSKRTMYLEMSLRARNTAVVYCAASGIALGSVA(TDYMGZGLVTI 120  
 QY 119 SS 120  
 DB 121 SS 122  
 RESULT 5  
 HV3K\_HUMAN STANDARD; PRT; 126 AA.  
 ID P01772;  
 AC 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region KOL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE, AND DISULFIDE BONDS.  
 RX MEDLINE=83289131; PubMed=6884994;  
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
 RT "Three-dimensional structure determination of antibodies. Primary  
 structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=81072295; PubMed=7441755;  
 RA Marguaret M., Delsenhofer J., Huber R., Palm W.;  
 RT "Cryoelectronographic refinement and atomic models of the intact  
 immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A  
 and 1.0-A resolution.";  
 RL J. Mol. Biol. 141:369-391(1980).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR: A02055; G1HUKL.  
 DR PDB: 2FB4; 12-JUL-89.  
 DR PDB: 2IG2; 12-JUL-89.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding activity; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; IG-LIKE.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin V region; 3D-structure; Pyridone carboxylic acid.  
 FT DOMAIN 1 112  
 FT MOD\_RES 1 1 IG-LIKE.  
 FT NON\_TER 1 1 PYRROLIDONE CARBOXYLIC ACID  
 FT DISULFID 22 96

FT DISULFID 105 110  
 FT STRAND 3 7  
 FT STRAND 11 12  
 FT TURN 14 15  
 FT STRAND 18 25  
 FT HELIX 29 31  
 FT STRAND 34 39  
 FT TURN 41 42  
 FT STRAND 45 51  
 FT TURN 53 54  
 FT STRAND 58 60  
 FT HELIX 62 64  
 FT STRAND 65 65  
 FT TURN 66 67  
 FT STRAND 68 73  
 FT TURN 74 77  
 FT STRAND 78 83  
 FT HELIX 88 90  
 FT STRAND 92 99  
 FT TURN 106 106  
 FT TURN 107 108  
 FT STRAND 109 109  
 FT STRAND 113 116  
 FT STRAND 120 124  
 FT NON\_TER 126 126  
 SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;  
 Query Match 69.6%; Score 433; DB 1; Length 126;  
 Best Local Similarity 68.3%; Pred. No. 9.6e-39;  
 Matches 86; Conservative 12; Mismatches 22; Indels 6; Gaps 1;  
 QY 1 EVOLVESGGGLVQPGSRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYGNDKRY 60  
 DB 1 QVQLVVSQGGAVZPQSRSLRLSCSSGFSFSTYAMHWVRQAPGKGLZWI:IMWDGSDQHY 60  
 QY 61 ADSVKGRAISRDAKNTLYIQMNSLTIEDTAVVYCAKD-----LIESNI/EAALMGQCT 114  
 DB 61 ADSVKGRTISRDSKNTLYIQMNSLTIEDTAVVYCAKD-----LIESNI/EAALMGQCT 120  
 QY 115 LVTVSS 120  
 DB 121 PVTVSS 126  
 RESULT 6  
 HV3T\_HUMAN STANDARD; PRT; 116 AA.  
 ID P01781;  
 AC 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-III region GAL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=75059123; PubMed=4803843;  
 RA Watanabe S., Barnikol H.U., Horn J., Berttram J., Hilschmann N.;  
 RT "The primary structure of a monoclonal IgM-immunoglobulin  
 (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-  
 type), subgroup H III. Architecture of the complete IgM-molecule.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).  
 RN [2]  
 RP REVISION TO 28-33.  
 RA Hilschmann N.;  
 RL Submitted (JUN-1975) to the PIR data bank.  
 CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
 MACROGLOBULIN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR: A02064; M3HUGL.  
 DR HSSP: P01772; 2FB4.



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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 6.43379 Seconds  
(without alignments)  
877.119 Million cell updates/sec

Title: US-09-674-752-46

Perfect score: 622  
Sequence: 1 EVOLVESGGGLVQPGKSLRL.....IESNTAALMGQGLTVTVSS 120

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description        |
|------------|-------|-------------|--------|--------------|--------------------|
| 1          | 477   | 76.7        | 122    | 1 HV3G_HUMAN | P01768 homo sapien |
| 2          | 453.5 | 72.9        | 119    | 1 HV3I_HUMAN | P01770 homo sapien |
| 3          | 452.5 | 72.7        | 121    | 1 HV3J_HUMAN | P01771 homo sapien |
| 4          | 441   | 70.9        | 122    | 1 HV3H_HUMAN | P01769 homo sapien |
| 5          | 433   | 69.6        | 126    | 1 HV3K_HUMAN | P01772 homo sapien |
| 6          | 417   | 67.0        | 116    | 1 HV3T_HUMAN | P01781 homo sapien |
| 7          | 416.5 | 67.0        | 119    | 1 HV3I_HUMAN | P01782 homo sapien |
| 8          | 413   | 66.4        | 120    | 1 HV3U_HUMAN | P01782 homo sapien |
| 9          | 405   | 65.1        | 117    | 1 HV3C_HUMAN | P01764 homo sapien |
| 10         | 405   | 65.1        | 136    | 1 HV16_MOUSE | P01783 mus musculu |
| 11         | 402   | 64.6        | 114    | 1 HV3B_HUMAN | P01763 homo sapien |
| 12         | 399.5 | 64.2        | 115    | 1 HV3F_HUMAN | P01767 homo sapien |
| 13         | 398.5 | 64.1        | 117    | 1 HV02_CANFA | P01785 canis famli |
| 14         | 396   | 63.7        | 119    | 1 HV3M_HUMAN | P01773 homo sapien |
| 15         | 391   | 62.9        | 119    | 1 HV3N_HUMAN | P01774 homo sapien |
| 16         | 389.5 | 62.6        | 120    | 1 HV3E_HUMAN | P01775 homo sapien |
| 17         | 385   | 61.9        | 114    | 1 HV01_CANFA | P01766 homo sapien |
| 18         | 384   | 61.7        | 122    | 1 HV3A_HUMAN | P01766 homo sapien |
| 19         | 383.5 | 61.7        | 116    | 1 HV05_CARAU | P01818 carassius a |
| 20         | 379.5 | 61.0        | 115    | 1 HV3D_HUMAN | P01765 homo sapien |
| 21         | 373.5 | 60.0        | 115    | 1 HV32_MOUSE | P01801 mus musculu |
| 22         | 368.5 | 59.2        | 113    | 1 HV30_MOUSE | P01799 mus musculu |
| 23         | 368   | 59.2        | 119    | 1 HV37_MOUSE | P01807 mus musculu |
| 24         | 367   | 59.0        | 119    | 1 HV3P_HUMAN | P01777 homo sapien |
| 25         | 365   | 58.7        | 122    | 1 HV20_MOUSE | P01789 mus musculu |
| 26         | 364.5 | 58.6        | 142    | 1 HV01_PAT   | P01805 ratcus notv |
| 27         | 364   | 58.5        | 117    | 1 HV55_MOUSE | P18526 mus musculu |
| 28         | 363.5 | 58.4        | 113    | 1 HV27_MOUSE | P01796 mus musculu |
| 29         | 363   | 58.4        | 117    | 1 HV54_MOUSE | P18525 mus musculu |
| 30         | 363   | 58.4        | 119    | 1 HV40_MOUSE | P01810 mus musculu |
| 31         | 362.5 | 58.3        | 115    | 1 HV33_MOUSE | P01802 mus musculu |
| 32         | 362   | 58.2        | 98     | 1 HV57_MOUSE | P18528 mus musculu |
| 33         | 361.5 | 58.1        | 113    | 1 HV31_MOUSE | P01800 mus musculu |

|    |       |      |     |              |                    |
|----|-------|------|-----|--------------|--------------------|
| 34 | 359   | 57.7 | 117 | 1 HV3O_HUMAN | P01776 homo sapien |
| 35 | 358.5 | 57.6 | 113 | 1 HV34_MOUSE | P01803 mus musculu |
| 36 | 358.5 | 57.6 | 123 | 1 HV18_MOUSE | P01787 mus musculu |
| 37 | 357.5 | 57.5 | 113 | 1 HV28_MOUSE | P01797 mus musculu |
| 38 | 357.5 | 57.5 | 117 | 1 HV17_MOUSE | P01786 mus musculu |
| 39 | 356.5 | 57.3 | 123 | 1 HV19_MOUSE | P01788 mus musculu |
| 40 | 356   | 57.2 | 119 | 1 HV38_MOUSE | P01808 mus musculu |
| 41 | 356   | 57.2 | 122 | 1 HV21_MOUSE | P01790 mus musculu |
| 42 | 355.5 | 57.2 | 123 | 1 HV22_MOUSE | P01791 mus musculu |
| 43 | 355.5 | 57.2 | 123 | 1 HV25_MOUSE | P01794 mus musculu |
| 44 | 355   | 57.1 | 115 | 1 HV35_HUMAN | P01780 homo sapien |
| 45 | 353.5 | 56.8 | 113 | 1 HV29_MOUSE | P01798 mus musculu |

## ALIGNMENTS

|                                                                       |           |      |         |  |  |
|-----------------------------------------------------------------------|-----------|------|---------|--|--|
| RESULT 1                                                              |           |      |         |  |  |
| HV3G_HUMAN                                                            |           |      |         |  |  |
| ID HV3G_HUMAN                                                         | STANDARD; | PRT; | 122 AA. |  |  |
| AC P01768;                                                            |           |      |         |  |  |
| DT 21-JUL-1986 (Rel. 01, Created)                                     |           |      |         |  |  |
| DT 21-JUL-1986 (Rel. 01, Last sequence update)                        |           |      |         |  |  |
| DT 15-SEP-2003 (Rel. 42, Last annotation update)                      |           |      |         |  |  |
| DE Ig heavy chain V-II region CM.                                     |           |      |         |  |  |
| OS Homo sapiens (Human).                                              |           |      |         |  |  |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |           |      |         |  |  |
| OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.          |           |      |         |  |  |
| OX NCBI_TaxID=9606;                                                   |           |      |         |  |  |
| RN [1]                                                                |           |      |         |  |  |
| RP SEQUENCE.                                                          |           |      |         |  |  |
| RA MEDLINE=81013859; PubMed=6774332;                                  |           |      |         |  |  |
| RX Lehman D.W., Putnam F.W.;                                          |           |      |         |  |  |
| RT "Amino acid sequence of the variable region of a human mu chain:   |           |      |         |  |  |
| RL location of a possible JH segment."                                |           |      |         |  |  |
| RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).                  |           |      |         |  |  |
| CC -I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A |           |      |         |  |  |
| CC PATIENT WITH MACROGLOBULINEMIA.                                    |           |      |         |  |  |
| CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.             |           |      |         |  |  |
| DR PIR: A02051; M3HUM.                                                |           |      |         |  |  |
| DR HSRP: P01772; 2PB4.                                                |           |      |         |  |  |
| DR GO: GO:0005576; C:extracellular; NAS.                              |           |      |         |  |  |
| DR GO: GO:0003823; F:antigen binding activity; NAS.                   |           |      |         |  |  |
| DR GO: GO:0006955; P:immune response; NAS.                            |           |      |         |  |  |
| DR InterPro: IPR007110; IG-like.                                      |           |      |         |  |  |
| DR InterPro: IPR003006; IG_MHC.                                       |           |      |         |  |  |
| DR InterPro: IPR003596; IG_v.                                         |           |      |         |  |  |
| DR Pfam: PF0047; Ig_1.                                                |           |      |         |  |  |
| DR SMART: SM00406; IGv_1.                                             |           |      |         |  |  |
| DR PROSITE: PS50835; IG LIKE; 1.                                      |           |      |         |  |  |
| KW Immunoglobulin V region; Pyroliidone carboxylic acid.              |           |      |         |  |  |
| FT DOMAIN 1 112 IG-LIKE.                                              |           |      |         |  |  |
| FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.                            |           |      |         |  |  |
| FT NON_TER 122 122                                                    |           |      |         |  |  |
| SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;                    |           |      |         |  |  |
| Query Match 76.7%; Score 477; DB 1; Length 122;                       |           |      |         |  |  |
| Best Local Similarity 73.0%; Pred. No. 2,1e-43;                       |           |      |         |  |  |
| Matches 89; Conservative 14; Mismatches 17; Indels 2; Gaps 1;         |           |      |         |  |  |
| QY 1 EVOLVESGGGLVQPGKSLRLSCVDSGLTFSSYGMMWRQAFAGAGLEWVAISYDGNDRY 60    |           |      |         |  |  |
| DB 1 QVRLVESGGGVVZPGRSRLISCAASGTFPSVYAMHWYQPGKGLWVAIVSYGBBKY 60       |           |      |         |  |  |
| QY 61 ADSIKGPAISRDAAKNTLYQNMSLTIEDAVYYCAKD--LIISNTAALMGQGLTVTV 118    |           |      |         |  |  |
| DB 61 ABSYKGFRTISRDASKNTLYQNMSLTAEBAVYYCAKDRPLVGBYRPAFNTMGQGLTVTV 120 |           |      |         |  |  |
| QY 119 SS 120                                                         |           |      |         |  |  |
| DB 121 SS 122                                                         |           |      |         |  |  |



QY 61 ADSVKGFAISRDNKNTLYLQNMSLTIEDTAVYYCAKDLIESNIAELMGOGTLTVSS 120  
 DB 80 ADSVKGFTISRDNKNTLYLQNMSLRAEDTAVYYCARE-----SRGDYGGGTTLTVSS 134

RESULT 11

S70442  
 Ig heavy chain precursor V region (mu) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 21-Jan-2000  
 C/Accession: S70442  
 R/Cislinier, A.M.; Fougereau, M.; Tonnelle, C.  
 M.Ol. Immunol. 29, 1363-1373, 1992  
 A/Title: IGM kappa/lambda BBV human B cell clone: an early step of differentiation of B  
 A/Reference number: S70442; MUID:93024508; PMID:1383655  
 A/Accession: S70442  
 A/Status: not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-140 <CUI>  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 78.5%; Score 488; DB 2; Length 140;  
 Best Local Similarity 78.3%; Pred. No. 8.8e-39;  
 Matches 94; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVQPGSRSLRSCVDSGLTFSSYGMMHWRQAPGAGLEWAVISYDGNKYY 60  
 DB 20 QVQLVSGGQVQPGSRSLRSCAASGFTFSYGMMHWRQAPGKLEWAVAFIRYDGSNKYY 79  
 QY 61 ADSVKGFAISRDNKNTLYLQNMSLTIEDTAVYYCAKDLIESNIAELMGOGTLTVSS 120  
 DB 80 ADSVKGFTISRDNKNTLYLQNMSLRAEDTAVYYCARDHVGATYDYGGGTTLTVSS 139

RESULT 12

A49028  
 Ig heavy chain V-III region - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
 C/Accession: A49028  
 R/Timmers, B.; Kenter, M.; Thompson, A.; Kraakman, M.B.; Berman, J.E.; Alt, F.W.; Schuur  
 Eur. J. Immunol. 21, 2355-2363, 1991  
 A/Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob  
 A/Reference number: A49028; MUID:92008140; PMID:1915549  
 A/Accession: A49028  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-133 <TIM>  
 A/Cross-references: GB:S64471; NID:g236904; PIDN:AAB20011.1; PID:g236905  
 A/Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines  
 A/Note: sequence extracted from NCBI backbone (NCBI:64471, NCBI:P:64470)  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 485.5; DB 2; Length 133;  
 Best Local Similarity 78.2%; Pred. No. 1.4e-38;  
 Matches 97; Conservative 6; Mismatches 16; Indels 5; Gaps 2;

QY 1 EVOLVESGGGLVQPGSRSLRSCVDSGLTFSSYGMMHWRQAPGAGLEWAVISYDGNKYY 60  
 DB 1 QVQLVSGGQVQPGSRSLRSCAASGFTFSYGMMHWRQAPGKLEWAVAFIRYDGSNKYY 60  
 QY 61 ADSVKGFAISRDNKNTLYLQNMSLTIEDTAVYYCAKDLIESNIAELMGOGTLTV 116  
 DB 61 ADSVKGFTISRDNKNTLYLQNMSLRAEDTAVYYCARDHVGATYDYGGGTTLTV 119  
 QY 117 TVSS 120  
 DB 120 TVSS 123

RESULT 13  
 S48797  
 Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 13-Jan-1995 #sequence\_revision 13-Sep-1998 #text\_change 23-Jul-1999  
 C/Accession: S48797; S26893  
 R/Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.  
 Submitted to the EMBL Data Library, October 1994  
 A/Description: Molecular characterization of natural human anti-Sm autoantibodies.  
 A/Reference number: S48797  
 A/Accession: S48797  
 A/Molecule type: mRNA  
 A/Residues: 1-128 <MAH>  
 A/Cross-references: EMBL:246379; NID:9587147; PIDN:CAA86512.1; PID:g1340168  
 R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
 J. Mol. Biol. 227, 776-798, 1992  
 A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of  
 A/Reference number: S26885; MUID:93021117; PMID:1404388  
 A/Accession: S26893  
 A/Molecule type: DNA  
 A/Residues: 1-98 <TOM>  
 A/Cross-references: EMBL:212350; NID:g32922; PIDN:CAA78220.1; PID:g32923  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 485; DB 2; Length 128;  
 Best Local Similarity 75.0%; Pred. No. 1.5e-38;  
 Matches 96; Conservative 9; Mismatches 15; Indels 8; Gaps 2;

QY 1 EVOLVESGGGLVQPGSRSLRSCVDSGLTFSSYGMMHWRQAPGAGLEWAVISYDGNKYY 60  
 DB 1 QVQLVSGGQVQPGSRSLRSCAASGFTFSYGMMHWRQAPGKLEWAVAFIRYDGSNKYY 60  
 QY 61 ADSVKGFAISRDNKNTLYLQNMSLTIEDTAVYYCAKDLIESNIAELMGOGTLTVSS 120  
 DB 61 ADSVKGFTISRDNKNTLYLQNMSLRAEDTAVYYCARDHVGATYDYGGGTTLTVSS 120

RESULT 14

S31701  
 Ig heavy chain V region - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C/Accession: S31701  
 R/Cislinier, A.M.; Gaubier, L.; Boudli, L.; Fougereau, M.; Tonnelle, C.  
 submitted to the EMBL Data Library, June 1992  
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
 A/Reference number: S31585  
 A/Accession: S31701  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-137 <CUI>  
 A/Cross-references: EMBL:214177; NID:g31020; PIDN:CAA78546.1; PID:g31021  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 484; DB 2; Length 137;  
 Best Local Similarity 78.3%; Pred. No. 2e-38;  
 Matches 94; Conservative 8; Mismatches 16; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVQPGSRSLRSCVDSGLTFSSYGMMHWRQAPGAGLEWAVISYDGNKYY 60  
 DB 20 QVQLVSGGQVQPGSRSLRSCAASGFTFSYGMMHWRQAPGKLEWAVAFIRYDGSNKYY 79  
 QY 61 ADSVKGFAISRDNKNTLYLQNMSLTIEDTAVYYCAKDLIESNIAELMGOGTLTVSS 120

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| D6 | 61  | ADSVAGRTTISKDNKNTLYLOMNSLRADDTAVVYCARD--RKDWGMAFLPDYWGQSTLVY | 118 |
| OY | 118 | VSS                                                          | 120 |
| D6 | 119 | VSS                                                          | 121 |

## RESULT 7

IG heavy chain V region (M72) - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Dec-1998  
C:Accession: E36005  
R:Schroeder Jr., H.W.; Wang, J.Y.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
A:Reference number: A60005; MUID: 90349571; PMID:2117273  
A:Accession: E36005  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-122 <SCH>  
A:Cross-references: GB:M34030  
C:Genetic8:  
A:Gene: GDB:IGH@; IGHDI1  
A:Cross-references: GDB:118731; OMIM:146910  
A:Map position: 14q32.33-14q32.33  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
C:15-98/Domain: immunoglobulin homology <IMM>

|                          |       |                    |           |             |
|--------------------------|-------|--------------------|-----------|-------------|
| Query Match              | 79.4% | Score 494,         | DB 2,     | Length 122, |
| Best Local Similarity    | 78.7% | Pred. No. 2.1e-39, |           |             |
| Matches 96; Conservative |       | 8; Mismatches 16;  | Indels 2; | Gaps 1      |

QY 1 EVLVESGGGLVQPSRLSLRLSCVDSGLTFSSYGMHWVRQAGAGLEWVAIVSYDGDNKKY 60

Db 1 QVLVESGGGVQPSRLSLRLSCAASEFTFSYAMHWVRQAGKGLEWVAIVSYDGSNKKY 60

QY 6 ADSYKGRFALSRDNKNTLYLQMNLSLTIEDPAAVYVYCAKDILIESN--IAEALMGQGLTVV 118

Db 61 ADSYKGRFTLSRDNSKNTLYLQMNLSLRAEDPAAVYVYCARDRSSWYGMQDVGGLTVV 120

|    |     |    |     |
|----|-----|----|-----|
| QY | 119 | SS | 120 |
|    |     |    |     |
| Pb | 121 | SS | 122 |

## RESULT 8

S19666  
Ig heavy chain V region (VH3DJH4) - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000  
A:Accession: S19666  
R:Marks: J.D., Hoogenboom, H.R.; Bonnett, T.P.; McCafferty, J.; Griffiths, A.D.; Winter  
J. Mol. Biol. 222, 581-597, 1991  
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage  
A:Reference number: S19663; MUID:92085276; PMID:1748994  
A:Accession: S19666  
A:Molecule type: mRNA  
A:Residues: 1-121 <MAR>  
A:Cross-references: EMBL:X61646; NID:g37688; PIDN:CAA43827.1; PID:g1335369  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
A:Keywords: heterotetramer; immunoglobulin  
P:15-98/Domain: immunoglobulin homology <IM>

|                          |       |                    |           |             |
|--------------------------|-------|--------------------|-----------|-------------|
| Query Match              | 79.3% | Score 493.5;       | DB 2;     | Length 121; |
| Best Local Similarity    | 80.2% | Pred. No. 2.3e-39; |           |             |
| Matches 97; Conservative |       | 6; Mismatches 17;  | Indels 1; | Gaps 1;     |

**Oy**      1 EVQLVESGGGLVQPGSRSLRLSCTVDSGLTPTSSYGMHWVRPAAGAGEFWAVISYDGNDKYY 60  
         :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
**Db**      1 QVQLVDSGGSVVQPGSRSLRLSCASGFTPTSSYGMHWVRAPKGIKEFWAVISYDGSNKYY 60

|    |    |                                                              |     |
|----|----|--------------------------------------------------------------|-----|
| QY | 61 | ADSYKGRFAISRDNAKNTLYLONNSLTIEPTAVVYCAKOLIESNIAE-ALMGOGTLVTSS | 119 |
| Db | 61 | ADSYKGRFETISRDSKNTLYLONNSLRAEEDTAVVYCAKTGYSSGWSGFDMYGOGLTVTS | 120 |

|    |       |     |
|----|-------|-----|
| QY | 120 S | 120 |
| Db | 121 S | 121 |

## RESULT 9

S3117  
Ig heavy chain - human  
C|Species: Homo sapiens (man)  
C|Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C|Accession: S3117  
R|Raschovsky, F.M.; Timmer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
Eur. J. Immunol. 22, 247-251, 1992  
A|Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement  
A|Reference number: S31104; M|ID:9211633; P|ID:1730252  
A|Accession: S3117  
A|Status: preliminary; nucleic acid sequence not shown; translation not shown  
A|Molecule type: mRNA  
A|Residues: 1-122 <RAA>  
A|Cross-references: EMBL:X62967  
A|Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C|Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C|Keywords: heterotetramer; immunoglobulin  
F|15-98/Domain: immunoglobulin homology <IMM>

|                          |       |                  |       |             |
|--------------------------|-------|------------------|-------|-------------|
| Query Match              | 78.9% | Score 491;       | DB 2; | length 122; |
| Best Local Similarity    | 79.5% | Pred. No. 4e-39; |       |             |
| Matches 97; Conservative | 7;    | Mismatches       | 16;   | Indels 2;   |
|                          |       |                  |       | Gaps 2.     |

| QY                                                         | DB                                                         |
|------------------------------------------------------------|------------------------------------------------------------|
| 1                                                          | 1                                                          |
| EVOLVESGGGLVQPRSLRLSCVDSGLTFSYSGMHVVRQAPGAGLEMAVATSYDGNKYY | QVQLVDSGGGVQPRSLRLSCAASGFTFSYSGMHVVRQAPGKGLEMAVATWYDGSNKYY |
| 60                                                         | 60                                                         |

| QY                                                               | DB                                                               |
|------------------------------------------------------------------|------------------------------------------------------------------|
| 61                                                               | 61                                                               |
| ADSVKGRFPAISRDNAKNTLYLQNNSLTIETAVVYCAKDLI - ESNIAE - ALMGOGGLTVV | ADSVKGRFPAISRDNAKNTLYLQNNSLTIETAVVYCAKDLI - ESNIAE - ALMGOGGLTVV |
| 118                                                              | 120                                                              |

|    |     |    |     |
|----|-----|----|-----|
| QY | 119 | SS | 120 |
|    |     |    |     |
| Db | 121 | SS | 122 |

## RESULT 10

S31679 Ig heavy chain V region - human (fragment)  
C|Species: Homo sapiens (man)  
C|Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C|Accession: S31679  
R|Cuijster, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
Submitted to the EMBL Data Library, June 1992  
A|Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A|Reference number: S31585  
A|Accession: S31679  
A|Status: preliminary  
A|Molecule type: mRNA  
A|Residues: 1-134 < EMBL>  
A|Cross-references: CUIB:214203; NID:G30965; PIDN:CAA78572.1; PID:G30966  
C|Superfamily: immunoglobulin V region; immunoglobulin homology  
C|Keywords: heterotetramer; immunoglobulin  
P|3-4-117|Domain: immunoglobulin homology <IMM>

|                          |       |                    |           |             |
|--------------------------|-------|--------------------|-----------|-------------|
| Query Match              | 78.7% | Score 489.5;       | DB 2;     | Length 134; |
| Best Local Similarity    | 79.2% | Pred. No. 6.1e-39; |           |             |
| Matches 95; Conservative | 7;    | Mismatches 13;     | Indels 5; | Gaps 1;     |

```
QY      1 EVQLVESGGGLVQPGKSLRLSCVDSGLTPSSVGMHWQAQPGAGLEWNAVISYDGNKYY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      20 QVQLVESGGGVQPGKSLRLSCAASGTFSSYAMHWQAQPGKLEWNAVISYDSNKYY 79
```





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 / Search time 11.5028 Seconds  
(without alignment)  
1003.251 Million cell updates/sec

Title: US-09-674-752-46

Perfect score: 622  
Sequence: 1 EVQLVESGGGVQPGSRSLRL.....IESNIAELMGQGLTVTVSS 120

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 502.5 | 80.8        | 132    | 2 S31603 | Ig heavy chain V r |
| 2          | 502   | 80.7        | 118    | 2 S31116 | Ig heavy chain - h |
| 3          | 501.5 | 80.6        | 119    | 2 P36005 | Ig heavy chain V r |
| 4          | 500   | 80.4        | 120    | 2 S31112 | Ig heavy chain - h |
| 5          | 499   | 80.2        | 114    | 2 S46390 | Ig heavy chain V r |
| 6          | 494.5 | 79.5        | 121    | 2 G36005 | Ig heavy chain V r |
| 7          | 494   | 79.4        | 122    | 2 E36005 | Ig heavy chain V r |
| 8          | 493.5 | 79.3        | 121    | 2 S19666 | Ig heavy chain V r |
| 9          | 491   | 78.9        | 122    | 2 S31117 | Ig heavy chain - h |
| 10         | 489.5 | 78.7        | 132    | 2 S31679 | Ig heavy chain V r |
| 11         | 488   | 78.5        | 140    | 2 S70442 | Ig heavy chain pre |
| 12         | 485.5 | 78.1        | 133    | 2 A49028 | Ig heavy chain V r |
| 13         | 485   | 78.0        | 128    | 2 S48797 | Ig heavy chain V r |
| 14         | 484   | 77.8        | 137    | 2 S31701 | Ig heavy chain V r |
| 15         | 483   | 77.7        | 139    | 2 S31674 | Ig heavy chain V r |
| 16         | 482.5 | 77.6        | 130    | 2 S31601 | Ig heavy chain V r |
| 17         | 482   | 77.5        | 114    | 2 S46392 | Ig heavy chain V r |
| 18         | 481.5 | 77.4        | 135    | 2 S31598 | Ig heavy chain V r |
| 19         | 480.5 | 77.3        | 130    | 2 PLO098 | Ig heavy chain pre |
| 20         | 478.5 | 76.9        | 111    | 2 P16143 | Ig heavy chain V r |
| 21         | 478   | 76.8        | 151    | 2 A60943 | Ig heavy chain pre |
| 22         | 477   | 76.7        | 122    | 1 M3HDM  | Ig heavy chain V r |
| 23         | 477   | 76.4        | 122    | 1 S31119 | Ig heavy chain - h |
| 24         | 473   | 76.0        | 114    | 2 S46391 | Ig heavy chain V r |
| 25         | 472.5 | 76.0        | 109    | 2 P16146 | Ig heavy chain V r |
| 26         | 470   | 75.6        | 136    | 2 S31587 | Ig heavy chain V r |
| 27         | 468   | 75.2        | 133    | 2 S31500 | Ig heavy chain - h |
| 28         | 466.5 | 75.0        | 123    | 2 S38493 | Ig heavy chain - h |
| 29         | 466   | 74.9        | 108    | 2 P16142 | Ig heavy chain V r |

|    |       |      |     |          |                    |
|----|-------|------|-----|----------|--------------------|
| 30 | 460.5 | 74.0 | 109 | 2 P16144 | Ig heavy chain V r |
| 31 | 460   | 74.0 | 147 | 2 I37780 | Ig variable region |
| 32 | 459   | 73.8 | 98  | 2 PLO116 | Ig heavy chain V r |
| 33 | 458.5 | 73.7 | 111 | 2 P16145 | Ig heavy chain V r |
| 34 | 457.5 | 73.6 | 119 | 2 S31107 | Ig heavy chain - h |
| 35 | 456.5 | 73.4 | 119 | 2 S31111 | Ig heavy chain - h |
| 36 | 456   | 73.3 | 128 | 2 S31595 | Ig heavy chain V r |
| 37 | 455.5 | 73.2 | 140 | 2 S31588 | Ig heavy chain V r |
| 38 | 455   | 73.2 | 122 | 2 S69910 | Ig V-D-J region (K |
| 39 | 454.5 | 73.1 | 117 | 2 S78486 | Ig heavy chain V r |
| 40 | 454.5 | 73.1 | 123 | 2 S31114 | Ig heavy chain - h |
| 41 | 454   | 73.0 | 120 | 2 S48798 | Ig heavy chain V r |
| 42 | 454   | 73.0 | 120 | 2 S44111 | Ig heavy chain V-D |
| 43 | 453.5 | 72.9 | 113 | 2 S38490 | Ig heavy chain - h |
| 44 | 453.5 | 72.9 | 119 | 1 GHUM1  | Ig heavy chain V r |
| 45 | 453.5 | 72.9 | 119 | 2 S31108 | Ig heavy chain - h |

#### ALIGNMENTS

##### RESULT 1

S31603

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 03-Mar-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C/Accession: S31603

R/Cuifinler, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31603

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-132 <CUI>

A/Cross-references: EMBL:Z14168; NID:930999; PIDN:CAW78537.1; PID:G31000

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heterodimer; immunoglobulin

F/30-113/Domain: immunoglobulin homology <IMM>

Query Match Score 502.5; DB 2; Length 132;  
Best Local Similarity 81.7%; Pred. No. 3.6e-40;  
Matches 98; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

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Qy      1 EVQLVESGGGVQPGSRSLRLSCVDSGLTFSSYGMAHWROAPAGLEWVAIVISDNDKY 60
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      16 QVQLVESGGGVQPGSRSLRLSCAASGFTFSYGMIHWROAPGKLEWVAIVISDGNKY 75
Qy      61 ADSVGRPAISRDNKNTLYLQNSLTIEDTAVYVCADLIISNIAELMGQGLTVTVSS 120
       |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      76 ADSVGRFTISRDNKNTLYLQNSLTIEDTAVYVCADLP---YFDYWGQGLTVTVSS 132

```

##### RESULT 2

S31116

Ig heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999

C/Accession: S31116

R/Asphoret, F.M.; Timmerg, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar

Eur. J. Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple

A/Reference number: S31104; M0ID:92111633; PMID:173052

A/Accession: S31116

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-118 <RBA>

A/Cross-references: EMBL:X62966

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heterodimer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

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/ FILE REFERENCE: 2183-4080US
/ CURRENT APPLICATION NUMBER: US/09/315,926A
/ CURRENT FILING DATE: 1999-05-20
/ PRIOR APPLICATION NUMBER: EP 99201593.3
/ PRIOR FILING DATE: 1999-05-20
/ PRIOR APPLICATION NUMBER: EP 98201693.3
/ PRIOR FILING DATE: 1998-05-20
/ NUMBER OF SEQ ID NOS: 81
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO: 80
/ LENGTH: 248
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Description of Artificial Sequence: phage
/ NAME/KEY: PEPTIDE
/ LOCATION: (1)..(248)
/ OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-80
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Query Match 70.2%; Score 467; DB 4; Length 248;
Best Local Similarity 69.2%; Pred. No. 3.4e-37;
Matches 90; Conservative 16; Mismatches 10; Indels 14; Gaps 2;
```

```
QY 1 QVOLVSGGLVOPGKSLRLSCAASGFTFGDPAIHVROAPGEGLEWVGVTSGTTIGF 60
Db 23 QVOLVSGGGLVOPGKSLRLSCAASGFTFGDPAIHVROAPGEGLEWVGVTSGTTIGF 82
QY 61 ADSVKGKFTISRDNKNSLYLYMNSLRAPETALYYCALPYINSSNYRGV---AAPDIW 116
Db 83 ADSVKGKFTISRDNKNSLYLYMNSLRAPETALYYCA-----RGITVTKSRPDYW 132
QY 117 GCGTMTVSS 126
Db 133 GCGTLTVSS 142
```

Search completed: December 30, 2003, 11:05:35  
Job time : 13.8778 secs

APPLICANT: Hoogenboom, Hendricus R.J.M.  
APPLICANT: Kaymakcalan, Zehra  
APPLICANT: Labkovsky, Boris  
APPLICANT: Mankovich, John A.  
APPLICANT: McGuinness, Brian T.  
APPLICANT: Roberts, Andrew J.  
APPLICANT: Sakorafas, Paul  
APPLICANT: Schoenhaut, David  
APPLICANT: Vaughan, Tristan J.  
APPLICANT: White, Michael  
APPLICANT: Milton, Andrew J.  
TITLE OF INVENTION: Human Antibodies that Bind Human TNF $\alpha$   
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/125,098  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/599,226  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A., Jr.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: BBI-043  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-09-125-098-10

Query Match 70.3%; Score 467.5; DB 3; Length 121;  
Best Local Similarity 69.0%; Pred. No. 1.4e-37;  
Matches 87; Conservative 17; Mismatches 17; Indels 5; Gaps 1;

QY 1 OVQLVOSGGGLVPGKSLRLSCAASGFTFGDVAIHVWQAQPGEGLEWVSGYTWSGTTIGF 60  
DB 1 OVQLVSSGGGLVPGKSLRLSCAASGFTFDYAHMHWQAQPGKGLDWVAITWNSGHIDY 60

QY 61 ADSVAGRFTISRDNKNSLYLYNNSLRADETALYYCALPYINSSNYRRGVAAPDIWGCGT 120  
DB 61 ADSVGRFAVSRDNKAKNALYLQWNSLRPEDTAVVYC-----TKASYLSTSSSLDWWGCGT 115

QY 121 MVTWSS 126  
DB 116 LVTWSS 121

RESULT 14  
US-09-540-018-10  
Sequence 10, Application US/09540018  
Patent No. 6509015  
GENERAL INFORMATION:  
APPLICANT: Salfeld, Jochen G.  
APPLICANT: Allen, Deborah J.  
APPLICANT: Hoogenboom, Hendricus R.J.M.

APPLICANT: Kaymakcalan, Zehra  
APPLICANT: Labkovsky, Boris  
APPLICANT: Mankovich, John A.  
APPLICANT: McGuinness, Brian T.  
APPLICANT: Roberts, Andrew J.  
APPLICANT: Sakorafas, Paul  
APPLICANT: Schoenhaut, David  
APPLICANT: Vaughan, Tristan J.  
APPLICANT: White, Michael  
APPLICANT: Milton, Andrew J.  
TITLE OF INVENTION: Human Antibodies that Bind Human TNF $\alpha$   
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/540,018  
FILING DATE: 31-MARCH-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/599,226  
FILING DATE: 08-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A., Jr.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: BBI-043  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-09-540-018-10

Query Match 70.3%; Score 467.5; DB 4; Length 121;  
Best Local Similarity 69.0%; Pred. No. 1.4e-37;  
Matches 87; Conservative 17; Mismatches 17; Indels 5; Gaps 1;

QY 1 OVQLVOSGGGLVPGKSLRLSCAASGFTFGDVAIHVWQAQPGEGLEWVSGYTWSGTTIGF 60  
DB 1 OVQLVSSGGGLVPGKSLRLSCAASGFTFDYAHMHWQAQPGKGLDWVAITWNSGHIDY 60

QY 61 ADSVAGRFTISRDNKNSLYLYNNSLRADETALYYCALPYINSSNYRRGVAAPDIWGCGT 120  
DB 61 ADSVGRFAVSRDNKAKNALYLQWNSLRPEDTAVVYC-----TKASYLSTSSSLDWWGCGT 115

QY 121 MVTWSS 126  
DB 116 LVTWSS 121

RESULT 15  
US-09-315-926A-80  
Sequence 80, Application US/09315926A  
Patent No. 6498027  
GENERAL INFORMATION:  
APPLICANT: Es van, Helmut  
APPLICANT: Havenga, Menzo  
APPLICANT: Verlinden, Stefan  
TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER



LENGTH: 123 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-315-574-30

Query Match 71.1%; Score 472.5; DB 4; Length 123;  
Best Local Similarity 73.8%; Pred. No. 4.7e-38;  
Matches 93; Conservative 11; Mismatches 19; Indels 3; Gaps 1;

QY 1 QVQLVDSGGGLVPGGSLRLSCAASGFTPEGVAIHWVROAPGSEGLMWSGVTMSGTTIGF 60  
DB 1 QVQLVDSGGGLVPGGSLRLSCAASGFTPEGVAIHWVROAPGSEGLMWSGVTMSGTTIGF 60  
QY 61 ADSVKGRFTISRDNANKNSLYLYNNSLRADDTALYYCALPYINSSNYRRCVAAFDIWGQGT 120  
DB 61 ADSVKGRFTISRDNANKNSLYLYNNSLRADDTALYYCALPYINSSNYRRCVAAFDIWGQGT 117  
QY 121 MWTVSS 126  
DB 118 LVTVSS 123

RESULT 9  
US-08-652-816A-14  
Sequence 14, Application US/08652816A  
Patent No. 5872215

GENERAL INFORMATION:  
APPLICANT: Oobourn, JK  
APPLICANT: Allen, DJ  
TITLE OF INVENTION: Specific binding members, materials and  
TITLE OF INVENTION: methods.  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Garstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,816A  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.4  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.8  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9525004.9  
FILING DATE: 07-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02240  
FILING DATE: 02-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/244,597  
FILING DATE: 01-JUN-1994

ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33308  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-652-816A-14

Query Match 70.8%; Score 471; DB 2; Length 116;  
Best Local Similarity 72.0%; Pred. No. 6.2e-38;  
Matches 90; Conservative 12; Mismatches 13; Indels 10; Gaps 1;

QY 1 QVQLVDSGGGLVPGGSLRLSCAASGFTPEGVAIHWVROAPGSEGLMWSGVTMSGTTIGF 60  
DB 1 EVQLVDSGGGLVPGGSLRLSCAASGFTPEGVAIHWVROAPGSEGLMWSGVTMSGTTIGF 60  
QY 61 ADSVKGRFTISRDNANKNSLYLYNNSLRADDTALYYCALPYINSSNYRRCVAAFDIWGQGT 120  
DB 61 ADSVKGRFTISRDNANKNSLYLYNNSLRADDTALYYCALPYINSSNYRRCVAAFDIWGQGT 110  
QY 121 MWTVSS 125  
DB 111 LVTVSS 115

RESULT 10  
US-08-918-148-75  
Sequence 75, Application US/08918148A  
Patent No. 6342220

GENERAL INFORMATION:  
APPLICANT: Adams, Camellia  
APPLICANT: W.  
APPLICANT: Carter, Paul J.  
APPLICANT: Fendly, Brian M.  
APPLICANT: Gurney, Austin L.  
TITLE OF INVENTION: Agonist Antibodies  
FILE REFERENCE: P0979  
CURRENT APPLICATION NUMBER: US/08/918,148A  
CURRENT FILING DATE: 1997-08-25  
NUMBER OF SEQ ID NOS: 79  
SEQ ID NO 75  
LENGTH: 245  
TYPE: PRT  
ORGANISM: artificial  
US-08-918-148-75

Query Match 70.7%; Score 470; DB 4; Length 245;  
Best Local Similarity 73.8%; Pred. No. 1.7e-37;  
Matches 93; Conservative 12; Mismatches 13; Indels 8; Gaps 1;

QY 1 QVQLVDSGGGLVPGGSLRLSCAASGFTPEGVAIHWVROAPGSEGLMWSGVTMSGTTIGF 60  
DB 3 EVQLVDSGGGLVPGGSLRLSCAASGFTPEGVAIHWVROAPGSEGLMWSGVTMSGTTIGF 62  
QY 61 ADSVKGRFTISRDNANKNSLYLYNNSLRADDTALYYCALPYINSSNYRRCVAAFDIWGQGT 120  
DB 61 ADSVKGRFTISRDNANKNSLYLYNNSLRADDTALYYCALPYINSSNYRRCVAAFDIWGQGT 114  
QY 121 MWTVSS 126  
DB 115 MWTVSS 120

RESULT 11  
US-08-983-607-28  
Sequence 28, Application US/08983607  
Patent No. 6140470  
GENERAL INFORMATION:

```
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: in house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-24

Query Match          71.3%; Score 474; DB 1; Length 117;
Best Local Similarity 75.6%; Pred. No. 3-2e-38;
Matches 90; Conservative 11; Mismatches 14; Indels 4; Gaps 2;

Cy 1 QVQLVSGGGLVOPGSLRLSCAASGFTFGDIAIMHWROAPGLEGVSGVTSGTTIGF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGGLVOPGSRSLRLSCAASGFTFNDYAMHWROAPGKLEWVSGISWSSSTIG 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Cy 61 ADSVKGRTISRDNANKSLYLNNSLRAEDTALYYCC-ALPYINSSNRRGVAAFDIWG 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTISRDNANKSLYLQNNSLRAEDMALYYCVKGRDYDSGGY-FTVAFDIWG 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
US-08-665-202-30
Sequence 30, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
```

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-30

Query Match          71.1%; Score 472.5; DB 2; Length 123;
Best Local Similarity 73.8%; Pred. No. 4.7e-38;
Matches 93; Conservative 11; Mismatches 19; Indels 3; Gaps 1;

Cy 1 QVQLVSGGGLVOPGSLRLSCAASGFTFGDIAIMHWROAPGLEGVSGVTSGTTIGF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGGLVOPGSLRLSCAASGFTFSYEMHWROAPGKLEWVSISSSGTITY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Cy 61 ADSVKGRTISRDNANKSLYLNNSLRAEDTALYYCALPYINSSNRRGVAAFDIWGQT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTISRDNANKSLYLQNNSLRAEDTALYYCAR---DLGGYSGYVGLDYWGQT 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Cy 121 MVTVSS 126
   :||||
Db 118 LVTVSS 123

RESULT 8
US-09-315-574-30
Sequence 30, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
```

```

APPLICANT: Vaughan, Triстан J.
APPLICANT: White, Michael
APPLICANT: Wilton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNFA
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/125,098
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,226
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-125-098-2

```

```

Query Match          73.2%; Score 486.5; DB 3; Length 121;
Best Local Similarity 73.0%; Pred. No. 2.2e-39;
Matches 92; Conservative 14; Mismatches 15; Indels 5; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDVAIHVRQAPGQGLEWVSGVTWGTTIGF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  :
DB 1 EVQLVESGGGLVQPGKSLRLSCAASGFTFDYAMHWYQAQPGKLEWVSATITWNGHIDY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  :
QY 61 ADSVKGRTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRQVAAFDIWGQGT 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  :
DB 61 ADSVKGRTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRQVAAFDIWGQGT 115
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  :
QY 121 MVTWSS 126
   :|||:|||||
DB 116 LVTWSS 121
   :|||:|||||

```

```

RESULT 5
US-09-540-018-2
Sequence 2, Application US/09540018
Patent No. 6509015
GENERAL INFORMATION:
APPLICANT: Salfeld, Joehen G.
APPLICANT: Allen, Deborah J.
APPLICANT: Hoogenboom, Hendricus R.J.M.
APPLICANT: Kaymakcalan, Zeyra
APPLICANT: Labkovsky, Boris
APPLICANT: Mankovich, John A.
APPLICANT: McGuinness, Brian T.
APPLICANT: Roberts, Andrew J.
APPLICANT: Sakorafas, Paul
APPLICANT: Schoenhaut, David
APPLICANT: Vaughan, Tlstan J.

```

```

APPLICANT: White, Michael
APPLICANT: Wilton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNFA
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/540,018
FILING DATE: 31-MARCH-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/599,226
FILING DATE: 08-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-540-018-2

```

```

Query Match          73.2%; Score 486.5; DB 4; Length 121;
Best Local Similarity 73.0%; Pred. No. 2.2e-39;
Matches 92; Conservative 14; Mismatches 15; Indels 5; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDVAIHVRQAPGQGLEWVSGVTWGTTIGF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  :
DB 1 EVQLVESGGGLVQPGKSLRLSCAASGFTFDYAMHWYQAQPGKLEWVSATITWNGHIDY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  :
QY 61 ADSVKGRTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRQVAAFDIWGQGT 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  :
DB 61 ADSVKGRTISRDNKNSLYLYMNSLRADTALYYCALPYINSSNYRQVAAFDIWGQGT 115
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  :
QY 121 MVTWSS 126
   :|||:|||||
DB 116 LVTWSS 121
   :|||:|||||

```

```

RESULT 6
US-07-942-245-24
Sequence 24, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERERING OF RODENT
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESS: Sughrue, Mion, Zimm, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington

```







Search completed: December 30, 2003, 11:45:24  
Job time : 28.0219 secs

```
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1324
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1324
```

```
Query Match          73.1%; Score 486; DB 11; Length 246;
Best Local Similarity 73.8%; Pred. No. 7e-40; Indels 14; Gaps 2;
Matches 96; Conservative 11; Mismatches 9;
```

```
OY      1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTMSGTTIGF 60
Db      1 QVQLVESGGGLVQPGKSLRLSCTASGFTFGDYAMSWVRQAPGKGLWVSAISGSGSTYY 60
```

```
OY      61 ADSYKGRFTISRDNKNSLYLYMNSLRADETALYYCA-----LPYINSSNTRRGVAAFDIW 116
Db      61 ADSYKGRFTISRDNKNSKNTLYLQMNLSLRADETAVYYCAKQOWLPY-----DAFDIW 110
```

```
OY      117 GGGMTVTYSS 126
Db      111 GGGMTVTYSS 120
```

```
RESULT 15
US-09-972-656-76
; Sequence 76, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Teal, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 76
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-76
```

```
Query Match          72.6%; Score 483; DB 11; Length 227;
Best Local Similarity 73.0%; Pred. No. 1.3e-39; Indels 2; Gaps 1;
Matches 92; Conservative 17; Mismatches 15;
```

```
OY      1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTMSGTTIGF 60
Db      1 QVQLVETGGGVVQPGKSLRLSCAASGFTFSSYAMHWVRQAPGKGLWVAIVSYDSNKYY 60
```

```
OY      61 ADSYKGRFTISRDNKNSLYLYMNSLRADETALYYCALPYINSSNTRRGVAAFDIWGGGT 120
Db      61 ADSYKGRFTISRDNKNSKNTLYLQMNLSLRADETAVYYCASDLVLTWTSRR--AAFDIWGGGT 118
```

```
OY      121 MVTYSS 126
Db      119 MVTYSS 124
```



```

RESULT 8
US-09-791-153A-66
; Sequence 66, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Hiltz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791.153A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-66

Query Match      73.5%; Score 488.5; DB 11; Length 123;
Best Local Similarity 73.8%; Pred.No. 1.8e+40;
Matches 93; Conservative 13; Mismatches 17; Indels 3; Gaps 1;

QY      1 OVQLVVGSGGLVOPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWGTTIGF 60
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      1 EVQLLESQGGVLQPPRSIRLRLSCAASGFTFDYAMHWVRQAPGKGLEWVSGISNWSGRIGY 60

        61 ADSVKGRTTISRDNAKNSLYLVNMSLRADPTALYYCALPYINSNYRGVAAPDIMGCGT 120
QY      61 ADSVKGRTTISRDNAKNSLYLVNMSLRADPTALYYCALPYINSNYRGVAAPDIMGCGT 120
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      61 ADSVKGRTTISRDNAKNSLYLVNMSLRADPTAFYICAKGSGTSARYSNG---WTYMGCGT 117

QY      121 MTWVS 126
       :|||
Db      118 LTVVSS 123

RESULT 9
US-09-791-153A-59
; Sequence 59, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Hiltz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791.153A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 59
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-59

Query Match      73.5%; Score 488.5; DB 11; Length 227;
Best Local Similarity 73.8%; Pred.No. 3.6e+40;
Matches 93; Conservative 13; Mismatches 17; Indels 3; Gaps 1;

QY      1 OVQLVVGSGGLVOPGKSLRLSCAASGFTFGDYAIHWVRQAPGEGLEWVSGVTWGTTIGF 60
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      2 EVQLLESQGGVLQPPRSIRLRLSCAASGFTFDYAMHWVRQAPGKGLEWVSGISNWSGRIGY 61

        61 ADSVKGRTTISRDNAKNSLYLVNMSLRADPTALYYCALPYINSNYRGVAAPDIMGCGT 120
QY      61 ADSVKGRTTISRDNAKNSLYLVNMSLRADPTALYYCALPYINSNYRGVAAPDIMGCGT 120

```

```

Db      62 ADVSKGFTTISRDNKNSLYLQNNLSLRPEDTAFYYCKAGSTARSYSG---WYYWGCGT 118
OY      121 MWTVSS 126
       :|||||
Db      119 LVTYSS 124

RESULT 10
US-09-880-748-1416
; Sequence 1416, Application US/09880748
; Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1416
LENGTH: 252
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1416

Query Match          73.3%; Score 487.5; DB 11; Length 252;
Beet Local Similarity 71.2%; Pred. No. 5,1e-40;
Matches 94; Conservative 14; Mismatches 15; Indels 9; Gaps 2

OY      1 QVOVLQSGGGIVQPGKSLRLSCAASGFTFGDIAIMVRQAPGEGLIEWYSGVTWSGTITGF 60
       :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      1 EVOLVESGGGVQPGRSIRLSCAASGFTFDEYAAMTVRQAQPKGLEWYSGISWNSGSJAY 60
OY      61 ADVSKGRTTISRDNKNSLYLYMNSLRAEDTLAYCA-----LPYINSNRYRGVAARD 114
       :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      61 ADVSKGRTTISRDNKNSLYLYMNSLRAEDTLAYCAEDRGVGYDILTGRTTYGM---D 117
OY      115 IWGGTMTVSS 126
       :|||||
Db      118 VMGORTMTVSS 129

RESULT 11
US-09-801-185A-2
; Sequence 2, Application US/09801185A
; Publication No. US20030092059A1
GENERAL INFORMATION:
APPLICANT: BASF Aktiengesellschaft
TITLE OF INVENTION: Human Antibodies that Bind Human TNFalpha
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

```

Best Local Similarity 75.2%; Pred. No. 1.3e-41;  
Matches 97; Conservative 12; Mismatches 7; Indels 13; Gaps 2;

QY 1 QVQLVSGGGLVPGKSLRLSCAASGFTPDYAIHWVROAPGEGLEWVSGVTSGTTIGF 60  
1 QVQLVSGGGLVPGKSLRLSCAASGFTPDYAHMWVROAPGKGLEWVSGISNMSGTIGY 60

QY 61 ADSVKGRFTISRDNKNSLYLYNNSLRAEDTALYYCA-----AAPTIG 117  
61 ADSVKGRFTISRDNKNSLYLYNNSLRAEDTATYYCA-----RIGWGAPDIWG 110

QY 118 QGTMTVSS 126  
111 KGLVTVSS 119

Db

US-09-880-748-1427  
Sequence 1427, Application US/09880748

Publication No. US2003005937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: P5523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1427

LENGTH: 254

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-1427

Query Match 73.8%; Score 491; DB 11; Length 254;  
Best Local Similarity 71.9%; Pred. No. 2.3e-40;

Matches 92; Conservative 16; Mismatches 18; Indels 2; Gaps 1;

QY 1 QVQLVSGGGLVPGKSLRLSCAASGFTPDYAIHWVROAPGEGLEWVSGVTSGTTIGF 60  
1 QVQLVSGGGLVPGKSLRLSCAASGFTPDYAHMWVROAPGKGLEWVSGISNMSGTIGY 60

QY 61 ADSVKGRFTISRDNKNSLYLYNNSLRAEDTALYYC--ALPYINSSNYRGVAAPDIWG 118  
61 ADSVKGRFTISRDNKNSLYLYNNSLRAEDTAVYYCTRGVEYDILTGYNELGAFDIWG 120

QY 119 GIMTVSS 126  
121 GILVTVSS 128

Db

US-10-447-331-6  
Sequence 6, Application US/10447331

Publication No. US2003021943A1

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.

APPLICANT: Ridgway, John B.

TITLE OF INVENTION: ANTIBODIES FOR CANCER THERAPY AND

TITLE OF INVENTION: DIAGNOSIS

FILE REFERENCE: GENENT.122A

CURRENT APPLICATION NUMBER: US/10/447,331

CURRENT FILING DATE: 2003-05-28

PRIOR APPLICATION NUMBER: US/09/515,825

PRIOR FILING DATE: 2000-02-29

PRIOR APPLICATION NUMBER: 60/122262

PRIOR FILING DATE: 1999-03-01

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6

LENGTH: 122

TYPE: PRT

ORGANISM: Homo sapiens

US-10-447-331-6

Query Match 73.5%; Score 489; DB 12; Length 122;  
Best Local Similarity 74.8%; Pred. No. 1.6e-40;

Matches 95; Conservative 12; Mismatches 14; Indels 6; Gaps 2;

QY 1 QVQLVSGGGLVPGKSLRLSCAASGFTPDYAIHWVROAPGEGLEWVSGVTSGTTIGF 60  
1 EVQLVETGGGLVPGKSLRLSCAASGFTPDYAHMWVROAPGKGLEWVSGISNMSGTIGY 60

QY 61 ADSVKGRFTISRDNKNSLYLYNNSLRAEDTALYYCALPYINSS--NYRGVAAPDIWG 119  
61 ADSVKGRFTISRDNKNSLYLYNNSLRAEDTALYYCARDAFSGSYG-----WFDPMGQG 115

QY 120 TMTVSS 126  
116 TLVTVSS 122

Db

US-09-880-748-922  
Sequence 922, Application US/09880748

Publication No. US2003005937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: P5523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 922

LENGTH: 251

TYPE: PRT

ORGANISM: Homo sapiens

US-09-880-748-922

Query Match 73.5%; Score 489; DB 11; Length 251;  
Best Local Similarity 67.6%; Pred. No. 3.6e-40;

Matches 94; Conservative 14; Mismatches 7; Indels 24; Gaps 2;

QY 1 QVQLVSGGGLVPGKSLRLSCAASGFTPDYAIHWVROAPGEGLEWVSGVTSGTTIGF 60  
1 QVQLVSGGGLVPGKSLRLSCAASGFTPDYAHMWVROAPGKGLEWVSGISNMSGTIGY 60

QY 61 ADSVKGRFTISRDNKNSLYLYNNSLRAEDTALYYCA-----LPTINSSNR 107  
61 ADSVKGRFTISRDNKNSLYLYNNSLRAEDTALYYCARVPSYDILTGYYLPH----- 113

QY 108 RGVAAFDIWGQMTVSS 126  
114 ---APDVWGKGLTVSS 128

Db

RESULT 2  
US-09-840-459-88  
Sequence 88, Application US/09840459  
Patent No. US20020150576A1  
GENERAL INFORMATION:  
APPLICANT: Larosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
FILE REFERENCE: 1855,1052-012  
CURRENT APPLICATION NUMBER: US/09/840,459  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 88  
LENGTH: 119  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-840-459-88

Query Match 76.0%; Score 505.5; DB 10; Length 119;  
Best Local Similarity 77.0%; Pred. No. 3.8e-42;  
Matches 97; Conservative 12; Mismatches 10; Indels 7; Gaps 2;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTPDYAIHWVRQAPGKLEWVSQVTWGTTIGF 60  
DB 1 EVQLVESGGGLVQPGKSLRLSCAASGFTPDYAMHWVRQAPGKLEWVSQVTWGSSIGY 60

QY 61 ADSVKGRTTISRDNKNSLYLYNNSLRADTALYYCALPYINSSNYRGRVAAPDIWGCT 120  
DB 61 ADSVKGRTTISRDNKNSLYLYNNSLRADTALYYCATYH---YYGCM---DVIWGCT 113

QY 121 MVTVSS 126  
DB 114 TVTVSS 119

RESULT 3  
US-08-779-457-50  
Sequence 50, Application US/08779457  
Publication No. US20020193571A1  
GENERAL INFORMATION:  
APPLICANT: Carter, Paul J.  
APPLICANT: Chiang, Nancy Y.  
APPLICANT: Kyung, Jin Kim  
APPLICANT: Matchew, William  
APPLICANT: Rodriguez, Maria L.  
TITLE OF INVENTION: MSX RECEPTOR AGONIST ANTIBODIES  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpacin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/779,457  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/667197  
FILING DATE: 06/20/96  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585005  
FILING DATE: 01/08/96  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0986P2  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-779-457-50

Query Match 76.0%; Score 505.5; DB 8; Length 241;  
Best Local Similarity 77.0%; Pred. No. 8.4e-42;  
Matches 97; Conservative 12; Mismatches 10; Indels 7; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTPDYAIHWVRQAPGKLEWVSQVTWGTTIGF 60  
DB 1 QVRLQSGGGLVQPGKSLRLSCAASGFTPDYAMHWVRQAPGKLEWVSQVTWGSSIGY 60

QY 61 ADSVKGRTTISRDNKNSLYLYNNSLRADTALYYCALPYINSSNYRGRVAAPDIWGCT 120  
DB 61 ADSVKGRTTISRDNKNSLYLYNNSLRADTALYYCAEPNTD-----APDIWGCT 113

QY 121 MVTVSS 126  
DB 114 LVTVSS 119

RESULT 4  
US-09-880-748-1926  
Sequence 1926, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PFS23  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: Patencin Ver. 2.0  
SEQ ID NO 1926  
LENGTH: 245  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-1926

Query Match 75.7%; Score 503.5; DB 11; Length 245;

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 30, 2003, 11:01:15 ; Search time 27.0219 Seconds  
(without alignments)  
927.994 Million cell updates/sec

Title: US-09-674-752-43

Perfect score: 665  
Sequence: 1 QVQLVSGGGLVQPGKSLRL.....RRGVAAFDIWGQGTMTVSS 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCR\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCRUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match Length | ID     | Description                          |
|------------|-------|--------------------|--------|--------------------------------------|
| 1          | 512   | 77.0               | 132 11 | US-09-791-153A-65 Sequence 65, Appl  |
| 2          | 505.5 | 76.0               | 119 10 | US-09-840-459-88 Sequence 88, Appl   |
| 3          | 505.5 | 76.0               | 241 8  | US-08-779-457-50 Sequence 50, Appl   |
| 4          | 503.5 | 75.7               | 245 11 | US-09-880-748-1926 Sequence 1926, Ap |
| 5          | 491   | 73.8               | 254 11 | US-09-880-748-1427 Sequence 1427, Ap |
| 6          | 489   | 73.5               | 122 12 | US-10-447-731-6 Sequence 6, Appl1    |
| 7          | 489   | 73.5               | 251 11 | US-09-880-748-922 Sequence 922, App  |
| 8          | 488.5 | 73.5               | 123 11 | US-09-791-153A-66 Sequence 66, Appl  |
| 9          | 488.5 | 73.5               | 227 11 | US-09-791-153A-59 Sequence 59, Appl  |
| 10         | 487.5 | 73.3               | 252 11 | US-09-880-748-1416 Sequence 1416, Ap |
| 11         | 486.5 | 73.2               | 121 11 | US-09-801-185A-2 Sequence 2, Appl1   |
| 12         | 486.5 | 73.2               | 121 12 | US-10-133-715-2 Sequence 2, Appl1    |
| 13         | 486.5 | 73.1               | 121 12 | US-10-302-356A-2 Sequence 2, Appl1   |
| 14         | 486   | 73.1               | 246 11 | US-09-880-748-1324 Sequence 1324, Ap |
| 15         | 483   | 72.6               | 227 11 | US-09-972-656-6 Sequence 76, Appl    |

|    |       |      |        |                                      |
|----|-------|------|--------|--------------------------------------|
| 16 | 483   | 72.6 | 251 11 | US-09-880-748-1320 Sequence 1320, Ap |
| 17 | 481   | 72.3 | 251 11 | US-09-880-748-1542 Sequence 1542, Ap |
| 18 | 476   | 71.6 | 248 11 | US-09-880-748-1890 Sequence 1890, Ap |
| 19 | 475   | 71.4 | 128 15 | US-10-269-805-29 Sequence 29, Appl   |
| 20 | 475   | 71.4 | 239 11 | US-09-880-748-2038 Sequence 2038, Ap |
| 21 | 474   | 71.3 | 239 11 | US-09-880-748-2015 Sequence 2015, Ap |
| 22 | 473   | 71.1 | 239 11 | US-09-880-748-2022 Sequence 2022, Ap |
| 23 | 472.5 | 71.1 | 230 12 | US-09-969-748C-2 Sequence 2, Appl1   |
| 24 | 472.5 | 71.1 | 290 12 | US-09-949-039-2 Sequence 2, Appl1    |
| 25 | 472.5 | 71.1 | 296 12 | US-09-969-748C-12 Sequence 75, Appl  |
| 26 | 472.5 | 71.1 | 236 12 | US-09-949-039-75 Sequence 2023, Ap   |
| 27 | 472   | 71.0 | 239 11 | US-09-880-748-2023 Sequence 937, App |
| 28 | 471   | 70.8 | 239 11 | US-09-880-748-937 Sequence 9, Appl1  |
| 29 | 469.5 | 70.6 | 121 12 | US-10-010-942B-9 Sequence 1664, Ap   |
| 30 | 469.5 | 70.6 | 259 11 | US-09-880-748-1664 Sequence 1664, Ap |
| 31 | 469   | 70.5 | 116 15 | US-10-091-300-24 Sequence 24, Appl   |
| 32 | 469   | 70.5 | 122 15 | US-10-269-805-7 Sequence 7, Appl1    |
| 33 | 469   | 70.5 | 122 15 | US-10-269-805-11 Sequence 11, Appl   |
| 34 | 469   | 70.5 | 249 11 | US-09-880-748-1109 Sequence 1109, Ap |
| 35 | 468   | 70.4 | 136 12 | US-10-045-674-487 Sequence 487, App  |
| 36 | 468   | 70.4 | 248 11 | US-09-880-748-1974 Sequence 1974, Ap |
| 37 | 468   | 70.4 | 367 12 | US-10-045-674-453 Sequence 453, App  |
| 38 | 467.5 | 70.3 | 119 15 | US-10-073-644C-6 Sequence 6, Appl1   |
| 39 | 467.5 | 70.3 | 121 11 | US-09-801-185A-10 Sequence 10, Appl  |
| 40 | 467.5 | 70.3 | 121 12 | US-10-133-715-10 Sequence 10, Appl   |
| 41 | 467.5 | 70.3 | 121 12 | US-10-302-356A-10 Sequence 10, Appl  |
| 42 | 467.5 | 70.3 | 225 11 | US-09-453-234-68 Sequence 82, Appl   |
| 43 | 467.5 | 70.3 | 244 11 | US-09-880-748-82 Sequence 164, App   |
| 44 | 467.5 | 70.3 | 244 11 | US-09-880-748-164 Sequence 164, App  |
| 45 | 467.5 | 70.3 | 244 11 | US-09-880-748-280 Sequence 280, App  |

## ALIGNMENTS

```
RESULT 1
US-09-791-153A-65
; Sequence 65, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Hiltz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOCALCIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791,153A
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent version 3.0
; SEQ ID NO 65
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-65

Query Match 77.0%; Score 512; DB 11; Length 132;
Best Local Similarity 75.0%; Pred. No. 9.9e-43;
Matches 99; Conservative 12; Mismatches 15; Indels 6; Gaps 1;

QY 1 QVQLVSGGGLVQPGKSLRLAEDTALYYCAAPYINSNYRGVA-----FD 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EVQLVSGGGLVQPGKSLRLAEDTALYYCAAPYINSNYRGVA-----FD 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY ADSVKRPTISRNANKSLYLNNSLRAEDTALYYCAAPYINSNYRGVA-----FD 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 ADSVKRPTISRNANKSLYLNNSLRAEDTALYYCAAPYINSNYRGVA-----FD 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 115 YWGQGTMTVSS 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 YWGQGTMTVSS 132
```





inhibit the expression and activity of Blys. The antibodies bind to Blys and so may be used to detect and quantitate the presence of Blys in biological samples and may be used in this way to diagnose disease associated with aberrant expression of Blys. They may also be administered to treat diseases associated with aberrant Blys expression and actively such as cancer, immune, and autoimmune disorders and diseases, e.g., systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g., common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention.

Sequence 245 AA:

Query Match 75.7%; Score 503.5; DB 23; Length 245;  
Best Local Similarity 75.2%; Pred. No. 2e-40; 7; Indels 13; Gaps 2;  
Matches 97; Conservative 12; Mismatches 7; Indels 13; Gaps 2;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDVAIHVRQAPEGLEWVSGVTWSGTTIGF 60  
DB 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDVAIHVRQAPEGLEWVSGVTWSGTTIGF 60  
QY 61 ADSVKGRTTISRDNKNSLYLYMNSLRADPTALTYCALPYINSNYRQGV--AAFDTWG 117  
DB 61 ADSVKGRTTISRDNKNSLYLYMNSLRADPTALTYCA-----REIGWGAFDTWG 110  
QY 118 OCTWVTWVSS 126  
DB 111 RGLTWTWVSS 119

RESULT 13

AAV64737  
ID AAV64737 standard; Protein; 149 AA.

AAV64737;

DT 01-FEB-2000 (first entry)

DE Human 5' EST related polypeptide SEQ ID NO:898.

XX Human, 5' EST; expressed sequence tag; secreted protein; diagnosis;  
XX gene therapy; chromosome mapping; upstream regulatory sequence;  
XX forensic; location; development; protein synthesis; stability;  
XX regulation; identification.

OS Homo sapiens.

PN WO953051-A2.

PD 21-OCT-1999.

PF 09-APR-1999; 99WO-IB00712.

PR 09-APR-1998; 98US-0057719.

PR 28-APR-1998; 98US-0069047.

XX (GEST ) GENSET.

PI Dumas Milne Edwards J, Duclet A, Giordano J;

DR WPI; 2000-038446/03.

DR N-PSDB; AA242351.

PT Novel secreted protein 5' expressed sequence tag sequences used in  
PT diagnostic, forensic, gene therapy, and chromosome mapping procedures  
XX Claim 3; Page 627; 837pp; English.

CC AA242265 to AA243075 represent novel 5' expressed sequence tag (EST)  
CC sequences, corresponding to human secreted proteins. AAV64651 to  
CC AAV65438 represent the EST-related proteins corresponding to AA242265 to  
CC AA243052. The 5' ESTs can be used for producing secreted human gene

products. They can be used to identify and isolate 5' untranslated regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, as well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal gene expression. The products may also be used in gene therapy protocols. The nucleic acids encoding signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins is valuable. AA242249 to AA242264 and AAV64644 to AAV64650 represent sequences used in the exemplification of the present invention.

Sequence 149 AA:

Query Match 74.1%; Score 492.5; DB 21; Length 149;  
Best Local Similarity 70.4%; Pred. No. 1.3e-39;  
Matches 95; Conservative 11; Mismatches 12; Indels 17; Gaps 2;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDVAIHVRQAPEGLEWVSGVTWSGTTIGF 60  
DB 20 EVQLVESGGGLVQPGKSLRLSCAASGFTFGDVAIHVRQAPEGLEWVSGVTWSGTTIGF 79  
QY 61 ADSVKGRTTISRDNKNSLYLYMNSLRADPTALTYCA-----LPYINSNYRQGV 111  
DB 80 ADSVKGRTTISRDNKNSLYLYMNSLRADPTALTYCA-----LPYINSNYRQGV 111  
QY 112 AFDWVGQGTWVTVSS 126  
DB 132 AMDWVGQGTWVTVSS 146

RESULT 14

ABP45416  
ID ABP45416 standard; Protein; 254 AA.

ABP45416;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1427.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytotoxic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunostimulant; immunomodulatory; antineutritic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.





Db 115 LTVSS 120

RESULT 7  
AAV43254  
ID AAV43254 standard; Protein; 120 AA.

AC AAV43254;

DT 13-JAN-2000 (first entry)

DE VH domain CDR of anti-estradiol antibody.

XX Estradiol; complementarity determining region; CDR; estradiol-3-sulphate;  
XX antibody antigen binding domain; steroid hormone; estradiol; testosterone;  
XX dihydrotestosterone; progesterone; estradiol 3-beta-di-glucuronide;  
XX menstrual cycle; hormone replacement therapy; oestrogen secreting tumour;  
XX diagnosis; VH domain.

OS Homo sapiens.

PN US5977319-A.

PD 02-NOV-1999.

PF 21-OCT-1997; 97US-0958201.

PR 21-OCT-1996; 96US-0028897.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Johnson KS, Pope AR, Pritchard K, Williams AJ;

DR WPI; 1999-619713/53.

XX N-PSDB; AAZ31652.

PT New specific binding partners for estradiol, used for monitoring  
PT estradiol levels during the menstrual cycle, in hormone replacement  
PT therapy and for diagnosing oestrogen secreting tumours

XX Claim 1, Column 23-24; 26pp; English.

CC This sequence represents a VH domain complementarity determining region  
CC (CDR) from an antibody specific for estradiol. The invention relates to  
CC specific binding members (sbp) comprising a polypeptide that comprises an  
CC antibody antigen binding domain (AABD) which has a dissociation constant  
CC of less than  $1.0 \times 10^{-8}$ M for estradiol, and a dissociation constant of at  
CC least 500-fold higher for the steroid hormones selected from estradiol,  
CC testosterone, dihydrotestosterone, progesterone, estradiol-3-sulphate and  
CC estradiol 3-beta-di-glucuronide, where the polypeptide comprises an  
CC antibody VH domain. The sbps can be used in an immunoassay for  
CC determining the presence or absence of estradiol in a sample. They can be  
CC used for monitoring estradiol levels, e.g. during the menstrual cycle, in  
CC hormone replacement therapy and for diagnosing oestrogen secreting  
CC tumours. The sbps can provide for discrimination between estradiol and  
CC other related steroids.

XX Sequence 120 AA;

Query Match 76.4%; Score 508; DB 20; Length 120;  
Best Local Similarity 76.2%; Pred. No. 3.4e-41;  
Matches 96; Conservative 14; Mismatches 10; Indels 6; Gaps 2;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTPDVAIHVWVROAPGEGLEWVSGTWGSGTIGF 60  
DB 1 RQQLVSSGGGLVQPGKSLRLSCAASGFTPDVAMHVRQAPGKGLWVSGISWNSGISY 60  
QY 61 ADSVKGRTTISRDNKNSLYLYMNSLRADPTALYYCALPYINSSNRRGVAAFDIWGQST 120  
DB 61 ADSVKGRTTISRDNKNSLYLYMNSLRADPTALYYCARPL-----YPKG-TQYDFPGQST 114  
QY 121 MVTSS 126

Db 115 LTVSS 120

RESULT 8  
AAG65553  
ID AAG65553 standard; protein; 120 AA.

AC AAG65553;

DT 30-NOV-2001 (first entry)

DE Amino acid sequence of VH3-4.

XX Gene library; immunoglobulin; antibody library; VH3-4.

XX Homo sapiens.

XX MO200162907-A1.

XX 30-AUG-2001.

XX 22-FEB-2001; 2001WO-JP01298.

XX 22-FEB-2000; 2000JP-0050543.

XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.

XX Kurosawa Y, Akahori Y, Ida Y, Morino K, Shinohara M, Takahashi M;

XX Okuno Y, Shiraki K;

XX WPI; 2001-565420/63.

PT Producing gene libraries and antibody libraries, involves selecting a  
PT light chain that binds to a heavy chain product to produce a functional  
PT formation, and producing a gene library of the light chain variable  
PT regions

XX Disclosure; Page 20; 18pp; Japanese.

CC The invention relates to producing gene libraries, comprising  
CC immunoglobulin light and heavy variable region. The method involves  
CC selecting light chain that binds with the heavy chain product to produce  
CC a functional conformation, producing a gene library comprising a  
CC collection of these light chain variable genes, and combining with gene  
CC library of heavy chain variable genes. The method is used for production  
CC of gene and antibody libraries. The present sequence represents the amino  
CC acid sequence of VH3-4.

XX Sequence 120 AA;

Query Match 76.4%; Score 508; DB 22; Length 120;  
Best Local Similarity 77.8%; Pred. No. 3.4e-41;  
Matches 98; Conservative 11; Mismatches 11; Indels 6; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTPDVAIHVWVROAPGEGLEWVSGTWGSGTIGF 60  
DB 1 EVQLVSSGGGLVQPGKSLRLSCAASGFTPDVAMHVRQAPGKGLWVSGISWNSGISY 60

QY 61 ADSVKGRTTISRDNKNSLYLYMNSLRADPTALYYCALPYINSSNRRGVAAFDIWGQST 120  
DB 61 ADSVKGRTTISRDNKNSLYLYMNSLRADPTALYYCAKPGSGSPD-----AFDIWGQST 114

QY 121 MVTSS 126

RESULT 9  
ABB06276  
ID ABB06276 standard; Protein; 120 AA.  
AC ABB06276;

|    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                           |
|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------|
| PH | Key                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Location/Qualifiers                                                       |
| FT | Region                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 1..30<br>/label= FR1<br>/note= "framework region 1"                       |
| FT | Region                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 31..35<br>/label= CDR1<br>/note= "complementarity determining region 1"   |
| FT | Region                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 36..49<br>/label= FR2<br>/note= "framework region 2"                      |
| FT | Region                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 50..66<br>/label= CDR2<br>/note= "complementarity determining region 2"   |
| FT | Region                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 67..99<br>/label= FR3<br>/note= "framework region 3"                      |
| FT | Region                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 100..113<br>/label= CDR3<br>/note= "complementarity determining region 3" |
| FT | Region                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 114..124<br>/label= FR4<br>/note= "framework region 4"                    |
| PD | WO9855619-A1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                           |
| XX | 10-DEC-1998.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                           |
| XX | 05-JUN-1998;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 98WO-EP03397.                                                             |
| XX | 08-MAY-1998;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 98DE-1020663.                                                             |
| PR | 06-JUN-1997;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 97DE-1023904.                                                             |
| PR | 12-DEC-1997;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 97DE-1055227.                                                             |
| PA | (ASAT-) ASAT AG APPLIED SCI & TECHNOLOGY.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                           |
| XX | Berchold P, Escher RFA:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                           |
| PI | WPI; 1999-105496/09.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                           |
| DR | N-PSDB; AAV72231.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                           |
| XX | Nucleic acid encoding human autoantibodies against platelet glycoprotein IIb/IIIa - used for diagnosis, treatment and prevention of autoimmune thrombocytopenic purpura and for modulation of fibrinogen binding                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                           |
| PT | Fibrinogen binding                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                           |
| PS | Disclosure; Page 58-59; 93pp; German.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                           |
| XX | This invention describes novel nucleic acid fragments that encode human auto-antibodies and anti-idiotypic antibodies against blood platelet membrane protein, GPIIb/IIIa. The products of the invention are used for diagnosis (including monitoring and determining predisposition), prevention and treatment of autoimmune thrombocytopenic purpura (AITP) and also for modulating binding of fibrinogen to thrombocytes (particularly to dissolve thrombi and/or prevent their formation, e.g. in cases of cardiac infarction or pulmonary embolism). Unlike murine antibodies, human antibodies (hAb) do not induce adverse side effects and persist for longer in vivo than small peptides. |                                                                           |
| SQ | Sequence 124 AA:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                           |
| OY | Query Match                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 76.8%; Score 511; DB 20; Length 124;                                      |
| OY | Best Local Similarity                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 77.3%; Pred. No. 1.8e-41;                                                 |
| DB | Matches 99; Conservative 11; Mismatches 12; Indels 6; Gaps 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                           |
| OY | 1 OYVLVSGGGGLVPGKSLRLSCAAGTGTGDAIHWRAPGEGLEWVGVTMSTTGIF 60                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                           |
| DB | 1 OYVLSSGGGLVPGKSLRLSCAAGTFEDVALHWRAPEGGLEWVGISINDSCTIGY 60                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                           |
| OY | 61 ASVKRFTISRDNANKSLTYLNNSLRADETALYYCALPYINS--SNYRGVAAPDIWQ 118                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                           |
| DB | 61 ASVKRFTISRDNANKSLTYLNNSLRADETALYYCVKMGGSSVATYN----APIWQ 116                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                           |
| OY | 119 GTMTVTSS 126                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                           |

|                                                               |                                                                                      |                            |     |          |     |
|---------------------------------------------------------------|--------------------------------------------------------------------------------------|----------------------------|-----|----------|-----|
| Db                                                            |                                                                                      | <br>     <br>              | 117 | GTMVTVSS | 124 |
| RESULT 6                                                      |                                                                                      |                            |     |          |     |
| AAAY43255                                                     |                                                                                      |                            |     |          |     |
| ID                                                            | AAAY43255                                                                            | standard; Protein; 120 AA. |     |          |     |
| XX                                                            | AAAY43255;                                                                           |                            |     |          |     |
| AC                                                            |                                                                                      |                            |     |          |     |
| XX                                                            |                                                                                      |                            |     |          |     |
| DT                                                            | 13-JAN-2000                                                                          | (first entry)              |     |          |     |
| XX                                                            |                                                                                      |                            |     |          |     |
| DE                                                            | VH domain CDR of anti-estradiol antibody.                                            |                            |     |          |     |
| KM                                                            | Estradiol; complementarity determining region; CDR; estriol-3-sulphate;              |                            |     |          |     |
| KM                                                            | antibody antigen binding domain; steroid hormone; estriol; testosterone;             |                            |     |          |     |
| KM                                                            | dihydrotestosterone; progesterone; estriol 3-beta-di-glucuronide;                    |                            |     |          |     |
| KM                                                            | menstrual cycle; hormone replacement therapy; oestrogen secreting tumour;            |                            |     |          |     |
| KW                                                            | diagnosis; VH domain.                                                                |                            |     |          |     |
| XX                                                            |                                                                                      |                            |     |          |     |
| OS                                                            | Homo sapiens.                                                                        |                            |     |          |     |
| XX                                                            |                                                                                      |                            |     |          |     |
| PN                                                            | US5977319-A.                                                                         |                            |     |          |     |
| XX                                                            |                                                                                      |                            |     |          |     |
| PD                                                            | 02-NOV-1999.                                                                         |                            |     |          |     |
| XX                                                            |                                                                                      |                            |     |          |     |
| PF                                                            | 21-OCT-1997; 97US-0958201.                                                           |                            |     |          |     |
| XX                                                            |                                                                                      |                            |     |          |     |
| PR                                                            | 21-OCT-1996; 96US-0028897.                                                           |                            |     |          |     |
| XX                                                            |                                                                                      |                            |     |          |     |
| PA                                                            | (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.                                               |                            |     |          |     |
| XX                                                            |                                                                                      |                            |     |          |     |
| PI                                                            | Johnson KS, Pope AR, Pritchard K, Williams AJ;                                       |                            |     |          |     |
| XX                                                            |                                                                                      |                            |     |          |     |
| DR                                                            | WPI; 1999-619713/53.                                                                 |                            |     |          |     |
| DR                                                            | N-PSDB; AAZ31653.                                                                    |                            |     |          |     |
| XX                                                            |                                                                                      |                            |     |          |     |
| PT                                                            | New specific binding partners for estradiol, used for monitoring                     |                            |     |          |     |
| PT                                                            | estradiol levels during the menstrual cycle, in hormone replacement                  |                            |     |          |     |
| PT                                                            | therapy and for diagnosing oestrogen secreting tumours                               |                            |     |          |     |
| XX                                                            |                                                                                      |                            |     |          |     |
| PS                                                            | Claim 1; Column 25-26; 26pp; English.                                                |                            |     |          |     |
| XX                                                            |                                                                                      |                            |     |          |     |
| CC                                                            | This sequence represents a VH domain complementarity determining region              |                            |     |          |     |
| CC                                                            | (CDR) from an antibody specific for estradiol. The invention relates to              |                            |     |          |     |
| CC                                                            | specific binding members (sbp) comprising a polypeptide that comprises an            |                            |     |          |     |
| CC                                                            | antibody antigen binding domain (AABD) which has a dissociation constant             |                            |     |          |     |
| CC                                                            | of less than 1.0x10 <sup>-8</sup> M for estradiol, and a dissociation constant of at |                            |     |          |     |
| CC                                                            | least 500-fold higher for the steroid hormones selected from estriol,                |                            |     |          |     |
| CC                                                            | testosterone, dihydrotestosterone, progesterone, estriol-3-sulphate and              |                            |     |          |     |
| CC                                                            | estriol 3-beta-di-glucuronide, where the polypeptide comprises an                    |                            |     |          |     |
| CC                                                            | antibody VH domain. The sbps can be used in an immunoassay for                       |                            |     |          |     |
| CC                                                            | determining the presence or absence of estradiol in a sample. They can be            |                            |     |          |     |
| CC                                                            | used for monitoring estradiol levels, e.g. during the menstrual cycle, in            |                            |     |          |     |
| CC                                                            | hormone replacement therapy and for diagnosing oestrogen secreting                   |                            |     |          |     |
| CC                                                            | tumours. The sbps can provide for discrimination between estradiol and               |                            |     |          |     |
| CC                                                            | other related steroids.                                                              |                            |     |          |     |
| CC                                                            |                                                                                      |                            |     |          |     |
| SQ                                                            | Sequence                                                                             | 120 AA;                    |     |          |     |
|                                                               |                                                                                      |                            |     |          |     |
| Query Match                                                   | 76.5%; Score 509; DB 20; Length 120;                                                 |                            |     |          |     |
| Best Local Similarity                                         | 76.2%; Pred. No. 2.7e-41;                                                            |                            |     |          |     |
| Matches                                                       | 96; Conservative 14; Mismatches 10; Indels 6; Gaps 2                                 |                            |     |          |     |
| Db                                                            |                                                                                      |                            |     |          |     |
| OY                                                            | 1 QVALVDSGGGLVQPKSLRLSCAASGFTFGDYAIHWVAQPEGLGVSWGTSGTTIGF 60                         |                            |     |          |     |
|                                                               | :   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   :                    |                            |     |          |     |
| 1 EQVLVESGGGLVQPKSRLRLSCAASGFTFDYAWMWVAQPKGLEWSGISWNSGSIGY 60 |                                                                                      |                            |     |          |     |
| OY                                                            | 61 ADSVKGRTISDNANKSLIYLWMSLRBEDTLALTYCALPYINSNYRKGVAAFDIWGQT 120                     |                            |     |          |     |
|                                                               | ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   :                   |                            |     |          |     |
| Db                                                            | 61 ADSVKGRTISDNANKSLIYLNMLIRADTVAVYVCARPL-----YPKG-TQYDEWGQGT 114                    |                            |     |          |     |
| OY                                                            | 121 MTWTSS 126                                                                       |                            |     |          |     |

```

PN WO9118983-A.
XX
XX 12-DEC-1991.
XX
XX 28-MAY-1991; 91WO-1000067.
XX
XX 29-MAY-1990; 90AT-0001178.
XX
XX (JUNG/) JUNGBAUER A.
XX
XX Felgenhauer M, Himmler G, Kohl J, Steindl F;
XX WPI; 1992-007468/01.
XX DR N-PSDB; AAQ20068.
XX
XX Recombinant protein which binds to complex viral antigen and
XX HIV-1 - contains variable region of antibody derived from 3D6
XX cell line, used for detecting HIV-1 antigen
XX
XX Claim 4; Page 31; 52pp; German.
XX
XX The cell line 3D6 (87110301; Porton Down) produces a Mab of the
XX IgG1/Kappa type that reacts specifically with HIV-1 gp120 and also
XX weakly cross-reacts with HIV-1 gp120. Gene construct of the heavy
XX chain of the variable region coding region of the heavy chain
XX and light chain of antibody 3D6, joined by a linker. The
XX recombinant protein binds to HIV gp160.
XX See also AAQ20066 and AAQ20067.
XX
XX Sequence 248 AA:
SQ
Query Match 77.6%; Score 516; DB 13; Length 248;
Best Local Similarity 77.3%; Pred. No. 1,3e-41;
Matches 99; Conservative 11; Mismatches 14; Indels 4; Gaps 2;
QY 1 QVQLVDSGGGLVQPGKSLRLSCAASGFTPDYAIHWVR PGEGLEWVGVTWSGTTIGF 60
DB 2 EVQLVDSGGGLVQPGKSLRLSCAASGFTPDYAMHWVR PGKGLWVGSIWDSSTIGY 61
QY 61 ADSVKGRFTISRDNKNSLYLNMSLRADDTALYYC-- PYNNSNRRGVAAPFIWQ 118
DB 62 ADSVKGRFTISRDNKNSLYLNMSLRADDTALYYC-- DYVDSGY--FTVAAPFIWQ 119
QY 119 GTMVTWSS 126
DB 120 GTMVTWSS 127
RESULT 4
AAR20057
ID AAR20057 standard; Protein; 475 AA.
XX
XX AAR20057;
XX
XX 25-MAR-1992 (first entry)
XX
XX Heavy chain of 3D6 anti-HIV antibody.
XX
XX Plasmid pUC3D6HC; human immunodeficiency virus; IDS;
XX complementarity determining region.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..19 /label= signal
XX Region 20..49 /label= Framework_1
XX Region 50..54 /label= CDR-1
XX Region 55..68 /label= Framework_2
XX Region 69..85

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FT /label= CDR_2
FT Region 86..117 /label= Framework_3
FT Region 118..134 /label= CDR_3
FT Region 135..145 /label= Framework_4
FT Region 146..475 /label= Constant_region
XX
XX WO9118983-A.
XX
XX 12-DEC-1991.
XX
XX 28-MAY-1991; 91WO-1000067.
XX
XX 29-MAY-1990; 90AT-0001178.
XX
XX (JUNG/) JUNGBAUER A.
XX
XX Felgenhauer M, Himmler G, Kohl J, Steindl F;
XX WPI; 1992-007468/01.
XX DR N-PSDB; AAQ20068.
XX
XX Recombinant protein which binds to complex viral antigen and
XX HIV-1 - contains variable region of antibody derived from 3D6
XX cell line, used for detecting HIV-1 antigen
XX
XX Claim 2; Page 24; 52pp; German.
XX
XX The variable region of the heavy chain is used in a recombinant
XX CC protein with the variable region from the kappa light chain of 3D6,
XX CC the two V regions being joined by a linker. The recombinant protein
XX CC binds to HIV gp160.
XX See also AAQ20067 and AAQ20068.
XX
XX Sequence 475 AA:
SQ
Query Match 77.6%; Score 516; DB 13; Length 475;
Best Local Similarity 77.3%; Pred. No. 2,6e-41;
Matches 99; Conservative 11; Mismatches 14; Indels 4; Gaps 2;
QY 1 QVQLVDSGGGLVQPGKSLRLSCAASGFTPDYAIHWVRQAPGKGLWVGSIWDSSTIGY 60
DB 20 EVQLVDSGGGLVQPGKSLRLSCAASGFTPDYAMHWVRQAPGKGLWVGSIWDSSTIGY 79
QY 61 ADSVKGRFTISRDNKNSLYLNMSLRADDTALYYC--ALPYNNSNRRGVAAPFIWQ 118
DB 80 ADSVKGRFTISRDNKNSLYLNMSLRADDTALYYC--FTVAAPFIWQ 137
QY 119 GTMVTWSS 126
DB 138 GTMVTWSS 145
RESULT 5
AAW90286
ID AAW90286 standard; Protein; 124 AA.
XX
XX AAW90286;
XX
XX 07-SEP-1999 (first entry)
XX
XX Human anti-GPIIb/IIIa antibody heavy chain protein from phagemid A1-X40.
XX
XX Antibody; GPIIb/IIIa; human; auto-antibody; anti-idiotypic; diagnosis;
XX blood platelet membrane protein; predilection; prevention; treatment;
XX autoimmune thrombocytopenic purpura; AITP; fibrinogen binding; thrombi;
XX chromosome; cardiac infarction; pulmonary embolism; heavy chain.
XX
XX Homo sapiens.
XX

```



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# OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 40.5329 Seconds  
(without alignments)  
493.415 Million cell updates/sec

Title: US-09-674-752-43

Sequence: 1 QVQLVQSGGGLVQPGKSLRL.....RRGVAAPFDIWGGTMTVTS 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

A\_Geneseq\_19Jun03:\*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                 |
|------------|-------|-------------|--------|-------|-----------------------------|
| 1          | 665   | 100.0       | 126    | 21    | AA50961 Human FVIII antio   |
| 2          | 665   | 100.0       | 126    | 21    | AA50967 Human FVIII antio   |
| 3          | 516   | 77.6        | 248    | 13    | AA20059 Recombinant sc3D6   |
| 4          | 516   | 77.6        | 475    | 13    | AA20057 Heavy chain of 3D6  |
| 5          | 511   | 76.8        | 124    | 20    | AAW90286 Human anti-GPIIb/I |
| 6          | 509   | 76.5        | 120    | 20    | AA433255 VH domain CDR of a |
| 7          | 508   | 76.4        | 120    | 20    | AA433254 VH domain CDR of a |
| 8          | 508   | 76.4        | 120    | 22    | AA65553 Amino acid sequenc  |
| 9          | 508   | 76.4        | 120    | 23    | AB806276 VH3-4 amino acid s |

|    |       |      |     |    |                             |
|----|-------|------|-----|----|-----------------------------|
| 10 | 505.5 | 76.0 | 119 | 22 | AAE07025 Human heavy chain  |
| 11 | 505.5 | 76.0 | 241 | 18 | AAW24063 Human MSX receptor |
| 12 | 503.5 | 75.7 | 245 | 23 | ABP45915 Human Blys binding |
| 13 | 492.5 | 74.1 | 149 | 21 | AAV64737 Human 5' EST relat |
| 14 | 491   | 73.8 | 254 | 23 | ABP45416 Human Blys binding |
| 15 | 489   | 73.5 | 122 | 21 | AAV96065 Human anti-DAP ant |
| 16 | 489   | 73.5 | 251 | 23 | ABP44911 Human Blys binding |
| 17 | 488.5 | 73.3 | 127 | 22 | AAU08385 Anti-ORGP antiod   |
| 18 | 487.5 | 73.3 | 126 | 22 | AAU02623 Anti-CD40 monoclon |
| 19 | 487.5 | 73.3 | 146 | 24 | ABJ36923 Anti-hEDRF antiod  |
| 20 | 487.5 | 73.3 | 248 | 24 | ABG65590 Human Blys binding |
| 21 | 487.5 | 73.3 | 252 | 23 | ABP45405 Anti-adipocyte mon |
| 22 | 487.5 | 73.2 | 118 | 22 | AAU02560 Anti-TNF-alpha ant |
| 23 | 486.5 | 73.2 | 121 | 18 | AAW27569 Human anti-TNF-aip |
| 24 | 486.5 | 73.1 | 121 | 24 | AAO16460 Human Blys binding |
| 25 | 486   | 73.1 | 246 | 23 | ABP45313 Human Blys binding |
| 26 | 483   | 72.6 | 251 | 23 | ABP45309 Human Blys binding |
| 27 | 481   | 72.3 | 127 | 23 | ABG76513 HCV E1 antigen mon |
| 28 | 481   | 72.3 | 131 | 23 | ABG76547 HCV E1 antigen mon |
| 29 | 481   | 72.3 | 151 | 23 | ABP45531 Human Blys binding |
| 30 | 480.5 | 72.3 | 121 | 23 | ABP45531 Human Blys binding |
| 31 | 480   | 72.2 | 118 | 22 | AAU02605 Anti-adipocyte mon |
| 32 | 479   | 72.0 | 118 | 22 | AAU02593 Anti-adipocyte mon |
| 33 | 476   | 71.6 | 120 | 22 | AAU02501 Human Blys binding |
| 34 | 476   | 71.6 | 248 | 23 | ABP45879 Human Blys binding |
| 35 | 475   | 71.4 | 239 | 23 | ABP46027 Human Blys binding |
| 36 | 474   | 71.3 | 117 | 15 | AAAS2053 Heavy chain variab |
| 37 | 474   | 71.3 | 239 | 23 | ABP46004 Human Blys binding |
| 38 | 473   | 71.1 | 239 | 23 | ABP46011 Human Blys binding |
| 39 | 472.5 | 71.1 | 117 | 23 | AAO15187 Dig3 antibody heav |
| 40 | 472.5 | 71.1 | 123 | 18 | AAW08582 Human antibody C4  |
| 41 | 472.5 | 71.1 | 290 | 24 | ABP55318 Pelb/SAF/myc/6His  |
| 42 | 472.5 | 71.1 | 291 | 23 | ABG60632 Immunoglobulin rel |
| 43 | 472.5 | 71.1 | 296 | 23 | ABG60637 Immunoglobulin rel |
| 44 | 472.5 | 71.1 | 519 | 23 | AAU81993 Human secreted pro |
| 45 | 472   | 71.0 | 239 | 23 | ABP46012 Human Blys binding |

## ALIGNMENTS

|          |                                                                        |                                    |
|----------|------------------------------------------------------------------------|------------------------------------|
| RESULT 1 | AA50961                                                                | AA50961 standard; Protein; 126 AA. |
| ID       | AA50961;                                                               |                                    |
| AC       | AA50961;                                                               |                                    |
| XX       |                                                                        | (first entry)                      |
| DT       | 23-MAR-2000                                                            |                                    |
| XX       |                                                                        |                                    |
| DE       | Human FVIII antibody A3-C1 scFv heavy chain protein B18.               |                                    |
| XX       |                                                                        |                                    |
| KW       | Human; heavy chain; antibody; factor VIII; hemostatic;                 |                                    |
| KW       | hemophilia A; scFv; A3-C1.                                             |                                    |
| XX       |                                                                        |                                    |
| OS       | Homo sapiens.                                                          |                                    |
| XX       |                                                                        |                                    |
| PN       | MO9958680-A2.                                                          |                                    |
| XX       |                                                                        |                                    |
| XX       | 18-NOV-1999.                                                           |                                    |
| PD       |                                                                        |                                    |
| XX       |                                                                        |                                    |
| PF       | 07-MAY-1999;                                                           | 99MO-NL00285.                      |
| XX       |                                                                        |                                    |
| PR       | 08-MAY-1998;                                                           | 98EP-0201543.                      |
| XX       |                                                                        |                                    |
| PA       | (SANO-) STICHTING SANQUIN BLOEDVOORZIEENING.                           |                                    |
| XX       |                                                                        |                                    |
| PI       | Voorberg JJ, Van Den Brink EN, Turenhout EAM;                          |                                    |
| XX       |                                                                        |                                    |
| DR       | WPI; 2000-053102/04.                                                   |                                    |
| XX       |                                                                        |                                    |
| PT       | New polynucleotide, polypeptide and antibody useful for diagnosing the |                                    |
| PT       | presence of neutralizing antibodies against factor VIII and for        |                                    |
| PT       | treatment of hemophilia A patients with these antibodies -             |                                    |



|    |     |        |     |
|----|-----|--------|-----|
| Qy | 121 | MVTVSS | 126 |
|    |     | :      |     |
| Db | 135 | LVTVSS | 140 |

RESULT 14  
Q9UL72

|    |                                                                  |                                           |
|----|------------------------------------------------------------------|-------------------------------------------|
| AC | Q9UL72;                                                          |                                           |
| DT | 01-MAY-2000 (TrEMBLrel. 13, Created)                             |                                           |
| DT | 01-MAY-2000 (TrEMBLrel. 13, last sequence update)                |                                           |
| DT | 01-MAR-2003 (TrEMBLrel. 23, last annotation update)              |                                           |
| DE | Myosin-reactive Immunoglobulin heavy chain variable reg          |                                           |
| DE | (fragment).                                                      |                                           |
| OS | Homo sapiens (Human).                                            |                                           |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu           |                                           |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Ho           |                                           |
| OX | NCBI_TaxID=9606;                                                 |                                           |
| RA | [1]                                                              |                                           |
| RP | SEQUENCE FROM N.A.                                               |                                           |
| RX | MEDLINE=98271139; PubMed=9614934;                                |                                           |
| RA | Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berny S.M.,        |                                           |
| RA | Young D.C.;                                                      |                                           |
| RT | "Myosin-reactive autoantibodies in rheumatic carditis and normal |                                           |
| RT | fetus.";                                                         |                                           |
| RL | Clin. Immunol. Immunopathol. 87:184-192(1998).                   |                                           |
| DR | EMBL; AF035042; AAD56278.1; -.                                   |                                           |
| DR | HSSP; P01772; 2PB4.                                              |                                           |
| DR | InterPro; IPR007110; IG-11ke.                                    |                                           |
| DR | InterPro; IPR003006; IG_MHC.                                     |                                           |
| DR | InterPro; IPR003596; IG_V.                                       |                                           |
| DR | Pfam; PF00047; IG_1.                                             |                                           |
| DR | SMART; SM00406; IGV_1.                                           |                                           |
| DR | PROSITE; PSS0835; IG_Like; 1.                                    |                                           |
| FT | NON_TER                                                          | 1                                         |
| FT | NON_TER                                                          | 1                                         |
| FT | NON_TER                                                          | 118                                       |
| FT | NON_TER                                                          | 118                                       |
| SO | SEQUENCE                                                         | 118 AA; 12872 MW; BADA15944B2D5CCA CRC64; |

RESULT 15  
Q96K68  
ID Q96K68 PRELIMINARY; PRT; 494 AA

DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE Hypothetical protein FLJ14473.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Isegal T., Oca T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

RA Magatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.  
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.  
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.  
RA Yamamoto K., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,  
RA Minomiya K., Iwayanagi T.,  
RA "NEDO human cDNA sequencing project",  
RT Submitted (May-2001) to the EMBL/Genbank/DBD databases.  
BL

SQ SEQUENCE 494 AA; 5308 MW; 9A1D7AEB5AE4C0E CRC64;

|                       |        |                  |        |                |
|-----------------------|--------|------------------|--------|----------------|
| Query Match           | 62.7%; | Score 417;       | DB 4;  | Length 494;    |
| Best Local Similarity | 65.9%; | Pred. No. 4e-34; |        |                |
| Matches               | 83;    | Conservative     | 14;    | Mismatches 25; |
|                       |        |                  | Indels | 4;             |
|                       |        |                  | Gaps   | 1;             |

Search completed: December 30, 2003, 11:01:08  
Job time : 31.7067 secs

```

Q9Y509
ID Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vh3 protein (Fragment).
GN Vh3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vesicic R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:11948-1953(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAAATBC925C CRC64;

Query Match
Best Local Similarity 64.2%; Score 427; DB 4; Length 147;
Matches 84; Conservative 16; Mismatches 24; Indels 4; Gaps 2;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTGDAIHWVRQAPGQLEWVGVTWGGTIGF 60
DB 1 QVHLVSGGGGVVQPGKSLRLSCAASGFTGDAIHWVRQAPGQLEWVGVTWGGTIGF 60
QY 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALTYCALP--YINSSN--RGVAAPDIMGQ 118
DB 61 ADSVKGRTISRDNSKNTLYLQMTSLRVEDTAVYCAKQGNFDSV--YAGIDYWGQ 118
QY 119 GTMVTSS 126
DB 119 GTLVTVSS 126

RESULT 12
Q9UL84
ID Q9UL84 PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable regi
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Hom
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.V., Kalis N.N., Berney S.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis an normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56266.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.

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DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER
SQ SEQUENCE 122 AA; 13579 MW; 36054DA1366545B8 CRC64;

Query Match
Best Local Similarity 63.2%; Score 420; DB 4; Length 122;
Matches 82; Conservative 16; Mismatches 24; Indels 4; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTGDAIHWVRQAPGQLEWVGVTWGGTIGF 60
DB 1 EVQLVSGGGGVVQPGKSLRLSCAASGFTGDAIHWVRQAPGQLEWVAISNDGSKRFY 60
QY 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALTYCALTYINSSNVRGVAAPDIMGQGT 120
DB 61 ADSVKGRTISRDNSKNTLYLQMTSLRVEDTAVYCA---KDERGLVGTTFDYGQGT 116
QY 121 MVTSS 126
DB 117 LVTSS 122

RESULT 13
Q8NCL6
ID Q8NCL6 PRELIMINARY; PRT; 493 AA.
AC Q8NCL6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ90170.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Mammary gland;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahata K.,
RA Masuhio Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Nimomiya K.;
RT "NEO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/Genbank/DBD databases.
DR EMBL; AK074651; BA011114.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_CL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_4.
DR SMART; SM00409; IG_4.
DR SMART; SM00407; IGCL; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 493 AA; 53224 MW; 12BCD7E094777101 CRC64;

Query Match
Best Local Similarity 63.1%; Score 419.5; DB 4; Length 493;
Matches 83; Conservative 13; Mismatches 25; Indels 5; Gaps 2;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTGDAIHWVRQAPGQLEWVGVTWGGTIGF 60
DB 20 QVQLVSGGGGVVLPKSLRLSCAASGFTGDAIHWVRQAPGQLEWVAISNDGSKRFY 79
QY 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALTYCALTYINSSNVRGVAAPDIMGQGT 120
DB 80 SDVKGRLTVSRDNYKNTLYLEMKSLGABDTAVYCA----RDQY-AGYGVFDHMGQGT 134

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DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalie N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154D6061 CRC64;

Query Match
Best Local Similarity 66.8%; Score 443.5; DB 4; Length 116;
Matches 85; Conservative 15; Mismatches 16; Indels 9; Gaps 1;

QY 2 VOLVOSGGGLVOPGKSLRLSCAASGFTGDYAIHWYRQAPGEGLEWVSGVTMGSTTIGF 61
DB 1 VOLVESGGGVVOPGKSLRLSCAASGFTGSSYAMHWYRQAPGKLEWVAIVISYDSGNKRYA 60
QY 62 DSVKGRFTISRDNKNSLYLNNSLRAPDYLALYGCALYINSSNRRGVAAFDIWGQGTM 121
DB 61 DSVKGRFTISRDNKNSLYLNNSLRAPDYLALYGCALYINSSNRRGVAAFDIWGQGTM 111
QY 122 VTVSS 126
DB 112 VTVSS 116

RESULT 9
Q9NSK4 PRELIMINARY; PRT; 499 AA.
ID Q9NSK4
AC Q9NSK4
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/Genbank/DDBJ databases.
DR EMBL; BC032249; AAH32249.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGL1; 2.
DR SMART; SM00406; IGV; 1.

```

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DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
RM Hypothetical protein.
SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;

Query Match
Best Local Similarity 66.1%; Score 439.5; DB 4; Length 499;
Matches 86; Conservative 14; Mismatches 23; Indels 7; Gaps 2;

QY 1 QVOLVOSGGGLVOPGKSLRLSCAASGFTGDYAIHWYRQAPGEGLEWVSGVTMGSTTIGF 60
DB 20 EVOLVESGGGVVOPGKSLRLSCAASGFTGDSGAMWYRQAPGKLEWVSSINMGSTNY 79
QY 61 ADSVKGRFTISRDNKNSLYLNNSLRAPDYLALYGCALPYINSSNRRGVAAFDI 116
DB 80 ADSVKGRFTISRDNKNSLYLNNSLRAPDYLALYGCAR---DPTKCSGSGCLGYMDVW 136
QY 117 GQGTMTVSS 126
DB 137 GKGTMTVSS 146

RESULT 10
Q9UL90 PRELIMINARY; PRT; 113 AA.
ID Q9UL90
AC Q9UL90
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalie N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match
Best Local Similarity 67.5%; Score 437.5; DB 4; Length 113;
Matches 85; Conservative 14; Mismatches 14; Indels 13; Gaps 2;

QY 1 QVOLVOSGGGLVOPGKSLRLSCAASGFTGDYAIHWYRQAPGEGLEWVSGVTMGSTTIGF 60
DB 1 EVOLVESGGGVVOPGKSLRLSCAASGFTGSSYAMHWYRQAPGKLEWVAIFRYDSNRY 60
QY 61 ADSVKGRFTISRDNKNSLYLNNSLRAPDYLALYGCALPYINSSNRRGVAAFDI 120
DB 61 ADSVKGRFTISRDNKNSLYLNNSLRAPDYLALYGCAR---KDLNY-----WGQGT 107
QY 121 MTVSS 126
DB 108 LTVSS 113

RESULT 11

```

QY 121 MVTSS 126  
 |||||  
 Db 116 MVTSS 121

## RESULT 5

09HCC1

ID 09HCC1 PRELIMINARY; PRT; 112 AA.

AC 09HCC1;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Single chain Fv (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI\_TaxId=9606;

RN (1)

RP SEQUENCE FROM N.A.

RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.,

RT "An antibody fragment2A3 specific for native lysozyme: isolation from a

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB049915; BAB16829.1; -

DR HSSP; P01772; 2PB4.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_V.

DR Pfam; PF00047; IG\_1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG\_LIKE; 1.

FT NON\_TER 1

FT NON\_TER 112

SQ SEQUENCE 112 AA; 12243 MW; 24F1A45BC3B84788 CRC64;

Query Match

Best Local Similarity 68.8%; Score 456; DB 4; Length 112;

Matches 86; Conservative 13; Mismatches 13; Indels 10; Gaps 1;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGKLEWVSGVTSGTTIGF 60

Db 1 EVQLVESGGGVVRRPGSLRLISCAASGFTPDYGMVNRQAPGKLEWVSGVTSGTTIGF 60

QY 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALYYCALPYINSSNYRGVAAPDIWGQ 120

Db 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALYYCALPYINSSNYRGVAAPDIWGQ 120

QY 121 MV 122

Db 111 LV 112

RESULT 6

08TC77

ID 08TC77 PRELIMINARY; PRT; 471 AA.

AC 08TC77;

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI\_TaxId=9606;

RN (1)

RP SEQUENCE FROM N.A.

RA TISSUE=Splice;

RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC024289; AAH24289.1; -

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_V.

DR Pfam; PR00047; IGV; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 471 AA; 51791 MW; 388F7FACF588660E CRC64;

Query Match

Best Local Similarity 67.7%; Score 450; DB 4; Length 471;

Matches 90; Conservative 16; Mismatches 14; Indels 8; Gaps 2;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGKLEWVSGVTSGTTIGF 60

Db 20 EVQLVESGGGLVQPGKSLRLSCAASGFTSYISMMVNRQAPGKLEWVSGVTSSSYIYY 79

QY 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALYYCALPYINSSNYRGVAAPDIWGQ 118

Db 80 ADSVKGRTISRDNAKNSLYLNMSLRADDTALYYCALPYINSSNYRGVAAPDIWGQ 133

QY 119 GTMVTSS 126

Db 134 GTLVTVSS 141

RESULT 7

096BB9

ID 096BB9 PRELIMINARY; PRT; 597 AA.

AC 096BB9;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI\_TaxId=9606;

RN (1)

RP SEQUENCE FROM N.A.

RA TISSUE=B-cell;

RA Strausberg R.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC015760; AAH15760.1; -

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_V.

DR Pfam; PF00047; IGV; 5.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG\_LIKE; 5.

DR PROSITE; PS00290; IG\_MHC; 3.

KW Hypothetical protein.

SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;

Query Match

Best Local Similarity 67.1%; Score 446.5; DB 4; Length 597;

Matches 88; Conservative 17; Mismatches 17; Indels 7; Gaps 2;

QY 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTFGDYAIHWVRQAPGKLEWVSGVTSGTTIGF 60

Db 20 EVQLVESGGGLVQPGKSLRLSCAASGFTSYISMMVNRQAPGKLEWVSGVTSSSYIYY 79

QY 61 ADSVKGRTISRDNAKNSLYLNMSLRADDTALYYCALPYINSSNYRGVAAPDIWG 117

Db 80 ADSVKGRTISRDNAKNSLYLNMSLRADDTALYYCALPYINSSNYRGVAAPDIWG 135

QY 118 OGTMVTSS 126

Db 136 OGTLTVSS 144

RESULT 8

09UL93

ID 09UL93 PRELIMINARY; PRT; 116 AA.

AC 09UL93;

```

APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSER: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-35

Query Match 78.9%; Score 490.5; DB 1; Length 120;
Best Local Similarity 79.5%; Pred. No. 1,1e-41;
Matches 97; Conservative 7; Mismatches 13; Indels 5; Gaps 2;

QY 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMHWROAPGAGLEWVAIVISYDGNKYY 60
DB 1 QVQLVSGGSGVOPGRSLRLSCAASGFTFSYAMHWROAPGKLEWVAIVISYDGSNKYY 60
QY 61 ADSVKRFAISRDNAKNTLYLQNSLTIEDTAVYYCAKDLIESNIAEL---WGQTLVLT 117
DB 61 ADSVKRFTISRDNSKNTLYLQNSLTARADTAVYYCARD--KDWGVALPDYWGQTLVLT 118
QY 118 VS 119
DB 119 VS 120

RESULT 3
US-08-331-398A-46
Sequence 46, Application US/08331398A
Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Paetan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURES:
NAME/KEY: Protein
LOCATION: 1,119
OTHER INFORMATION: /note="Human fetal immunoglobulin"
US-08-331-398A-46

Query Match 78.2%; Score 486.5; DB 1; Length 119;
Best Local Similarity 78.3%; Pred. No. 2.7e-41;
Matches 94; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMHWROAPGAGLEWVAIVISYDGNKYY 60
DB 1 QVQLVSGGSGVOPGRSLRLSCAASGFTFSYAMHWROAPGKLEWVAIVISYDGSNKYY 60
QY 61 ADSVKRFAISRDNAKNTLYLQNSLTIEDTAVYYCAKDLIESNIAELWGQTLVTS 120
DB 61 ADSVKRFTISRDNSKNTLYLQNSLTARADTAVYYCARSAARTYYPD-YWGQTLVTS 119
QY 118 VS 119
DB 119 VS 120

RESULT 4
US-08-331-397B-46
Sequence 46, Application US/08331397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Paetan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:45 ; Search time 12.1852 Seconds  
(without alignments)  
416.677 Million cell updates/sec

Title: US-09-674-752-46

Perfect score: 1 EVOLVESGGGLVPGKSLRL.....IESNIAELWGQGLTVTVSS 120

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCtUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfilea1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 495   | 79.6        | 248    | 4     | US-09-315-926A-80 |
| 2          | 490.5 | 78.9        | 120    | 1     | US-07-942-245-35  |
| 3          | 486.5 | 78.2        | 119    | 1     | US-08-331-398A-46 |
| 4          | 486.5 | 78.2        | 119    | 2     | US-08-331-397B-46 |
| 5          | 486.5 | 78.2        | 119    | 2     | US-08-759-804A-46 |
| 6          | 486.5 | 78.2        | 119    | 3     | US-09-227-693-46  |
| 7          | 485.5 | 78.1        | 123    | 4     | US-09-560-198A-2  |
| 8          | 484.5 | 77.9        | 117    | 4     | US-09-025-769B-24 |
| 9          | 478.5 | 76.9        | 123    | 4     | US-09-560-198A-4  |
| 10         | 477.5 | 76.8        | 123    | 4     | US-09-560-198A-10 |
| 11         | 477.5 | 76.8        | 125    | 3     | US-09-240-274-8   |
| 12         | 477.5 | 76.8        | 125    | 3     | US-09-240-274-20  |
| 13         | 477.5 | 76.8        | 125    | 3     | US-09-240-274-21  |
| 14         | 477.5 | 76.8        | 125    | 3     | US-09-240-274-22  |
| 15         | 473.5 | 76.1        | 125    | 3     | US-09-240-274-9   |
| 16         | 472.5 | 76.0        | 125    | 3     | US-09-240-274-9   |
| 17         | 469.5 | 75.5        | 125    | 3     | US-09-240-274-23  |
| 18         | 469   | 75.4        | 310    | 4     | US-09-079-039-11  |
| 19         | 468   | 75.2        | 124    | 3     | US-09-240-274-4   |
| 20         | 468   | 75.2        | 141    | 1     | US-08-259-372A-2  |
| 21         | 468   | 75.2        | 141    | 1     | US-08-468-671-2   |
| 22         | 467.5 | 75.1        | 125    | 3     | US-09-240-274-140 |
| 23         | 467   | 75.1        | 124    | 3     | US-09-240-274-5   |
| 24         | 467   | 75.1        | 124    | 3     | US-09-240-274-6   |
| 25         | 467   | 75.1        | 126    | 3     | US-09-240-274-26  |
| 26         | 466   | 74.9        | 126    | 3     | US-09-240-274-149 |
| 27         | 464.5 | 74.7        | 125    | 3     | US-09-240-274-151 |

|    |       |      |     |   |                   |                   |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 464   | 74.6 | 124 | 3 | US-09-240-274-7   | Sequence 7, Appl  |
| 29 | 462   | 74.3 | 120 | 2 | US-07-934-373C-4  | Sequence 4, Appl  |
| 30 | 462   | 74.3 | 120 | 3 | US-08-437-642B-4  | Sequence 4, Appl  |
| 31 | 462   | 74.3 | 120 | 4 | US-08-146-206C-4  | Sequence 4, Appl  |
| 32 | 462   | 74.3 | 122 | 2 | US-07-934-373C-21 | Sequence 21, Appl |
| 33 | 462   | 74.3 | 122 | 3 | US-08-437-642B-21 | Sequence 21, Appl |
| 34 | 462   | 74.3 | 122 | 4 | US-08-146-206C-21 | Sequence 21, Appl |
| 35 | 462   | 74.3 | 124 | 5 | PCT-US93-07832-21 | Sequence 21, Appl |
| 36 | 462   | 74.3 | 122 | 3 | US-09-240-274-2   | Sequence 2, Appl  |
| 37 | 461.5 | 74.2 | 121 | 3 | US-09-202-181-4   | Sequence 4, Appl  |
| 38 | 461   | 74.1 | 123 | 3 | US-08-983-607-38  | Sequence 38, Appl |
| 39 | 461   | 74.1 | 126 | 3 | US-09-240-274-153 | Sequence 153, App |
| 40 | 459.5 | 73.9 | 113 | 3 | US-08-974-899-6   | Sequence 6, Appl  |
| 41 | 459.5 | 73.9 | 117 | 3 | US-09-240-274-18  | Sequence 18, Appl |
| 42 | 459.5 | 73.9 | 127 | 3 | US-09-240-274-19  | Sequence 19, Appl |
| 43 | 459   | 73.8 | 126 | 3 | US-09-240-274-25  | Sequence 25, Appl |
| 44 | 458.5 | 73.7 | 125 | 2 | US-08-428-197-5   | Sequence 5, Appl  |
| 45 | 458.5 | 73.7 | 125 | 2 | US-08-428-197-6   | Sequence 6, Appl  |

ALIGNMENTS

```
RESULT 1
US-09-315-926A-80
; Sequence 80, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
; APPLICANT: Es van, Helmut
; APPLICANT: Havenga, Menzo
; APPLICANT: Verlinden, Stefan
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
; FILE REFERENCE: 2183-4080US
; CURRENT APPLICATION NUMBER: US/09/315,926A
; PRIOR APPLICATION NUMBER: EP 99201593.3
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98201693.3
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: phage
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(248)
; OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-80

Query Match      79.6%  Score 495:  DB 4:  Length 248:
Best Local Similarity 78.3%  Pred. No. 9.1e+42;
Matches 94; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVPGKSLRLSCVDSGLTFSSGYGHWYRQPGAGLEWVAIVSYGNDKYY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 23 QVQLVQSGGGLVPGKSLRLSCAASGFTSSYAMHWYRQPGKLEWVAIVSYGSKITY 82
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 ADSYKGRFAISRDAKNTLYLQNMSLTIEDYAVYYCAKDLIESNIAELWGQGLTVTVSS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 83 ADSYKGRFTISRDAKNTLYLQNMSLTIAEDYAVYYCARGITVTKSRPRDYWGQGLTVTVSS 142
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RESULT 2
US-07-942-245-35
; Sequence 35, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
```

| SEQUENCE                                                             | 463 AA                                  | 51007 MW | EAA674CGBBC30783 | CRC64 |
|----------------------------------------------------------------------|-----------------------------------------|----------|------------------|-------|
| Q099LC4                                                              | PRELIMINARY                             | PRT      | 463 AA           |       |
| AC Q099LC4                                                           |                                         |          |                  |       |
| DT 01-JUN-2001                                                       | (TREMBLrel. 17, Created)                |          |                  |       |
| DT 01-JUN-2001                                                       | (TREMBLrel. 17, Last sequence update)   |          |                  |       |
| DT 01-MAR-2003                                                       | (TREMBLrel. 23, Last annotation update) |          |                  |       |
| DE Similar to RIKEN cDNA 181006009 gene.                             |                                         |          |                  |       |
| GN IGH-4.                                                            |                                         |          |                  |       |
| OS Mus musculus (Mouse).                                             |                                         |          |                  |       |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |                                         |          |                  |       |
| OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus |                                         |          |                  |       |
| NCBI_TaxID=10090;                                                    |                                         |          |                  |       |
| [1]                                                                  |                                         |          |                  |       |
| SEQUENCE FROM N.A.                                                   |                                         |          |                  |       |
| RA Strausberg R.;                                                    |                                         |          |                  |       |
| RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.           |                                         |          |                  |       |
| DR EMBL: BC003435; AA03435.1; ..                                     |                                         |          |                  |       |
| DR HSSP: P01842; 7FAB.                                               |                                         |          |                  |       |
| DR MGD: MGI:96446; Igh-4.                                            |                                         |          |                  |       |
| DR InterPro: IPR007110; Ig-like.                                     |                                         |          |                  |       |
| DR InterPro: IPR003006; Ig_MHC.                                      |                                         |          |                  |       |
| DR InterPro: IPR003596; Ig_v.                                        |                                         |          |                  |       |
| DR Pfam: PF00047; Ig_4.                                              |                                         |          |                  |       |
| DR SMART: SM00406; IGV. 1.                                           |                                         |          |                  |       |
| DR PROSITE: PS00835; IG_LIKE; 4.                                     |                                         |          |                  |       |
| DR PROSITE: PS00290; IG_MHC; 1.                                      |                                         |          |                  |       |
| Q0                                                                   |                                         |          |                  |       |

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Oy      1 OVOLVQSAEYKPKSSSVKVSCKAAGGTFPSSHAISMVQAOPQGLEMMGDIIPIIGTGNV 60
Db      20 QVOLVQSAEYKPKSPASVKVSCKVGITLTTELPHVMWGAAPKGLEWGSFDPESGESITY 79
Oy      61 AOKFGGRVTITADBESTSTAYNELSLTTSBDAVAVYCELD---DMPFYMGQTMTVYSS 114
Db      80 AREFGGSTVMTADISTDIAYNELSSLRBDDBTDIAVVCANVPDPAFDIKGGQIMTVYSS 136

RESULT 11
ID      092400 PRELIMINARY; PRT: 143 AA.
AC      092400.
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      V165-D-J-C mu protein (fragment).
OS      V165-D-J-C MU.
SN      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6;
RC      Kozono Y., Kozono H., Azuma T.;
RT      "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT      Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT      Hydroxy-3-Nitrophenyl)Acetyl (NP)."
RL      Submitted (AUG-2001) to the EMBL/genbank/DBJ databases.
DR      EMBL; AB069915; BAB63931.1; .
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF00047; Ig_1.
DR      SMART; SM00406; Igv_1.
DR      PROSITE; PS50835; IG_LINK; 1.
FT      NON TER 1
FT      NON TER 143
SO      SEQUENCE 143 AA; 15704 MW; C99D2433F2BAD8A0 CRC64;

Query Match 64.5%; Score 385; DB 11; Length 143;
Best Local Similarity 62.7%; Pred. No. 1.6e-32;
Matches 74; Conservative 20; Mismatches 20; Indels 4; Gaps 1.

Oy      1 OVOLVQSAEYKPKSSSVKVSCKAAGGTFPSSHAISMVQAOPQGLEMMGDIIPIIGTGNV 60
Db      1 OVOLAQPAAELVYKPKASVAKVMSCKSGVFTTSTWTWVKORPQGSEMGDIGDIPSGSNTY 60
Oy      61 AOKFGGRVTITADBESTSTAYNELSLTTSBDAVAVYCELD---DMPFYMGQTMTVYSS 114
Db      61 NEKFSKATLTLYDKRSSTAYNQLSLTSDSANVYCAPPDSNLHYTDYMGQGITLVYSS 118

RESULT 12
ID      08VDC9 PRELIMINARY; PRT: 168 AA.
AC      08VDC9.
DT      01-MAR-2002 (TREMBLrel. 20, Created)
DT      01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Anti-MOG 212 variable gamma 2a (Fragment).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/c;
RA      Chernajovsky Y.;
RL      Submitted (OCT-2001) to the EMBL/genbank/DBJ databases.

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RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Sembali P.;
RT "targeting T cells to the CNS.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ161312; CAC94867.1; -
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
DR PROSITE: PSS0290; IG_MHC; 1.
KW Hypothetical protein.
SQ
SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 63.7%; Score 378; DB 11; Length 168;
Best Local Similarity 59.4%; Pred. No. 4.2e-31;
Matches 76; Conservative 15; Mismatches 23; Indels 14; Gaps 2;

1 QVQLVSGAEVKKVSGSVKSCAKSGGTFSSHAISWYRQAPGQGLRWNGDIIPIILGTCNY 60
  QVQLVSGAEVKKVSGSVKSCAKSGGTFSSHAISWYRQAPGQGLRWNGDIIPIILGTCNY 60
  20 QVHLVSGAEVMSGASVYRVSCKTSGAFTHTSIWIRQAPGQGLRWNGWISPSDSNTRF 79
  61 AOKFGAEVITITADSTSTAYMELSTLTSEDAVYYC-----ELDMFY-1WGQTMVTSS 106
  AOKFGAEVITITADSTSTAYMELSTLTSEDAVYYC-----ELDMFY-1WGQTMVTSS 106
  80 AKKFGAEVITITDSTSTVYMEISSLSDSDPAVYCARRYCSYSSQNDYVYYTMDVWGK 139
  AKKFGAEVITITDSTSTVYMEISSLSDSDPAVYCARRYCSYSSQNDYVYYTMDVWGK 139
  140 GTVTVSS 147
  GTVTVSS 147

RESULT 13
Q9BRV0 PRELIMINARY; PRT; 500 AA.
Q9BRV0
ID Q9BRV0
AC Q9BRV0;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Prostate;
RC Strauberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005951; AAH05951.1; -
DR HSP: P01789; IMCP.
DR InterPro: IPR007110; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 4.
DR PROSITE: PSS0290; IG_MHC; 1.
KW Hypothetical protein.
SQ
SEQUENCE 500 AA; 18293 MW; 1E3719FCC0E72723 CRC64;

Query Match 63.7%; Score 380.5; DB 11; Length 168;
Best Local Similarity 60.5%; Pred. No. 5.8e-32;
Matches 72; Conservative 21; Mismatches 21; Indels 5; Gaps 2;

1 QVQLVSGAEVKKVSGSVKSCAKSGGTFSSHAISWYRQAPGQGLRWNGDIIPIILGTCNY 60
  QVQLVSGAEVKKVSGSVKSCAKSGGTFSSHAISWYRQAPGQGLRWNGDIIPIILGTCNY 60
  20 QVHLVSGAEVIMKRGASVTKISKATGYTFSSYWIWYQKRGHGLEWIGELLPSGGRNTY 79
  61 AOKFGAEVITITADSTSTAYMELSTLTSEDAVYYC-----ELDMFY-1WGQTMVTSS 114
  AOKFGAEVITITADSTSTAYMELSTLTSEDAVYYC-----ELDMFY-1WGQTMVTSS 114
  80 NEKFGAEVITITADSTSTAYMELSTLTSEDAVYYCAYSSRWYFDVWAGAGTIVTSS 138
  NEKFGAEVITITADSTSTAYMELSTLTSEDAVYYCAYSSRWYFDVWAGAGTIVTSS 138
  140 GTVTVSS 147
  GTVTVSS 147

```



Db 140 GCGTTVTSS 149

RESULT 8

| ID | Q9DBL4                                                                | PRELIMINARY; | PRT; | 473 AA. |
|----|-----------------------------------------------------------------------|--------------|------|---------|
| AC | Q9DBL4                                                                |              |      |         |
| DT | 01-JUN-2001 (TREMBlrel. 17, Created)                                  |              |      |         |
| DT | 01-JUN-2001 (TREMBlrel. 17, Last sequence update)                     |              |      |         |
| DT | 01-MAR-2003 (TREMBlrel. 23, Last annotation update)                   |              |      |         |
| DE | 181060009R1k protein.                                                 |              |      |         |
| GN | IGH-1 OR 181060009R1k.                                                |              |      |         |
| OS | Mus musculus (Mouse).                                                 |              |      |         |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |              |      |         |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.    |              |      |         |
| OX | NCBI_TaxID=10090;                                                     |              |      |         |
| RA | [1]                                                                   |              |      |         |
| RP | SEQUENCE FROM N.A.                                                    |              |      |         |
| RC | STRAIN=C57BL/6J; TISSUE=Pancreas;                                     |              |      |         |
| EX | MEDLINE=21085660; PubMed=11217851;                                    |              |      |         |
| RA | Kawai Y., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,    |              |      |         |
| RA | Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,     |              |      |         |
| RA | Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,    |              |      |         |
| RA | Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,    |              |      |         |
| RA | Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,       |              |      |         |
| RA | Flischiemann W., Gaesteland T., Gissi C., King B., Kochwa H.,         |              |      |         |
| RA | Kuehl P., Lewis S., Matheu Y., Nakaido I., Pesole G., Quackenbush J., |              |      |         |
| RA | Schriml L.M., Stubbli P., Suzuki R., Tomita M., Wagner L., Washio T., |              |      |         |
| RA | Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,      |              |      |         |
| RA | Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,      |              |      |         |
| RA | Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,       |              |      |         |
| RA | Guertlich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,    |              |      |         |
| RA | Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,     |              |      |         |
| RA | Nordone P., Ring B., Ringwald M., Rodriguez I., Salamito N.,          |              |      |         |
| RA | Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., |              |      |         |
| RA | Suzuki H., Toyooka K., Wang K.H., Woltz C., Whitaker C., Wilmink L.,  |              |      |         |
| RA | Wynshaw-Boris A., Yoshida K., Haegawa Y., Kawaji H., Kohlschki S.,    |              |      |         |
| RA | Hayashizaki Y.;                                                       |              |      |         |
| RT | "Functional annotation of a full-length mouse cDNA collection.";      |              |      |         |
| RL | Nature 409:685-690(2001).                                             |              |      |         |
| DR | EMBL; AK007918; BAB25349.1; -                                         |              |      |         |
| DR | HSSP; P01842; 7PAB.                                                   |              |      |         |
| DR | MCD; MGI:96443; Igh-1.                                                |              |      |         |
| DR | InterPro; IPR007110; Igh-1like.                                       |              |      |         |
| DR | InterPro; IPR003006; IGH_MHC.                                         |              |      |         |
| DR | InterPro; IPR003596; IGH_V.                                           |              |      |         |
| DR | Pfam; PF00047; Ig; 4.                                                 |              |      |         |
| DR | SMART; SM00406; IGV; 1.                                               |              |      |         |
| DR | PROSITE; PS50835; IGH_LIKE; 4.                                        |              |      |         |
| DR | PROSITE; PS00290; IGH_MHC; 1.                                         |              |      |         |
| SO | SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;                    |              |      |         |

Query Match 66.9%; Score 399.5; DB 11; Length 473;

Best Local Similarity 63.0%; Pred. No. 2.2e-33;

Matches 75; Conservative 22; Mismatches 17; Indels 5; Gaps 1.

| Qy | 1  | QVQLVQSGAEVKKPSSSVKSCSKAGCTFFSSHAISMVRCAPQCGHEMMGDIIPILGTGNY 60 |
|----|----|-----------------------------------------------------------------|
| Db | 20 | QVQLVQSGAEVKKPSSSVKSCSKAGCTFFSDYIMVRCAPQCGHEMMGDIIPILGTGNY 79   |
| Qy | 61 | AKPFGGRVITNDSESTAYNELSTLTSIEDIAYVC---ELDPFYWGQGTMTVSS 114       |
| Db | 80 | NEKFGKATLTADKSSSTAYMQLSTLSEDSAVYFCARSGYDWFAYWGQGTTLTVSA 138     |

RESULT 9

| ID | Q8VCX7                                              | PRELIMINARY; | PRT; | 613 AA. |
|----|-----------------------------------------------------|--------------|------|---------|
| AC | Q8VCX7;                                             |              |      |         |
| DT | 01-MAR-2002 (TREMBlrel. 20, Created)                |              |      |         |
| DT | 01-MAR-2002 (TREMBlrel. 20, Last sequence update)   |              |      |         |
| DT | 01-MAR-2003 (TREMBlrel. 23, Last annotation update) |              |      |         |
| DE | Hypothetical 67.9 kDa protein.                      |              |      |         |

OS Mus musculus (Mouse) .  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Salivary gland;  
 RA Strauberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC018315; AAH18315.1; .  
 DR MGD; MGI:96448; Igh-6.  
 DR InterPro; IPR007110; Ig\_Like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 5.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KM Hypothetical protein.  
 SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C2862 CRC64;

Query Match 65.3%; Score 390; DB 11; Length 613;  
 Best Local Similarity 62.7%; Pred. No. 3e-32;  
 Matches 74; Conservative 21; Mismatches 19; Indels 4; Gaps 2;

OY 1 QVVLVSGAELVKKRGSSVKKVSCAKSGGTFSSHAISWVRQAPGGLGEMGDIPLPLGKGY 60  
 DB 20 QVQLQSGAEILMKGKGAIVKISKKATGYTFSSYIEWKORPGHGLEWIGELLPGSGSTNY 79  
 OY 61 AAKRGAVITTDSDSTAYMELSTLSEPTAVYVCEL---DWPY-IMGGSTWTVSS 114  
 DB 80 NEKPKGATFTADTSSNTATWQLSLTSEDSAVYICARRLRGMYFDVWGAGITVSS 137

RESULT 10

OY9298 PRELIMINARY; PRT; 150 AA.  
 AC OY9298;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 GN Igg VH protein precursor (Fragment).  
 GE IGG VH.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RL MEDLINE=96322155; PubMed=9657749;  
 RA Jacobson M.G.; Vander Elst L.P.;  
 RT "Mechanism and kinetics of factor VIII inactivation: study with an  
 RT Igg4 monoclonal antibody derived from a hemophilia A patient with an  
 RT inhibitor.";  
 RL Blood 92:496-506(1998).  
 DR EMBL; AJ224083; CAAL1829.1; .  
 DR HSSP; P01772; 2PB4.  
 DR InterPro; IPR007110; Ig\_Like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KM Signal.  
 FT SIGNAL.  
 FT NON TER 1 19 POTENTIAL.  
 SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match 65.2%; Score 389.5; DB 4; Length 150;  
 Best Local Similarity 67.5%; Pred. No. 5.8e-33;  
 Matches 79; Conservative 11; Mismatches 24; Indels 3; Gaps 1;

Db 140 S 140

## RESULT 5

09UL95 PRELIMINARY; PRT; 125 AA.

AC 09UL95;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98271139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RA "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus."  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035019; AAD56255.1; -;  
 DR HSSP; P01810; 2FBJ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT NON\_TER 1 125  
 FT SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 68.8%; Score 410.5; DB 4; Length 125;  
 Best Local Similarity 68.0%; Pred. No. 2.9e-35;

Matches 85; Conservative 9; Mismatches 20; Indels 11; Gaps 1;

QY 1 QVQLVSGAEVKKPGSSSVKVCASGCTFSSHAISVNRQAPGQGLWMGDIIPILGTGY 60  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 1 EVQLVSGAEVKKPGSSSVKVCASGCTFSSHAISVNRQAPGQGLWMGDIIPILGTGY 60  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 61 AQLVSGAEVKKPGSSSVKVCASGCTFSSHAISVNRQAPGQGLWMGDIIPILGTGY 109  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 61 AQLVSGAEVKKPGSSSVKVCASGCTFSSHAISVNRQAPGQGLWMGDIIPILGTGY 120  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 110 VTSS 114  
 :|||||  
 :|||||  
 DB 121 VTSS 125

## RESULT 6

096DK0 PRELIMINARY; PRT; 496 AA.

AC 096DK0;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein FLJ25298.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Genetic mucosa;  
 RA Ishihashi T., Kanehori K., Yoshida M., Watanabe S., Ishida S., Ono Y.,  
 RA Hota T., Hirooka S., Murakawa K., Takiguchi S., Kusano J.,  
 RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chida Y.,  
 RA Suzuki Y., Hata H., Nakagawa K., Mitsuoka S., Morinaga M., Kawamura M.,

RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,  
 RA Kawakami B., Nagai K., Isogai T., Sugano S.;  
 RT "NEBO human cDNA sequencing project."  
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK058027; BAB71633.1; -;  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 4.  
 DR PROSITE; PSS0230; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 496 AA; 53532 MW; C72BE1E247C68FED CRC64;

Query Match 68.3%; Score 408; DB 4; Length 496;  
 Best Local Similarity 65.3%; Pred. No. 3e-34;

Matches 81; Conservative 13; Mismatches 20; Indels 10; Gaps 2;

QY 1 QVQLVSGAEVKKPGSSSVKVCASGCTFSSHAISVNRQAPGQGLWMGDIIPILGTGY 60  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 20 QVQLVSGAEVKKPGSSSVKVCASGCTFSSHAISVNRQAPGQGLWMGDIIPILGTGY 79  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 61 AQLVSGAEVKKPGSSSVKVCASGCTFSSHAISVNRQAPGQGLWMGDIIPILGTGY 110  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 80 AQLVSGAEVKKPGSSSVKVCASGCTFSSHAISVNRQAPGQGLWMGDIIPILGTGY 139  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 111 TVSS 114  
 :|||||  
 :|||||  
 DB 140 TVSS 143

## RESULT 7

096GSO PRELIMINARY; PRT; 159 AA.

AC 096GSO;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Putative matrix cell adhesion molecule-3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Tilson M.D.;  
 RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3  
 RT mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3)."  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY039025; AAK82649.1; -;  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 SQ SEQUENCE 159 AA; 17497 MW; 5D29537B881FAF02 CRC64;

Query Match 67.7%; Score 404; DB 4; Length 159;  
 Best Local Similarity 63.1%; Pred. No. 1.9e-34;

Matches 82; Conservative 18; Mismatches 14; Indels 16; Gaps 3;

QY 1 QVQLVSGAEVKKPGSSSVKVCASGCTFSSHAISVNRQAPGQGLWMGDIIPILGTGY 60  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 20 QVQLVSGAEVKKPGSSSVKVCASGCTFSSHAISVNRQAPGQGLWMGDIIPILGTGY 79  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 61 AQLVSGAEVKKPGSSSVKVCASGCTFSSHAISVNRQAPGQGLWMGDIIPILGTGY 110  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 80 AQLVSGAEVKKPGSSSVKVCASGCTFSSHAISVNRQAPGQGLWMGDIIPILGTGY 139  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 105 GQGTWTVSS 114  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

|                                                                                                                                                                         |                                                                           |                                           |                                                                  |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------|-------------------------------------------|------------------------------------------------------------------|-----|
| Dd                                                                                                                                                                      |                                                                           | 1                                         | VQSGAEVKKPSSSVKVCCKAAGCTFSSVAISGVRQAPQGLEMGGRIIPILGIANYAQKF      | 60  |
| Oy                                                                                                                                                                      |                                                                           | 65                                        | OGRTITDESTSTRAYMELSLTITSBDTAIVYICELD-----WFL-IGCGTMVTSS          | 114 |
|                                                                                                                                                                         |                                                                           |                                           | :     :     :     :     :     :     :     :     :     :          |     |
|                                                                                                                                                                         |                                                                           |                                           | :  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  : |     |
| Dd                                                                                                                                                                      |                                                                           | 61                                        | QGRVTTADKSTSTRAYMELSLRSEDIAVVYCASSNMGPMYPFDLMGRGLTVTSS           | 116 |
| <br>RESULT 2                                                                                                                                                            |                                                                           |                                           |                                                                  |     |
| ID                                                                                                                                                                      | Q9UL92                                                                    |                                           | PRELIMINARY; PRT; 124 AA.                                        |     |
| AC                                                                                                                                                                      | Q9UL92;                                                                   |                                           |                                                                  |     |
| DT                                                                                                                                                                      | 01-MAY-2000                                                               | (TREMBLrel. 13, Created)                  |                                                                  |     |
| DT                                                                                                                                                                      | 01-MAY-2000                                                               | (TREMBLrel. 13, Last sequence update)     |                                                                  |     |
| DT                                                                                                                                                                      | 01-MAR-2003                                                               | (TREMBLrel. 23, Last annotation update)   |                                                                  |     |
| DE                                                                                                                                                                      | Myosin-reactive Immunoglobulin heavy chain variable region<br>(Fragment). |                                           |                                                                  |     |
| OS                                                                                                                                                                      | Homo sapiens (Human).                                                     |                                           |                                                                  |     |
| OC                                                                                                                                                                      | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;         |                                           |                                                                  |     |
| CC                                                                                                                                                                      | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.                |                                           |                                                                  |     |
| OX                                                                                                                                                                      | NCBI_TaxId=9606;                                                          |                                           |                                                                  |     |
| RN                                                                                                                                                                      | [1]                                                                       |                                           |                                                                  |     |
| RP                                                                                                                                                                      | SEQUENCE FROM N.A.                                                        |                                           |                                                                  |     |
| RX                                                                                                                                                                      | MEDLINE=98277139; PubMed=9614934;                                         |                                           |                                                                  |     |
| RA                                                                                                                                                                      | Yu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,               |                                           |                                                                  |     |
| RA                                                                                                                                                                      | "Young D.C.;                                                              |                                           |                                                                  |     |
| RT                                                                                                                                                                      | "Myosin-reactive autoantibodies in rheumatic carditis and normal          |                                           |                                                                  |     |
| RL                                                                                                                                                                      | fetus";                                                                   |                                           |                                                                  |     |
| DR                                                                                                                                                                      | Clin. Immunol. Immunopathol. 87:184-192(1998).                            |                                           |                                                                  |     |
| DR                                                                                                                                                                      | EMBL; AF035022; AAD56258.1; -.                                            |                                           |                                                                  |     |
| DR                                                                                                                                                                      | HSSP; P01772; 2PB4.                                                       |                                           |                                                                  |     |
| DR                                                                                                                                                                      | InterPro; IPR007110; Ig-like.                                             |                                           |                                                                  |     |
| DR                                                                                                                                                                      | InterPro; IPR003006; Ig_MHC.                                              |                                           |                                                                  |     |
| DR                                                                                                                                                                      | InterPro; IPR003596; Ig_V.                                                |                                           |                                                                  |     |
| DR                                                                                                                                                                      | Pfam; PF00047; Ig_1.                                                      |                                           |                                                                  |     |
| DR                                                                                                                                                                      | SMART; SM00406; IGv_1.                                                    |                                           |                                                                  |     |
| DR                                                                                                                                                                      | PROSITE; PS00835; IG_LINK; 1.                                             |                                           |                                                                  |     |
| FT                                                                                                                                                                      | NON_TER                                                                   | 1                                         |                                                                  |     |
| FT                                                                                                                                                                      | NON_TER                                                                   | 1                                         |                                                                  |     |
| SQ                                                                                                                                                                      | SEQUENCE                                                                  | 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64; |                                                                  |     |
| <br>Query Match 70.7%; Score 422; DB 4; Length 124;<br>Best Local Similarity 68.5%; Pred. No. 1.8e-36;<br>Matches 85; Conservative 12; Mismatches 17; Indels 10; Gaps 1 |                                                                           |                                           |                                                                  |     |
| Oy                                                                                                                                                                      |                                                                           | 1                                         | OVQLVQSGAEVKKPSSSVKVCCKAAGCTFSSHAISMVRQAPQGLEMGGDIIPILGTNY       | 60  |
|                                                                                                                                                                         |                                                                           |                                           | :     :     :     :     :     :     :     :     :                |     |
|                                                                                                                                                                         |                                                                           |                                           | :  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  : |     |
| Dd                                                                                                                                                                      |                                                                           | 1                                         | EVQLVESGAIEVKPKASAVKVCCKAAGTFSSVYMVMHVRQAPQGLEMGGIINPSGSTSY      | 60  |
| Oy                                                                                                                                                                      |                                                                           | 61                                        | AQFGRGRTITDESTSTRAYMELSLTITSBDTAIVYICELDFIT-----WGQTMV           | 110 |
|                                                                                                                                                                         |                                                                           |                                           | :     :     :     :     :     :     :     :     :                |     |
|                                                                                                                                                                         |                                                                           |                                           | :  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  :~  : |     |
| Dd                                                                                                                                                                      |                                                                           | 61                                        | AQFGRGRTITRDTSTSTVYMELSLRSEDIAVVYCARGLYVVPAAFRPDYWGQTLV          | 120 |
| Oy                                                                                                                                                                      |                                                                           | 111                                       | TVSS 114                                                         |     |
|                                                                                                                                                                         |                                                                           |                                           |                                                                  |     |
| Dd                                                                                                                                                                      |                                                                           | 121                                       | TVSS 124                                                         |     |
| <br>RESULT 3                                                                                                                                                            |                                                                           |                                           |                                                                  |     |
| ID                                                                                                                                                                      | Q9UL94                                                                    |                                           | PRELIMINARY; PRT; 119 AA.                                        |     |
| AC                                                                                                                                                                      | Q9UL94;                                                                   |                                           |                                                                  |     |
| DT                                                                                                                                                                      | 01-MAY-2000                                                               | (TREMBLrel. 13, Created)                  |                                                                  |     |
| DT                                                                                                                                                                      | 01-MAY-2000                                                               | (TREMBLrel. 13, Last sequence update)     |                                                                  |     |
| DT                                                                                                                                                                      | 01-MAR-2003                                                               | (TREMBLrel. 23, Last annotation update)   |                                                                  |     |
| DE                                                                                                                                                                      | Myosin-reactive immunoglobulin heavy chain variable region<br>(Fragment). |                                           |                                                                  |     |
| OS                                                                                                                                                                      | Homo sapiens (Human).                                                     |                                           |                                                                  |     |
| OC                                                                                                                                                                      | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;         |                                           |                                                                  |     |
| CC                                                                                                                                                                      | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.                |                                           |                                                                  |     |
| OX                                                                                                                                                                      | NCBI_TaxId=9606;                                                          |                                           |                                                                  |     |
| RN                                                                                                                                                                      | [1]                                                                       |                                           |                                                                  |     |
| RP                                                                                                                                                                      | SEQUENCE FROM N.A.                                                        |                                           |                                                                  |     |
| RX                                                                                                                                                                      | MEDLINE=98277139; PubMed=9614934;                                         |                                           |                                                                  |     |

[illegible]



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QY 1 QVOLVSGAEVKKPGSSVKYSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTGNY 60
Db 1 QVOLVSGAEVKKPGSSVKYSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTGNY 60
QY 61 AQFPGG-----RYITADESTAYMEI-STLTSEDTAVYYCELDW-----FYIMGQ 106
Db 55 TDFPGGYIYMERVYTSLKPSFNOATMELVNLFNEDGAVYYCARWKGVNPNPDFYWGQ 114
QY 107 GTMTVTS 114
Db 115 GVLTVTS 122

RESULT 15
HV01 MOUSE STANDARD; PRT; 121 AA.
ID HV01 MOUSE
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MPC11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; Pubmed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning" and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A93708; GWS11.
DR HSSP: P01810; 2EBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KW Immunoglobulin V region.
KW DOMAIN 1 112 IG-LIKE.
FT NON TER 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 57.9%; Score 345.5; DB 1; Length 121;
Best Local Similarity 53.7%; Pred. No. 1.9e-28;
Matches 65; Conservative 24; Mismatches 25; Indels 7; Gaps 1;

QY 1 QVOLVSGAEVKKPGSSVKYSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTGNY 60
Db 1 EAQIQSGAEVLRPGISVKISCKRAAGITFTNWMIGWKERPGHLEWIGDIYFGGGFTNY 60
QY 61 AQFPGGVTITADESTAYMEI-STLTSEDTAVYYCELDWY-----IMGGTMTVTS 113
Db 61 NDWLKGRATITADTSSSTAYIQLSSLTSEDSATYHCARGIYNSSPYFDSMGGCTITLVS 120
QY 114 S 114
Db 121 S 121
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RX MEDLINE=81234548; PubMed=6788376;
RA Botheil A.L.M., Paekind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC (NAB ANTIBODIES) TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC MAKING ANTIBODIES.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: J00529; AAA8170.1; -.
CC PIR: A08089; MEMS18.
CC PDB: 1A6U; 27-MAY-98.
CC PDB: 1A6W; 15-JUL-98.
CC InterPro: IPR007110; IG-like.
CC InterPro: IPR003006; IG_MHC.
CC InterPro: IPR003596; IG_V.
CC Pfam: PF00047; Ig; 1.
CC SMART: SM00406; IGV; 1.
CC PROSITE: PS50835; IG LIKE; 1.
CC Immunoglobulin V region; Signal; 3D-structure.
KM FT CHAIN 1 19
FT SIGNAL 1 19
FT DOMAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 FRAMEWORK-3.
FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DADF0CC9F465 CRC64;

Query Match 59.0%; Score 352; DB 1; Length 139;
Best Local Similarity 57.5%; Pred. No. 4.9e-29;
Matches 69; Conservative 20; Mismatches 25; Indels 6; Gaps 1;

QY 1 QVQLVQSGAEVKKPGSSVKVSCKAASGTSSTSAISMVRQAPQGLEMWGDIIPIIGTNY 60
DB 20 QVQLQPGALVKGASVYLSCKASGYTFTSYMMHWKQRPGRLEWIGRIDPNSGTRY 79
QY 61 AOKFOGRVTITADSTAYMELSTLSEDTAVYCE-----LDMFYIWGGTMTVSS 114
DB 80 NEKFSKATLTIVDKSSATYMWELSLTSEDSAVYVCARYDYGSYFDYWGQGITLVSS 139

RESULT 13
HVS1 MOUSE STANDARD; PRT; 118 AA.
ID HVS1_MOUSE
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
OX NCBI_Taxid=10090;
RN (1)
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Boven J., Silevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";

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RL EMB0 J. 3:517-523(1984).
DR PIR: A02040; MEMS38.
DR HSSP: P01789; IMCP.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 58.8%; Score 351; DB 1; Length 118;
Best Local Similarity 57.6%; Pred. No. 5.2e-29;
Matches 68; Conservative 21; Mismatches 25; Indels 4; Gaps 1;

QY 1 QVQLVQSGAEVKKPGSSVKVSCKAASGTSSTSAISMVRQAPQGLEMWGDIIPIIGTNY 60
DB 1 EVQLQSGPELVKPGASVKISCKASGYTFTSYMMHWKQRPGRLEWIGRIDPNSGTRY 60
QY 61 AOKFOGRVTITADSTAYMELSTLSEDTAVYCE-----LDMFYIWGGTMTVSS 114
DB 61 NOKFKGKATLTIVDKSSATYMWELSLTSEDSAVYVCARYDYGSYFDYWGQGITLVSS 118

RESULT 14
HVS1 HUMAN STANDARD; PRT; 124 AA.
ID HVS1_HUMAN
AC P01761;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
OX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE.
RX MEDLINE=82046599; PubMed=7028111;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of heavy chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5822-5830(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR: A02044; MHUS1.
DR HSSP: P01825; 7FAB.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KM Immunoglobulin V region; Pyroliidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE
FT MOD_RES 1 1 PYROLIIDONE CARBOXYLIC ACID.
FT NON TER 124 124
SQ SEQUENCE 124 AA; 13732 MW; 62CEDA573BDE59F CRC64;

Query Match 58.0%; Score 346; DB 1; Length 124;
Best Local Similarity 56.2%; Pred. No. 1.8e-28;
Matches 72; Conservative 12; Mismatches 24; Indels 20; Gaps 3;

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DR EMBL: J00493; AAA38128.1; -
DR PIR: A94264; HVMG57.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Hybridoma; Signal.
FT CHAIN 1 19
FT DOMAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT NON TER 20 139 IG-LIKE.
FT SEQUENCE 140 AA; 15514 MW; 25A4CB831DA5CE8 CRC64;

Query Match 60.7%; Score 362.5; DB 1; Length 140;
Best Local Similarity 58.7%; Pred. No. 4.2e-30;
Matches 71; Conservative 21; Mismatches 22; Indels 7; Gaps 1;

QY 1 QVQVQSGAEVKKKPGSSVVKVSCKASGCTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY 60
DB 20 EVQLQSGAEVLRAGSSVVKVSCKASGCTFTTSYGINWVKRPGQGLEWIGYINPGNGYIN 79
QY 61 AQKQGRVITLADSTSTAYMELSTLTSEDTAVYVCEDMFWY-----IMGQITMTVSS 113
DB 80 NEKFKGKTLTVDKSSATYVQLRSLTSEDSAVYFCARSHYGGSYDPDWGQGTTLTVSS 139
QY 114 S 114
DB 140 S 140

RESULT 10
HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8313846; Pubmed=6186498;
RA Stekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiootype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT. JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP: P01789; IMCP.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON TER 120 120
SO SEQUENCE 120 AA; 13307 MW; FF0464A167B654AF CRC64;

Query Match 59.7%; Score 356.5; DB 1; Length 120;
Best Local Similarity 58.3%; Pred. No. 1.4e-29;
Matches 70; Conservative 20; Mismatches 23; Indels 7; Gaps 1;

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QY 2 VOLVQSGAEVKKKPGSSVVKVSCKASGCTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNYA 61
DB 1 VOLQSGAEVLRAGSSVVKVSCKASGCTFTTSYGINWVKRPGQGLEWIGYINPGNGYIN 60
QY 62 QKQGRVITLADSTSTAYMELSTLTSEDTAVYVCEDMFWY-----IMGQITMTVSS 114
DB 61 EKFKGKTLTVDKSSATYVQLRSLTSEDSAVYFCARSHYGGSYDPDWGQGTTLTVSS 120

RESULT 11
HV50_MOUSE STANDARD; PRT; 120 AA.
ID HV50_MOUSE
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; Pubmed=6201362;
RA Dildrop R., Bovens J., Stekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes";
RL EMBL J. 3:517-523(1984).
DR PIR: A02037; MEMS15.
DR HSSP: P01810; 2FBJ.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 120 120
SO SEQUENCE 120 AA; 13311 MW; 914453F426F09634 CRC64;

Query Match 59.1%; Score 353; DB 1; Length 120;
Best Local Similarity 58.3%; Pred. No. 3.3e-29;
Matches 70; Conservative 19; Mismatches 25; Indels 6; Gaps 2;

QY 1 QVQVQSGAEVKKKPGSSVVKVSCKASGCTFSSHAISWVRQAPGQGLEWMGDIIPILGTGNY 60
DB 1 QVQLPGELVLRAGSSVVKVSCKASGCTFTTSYGMHVRKPGQGLEWIGYINPGNGYIN 60
QY 61 AQKQGRVITLADSTSTAYMELSTLTSEDTAVYVCEDMFWY-----BLD-WFYWGQITMTVSS 114
DB 61 NEKFKGKTLTVDKSSATYVQLRSLTSEDSAVYFCARSHYGGSYDPDWGQGTTLTVSS 120

RESULT 12
HV07_MOUSE STANDARD; PRT; 139 AA.
ID HV07_MOUSE
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;

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Best Local Similarity 67.5%; Pred. No. 7.2e-31;  
Matches 77; Conservative 13; Mismatches 20; Indels 4; Gaps 1;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;

RP SEQUENCE  
RX MEDLINE=60078170; PubMed=6765983;  
RA Schilling J., Clevinger B., Davie J.M., Hood L.;  
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA  
rearrangements in heavy chain V-region gene segments.";  
RL Nature 283:35-40(1980).

CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO  
BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF  
WHICH OCCUR IN THE D AND J SEGMENTS.  
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.  
CC PIR: A26242; MEMSJS.  
DR HSP; P01789; IMCP.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; IG; 1.  
DR SMART: SM00406; IG; 1.  
DR PROSITE: PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.

FM DOMAIN 1 116 IG-LIKE.  
FT DISULFID 22 96 BY SIMILARITY.  
FT NON TER 117 117  
FT SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 60.9%; Score 363.5; DB 1; Length 117;  
Best Local Similarity 59.0%; Pred. No. 2.7e-30;  
Matches 69; Conservative 24; Mismatches 21; Indels 3; Gaps 2;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;

RP SEQUENCE FROM N.A.  
RC STRAIN=A/J;  
RX MEDLINE=82152818; PubMed=6801765;  
RA Sline J., Rabbitts T.H., Estees P., Slaughter C., Tucker P.W.,  
RA Capra J.D.;  
RT "Somatic mutation in genes for the variable portion of the  
immunoglobulin heavy chain.";  
RL Science 216:309-311(1982).

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

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Best Local Similarity 67.5%; Pred. No. 7.2e-31;  
Matches 77; Conservative 13; Mismatches 20; Indels 4; Gaps 1;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;

RP SEQUENCE  
RX MEDLINE=60078170; PubMed=6765983;  
RA Schilling J., Clevinger B., Davie J.M., Hood L.;  
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA  
rearrangements in heavy chain V-region gene segments.";  
RL Nature 283:35-40(1980).

CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO  
BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF  
WHICH OCCUR IN THE D AND J SEGMENTS.  
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.  
CC PIR: A26242; MEMSJS.  
DR HSP; P01789; IMCP.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; IG; 1.  
DR SMART: SM00406; IG; 1.  
DR PROSITE: PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.

FM DOMAIN 1 116 IG-LIKE.  
FT DISULFID 22 96 BY SIMILARITY.  
FT NON TER 117 117  
FT SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 60.9%; Score 363.5; DB 1; Length 117;  
Best Local Similarity 59.0%; Pred. No. 2.7e-30;  
Matches 69; Conservative 24; Mismatches 21; Indels 3; Gaps 2;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;

RP SEQUENCE FROM N.A.  
RC STRAIN=A/J;  
RX MEDLINE=82152818; PubMed=6801765;  
RA Sline J., Rabbitts T.H., Estees P., Slaughter C., Tucker P.W.,  
RA Capra J.D.;  
RT "Somatic mutation in genes for the variable portion of the  
immunoglobulin heavy chain.";  
RL Science 216:309-311(1982).

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

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EMBL, X07448, -; NOT\_ANNOTATED\_CDS.

DR PIR, S00476; HYH035.

DR HSSP, P01772; 2FB4.

DR GO, GO:0005576; C:extracellular; NAS.

DR GO, GO:0003823; P:antigen binding activity; NAS.

DR GO, GO:0006955; P:immune response; NAS.

DR InterPro, IPR007110; IG-Like.

DR InterPro, IPR003006; IG\_MHC.

DR Pfam, PF00047; Ig\_1.

DR SMART, SM00406; IGV, 1.

DR PROSITE, PS50835; IG\_Like; 1.

IMMUNOGLOBULIN V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.

FT DOMAIN 20 >117 IG-LIKE.

FT NON\_TER 117 117

SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match 62.1%; Score 371; DB 1; Length 117;

Best Local Similarity 77.1%; Pred. No. 4, 7e-31;

Matches 74; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPGSSVKVSCKASGCTFSSHAISWRVQAPGQGLEWMGDIPIILGTNY 60  
DB 20 QVQLVQSGAEVKKPGASVVSCKASGCTFTGYMHVRVQAPGQGLEWMGRINPNSGTTY 79

QY 61 AAKFGQRTVTADSTAYMELSTLTSEDTAVYYC 96  
DB 80 AAKFGQRTVTADSTAYMELSTLTSEDTAVYYC 115

RESULT 5  
HYVC\_HUMAN STANDARD; PRT; 147 AA.

AC P01741; 21-JUL-1986 (Rel. 01, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DR Ig heavy chain V-I region NP precursor (Fragments).

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

[1]

RP SEQUENCE FROM N.A.

RA MEDLINE=83065234; PubMed=6815656;

RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,

RA Bell L.O., Gould H.J.;

RT "Cloning and sequence determination of the gene for the human

RT immunoglobulin epsilon chain expressed in a myeloma cell line.";

RT Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665 (1982).

RN [2]

SEQUENCE OF 20-147.

RA Benlich H.H., Johanson S.G.O., von Bahr-Lindstrom H.;

RA (in) Bach M.K. (eds.);

RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,

RL Marcel Dekker, New York (1978).

-1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA

PROTEIN.

-1- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC HSSP, P01789; IMCP.

DR GO, GO:0005576; C:extracellular; NAS.

DR GO, GO:0003823; P:antigen binding activity; NAS.

DR GO, GO:0006955; P:immune response; NAS.

DR InterPro, IPR007110; IG-Like.

DR InterPro, IPR003006; IG\_MHC.

DR InterPro, IPR003596; IG\_V.

DR Pfam, PF00047; Ig; 1.

DR SMART, SM00406; IGV, 1.

DR PROSITE, PS50835; IG\_Like; 1.

KW Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.

FT SIGNAL 1 19

FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.

FT DOMAIN 20 131 IG-LIKE.

FT MOD\_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.

FT DISULFID 41 115

FT CONFLICT 21 21 T -> V (IN REF. 2).

FT CONFLICT 53 54 IH -> HI (IN REF. 2).

FT CONFLICT 67 68 VG -> GV (IN REF. 2).

FT CONFLICT 125 125 MISSING (IN REF. 2).

FT NON\_TER 147 147

SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 62.1%; Score 371; DB 1; Length 147;

Best Local Similarity 59.4%; Pred. No. 6e-31; 24; Indels 14; Gaps 2;

Matches 76; Conservative 14; Mismatches 24; Indels 14; Gaps 2;

QY 1 QVQLVQSGAEVKKPGSSVKVSCKASGCTFSSHAISWRVQAPGQGLEWMGDIPIILGTNY 60  
DB 20 QVQLVQSGAEVKKPGASVVSCKASGCTFTGYMHVRVQAPGQGLEWMGRINPNSGTTY 79

QY 61 AAKFGQRTVTADSTAYMELSTLTSEDTAVYYC-----ELDMFY---IMQ 106  
DB 80 AAKFGQRTVTADSTAYMELSTLTSEDTAVYYC-----ELDMFY---IMQ 139

RESULT 6  
HV00\_MOUSE STANDARD; PRT; 114 AA.

AC P01741; 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DR Ig heavy chain V region (Anti-arsenate antibody).

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

[1]

RP SEQUENCE.

RA STRAIN=A/J;

RA MEDLINE=79195438; PubMed=109536;

RA Capra J.D., Niseno A.;

RT "Structural studies on induced antibodies with defined idiotypic

RT specificities. VII. The complete amino acid sequence of the heavy

RT chain variable region of anti-p-azophenylarsenate antibodies from A/J

RT mice bearing a cross-reactive idiotype.";

RT J. Immunol. 123:279-284 (1979).

RT -1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF

CC THE IG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V

REGION SEQUENCE

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC PIR, A02022; GIMSA.

DR HSSP, P01772; 2FB4.

DR InterPro, IPR007110; IG-Like.

DR InterPro, IPR003006; IG\_MHC.

DR InterPro, IPR003596; IG\_V.

DR Pfam, PF00047; IGV, 1.

DR SMART, SM00406; IGV, 1.

DR PROSITE, PS50835; IG\_Like; 1.

IMMUNOGLOBULIN V region.

FT DOMAIN 1 106 IG-LIKE.

FT NON\_TER 114 114

SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A69F4BE CRC64;

Query Match 61.8%; Score 369; DB 1; Length 114;

QY 61 AOKFOGRTITADESTAYMELSTLTSDETAIVYCCEDLWFIYWG-----OGTMVTSS 114  
 DB 61 AOKFOGRTITADESTAYMELSSLRSDTAIFYC-AGGYGIVYBPBEKNGSLVTSS 117

## RESULT 2

HV1B\_HUMAN STANDARD; PRT; 117 AA.  
 ID HV1B\_HUMAN  
 AC P01743;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-I region H03 precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_Taxid=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83144028; PubMed=6298778;  
 RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;  
 RT "Evolutionary aspects of immunoglobulin heavy chain variable region  
 (VH) gene subgroups.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC -----  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; J00240; AAMS2988.1; -  
 DR PIR; A02024; HVH0HG.  
 DR HSSP; P01772; 2PB4.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; P:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION H03.  
 FT DOMAIN 20 >117 IG-LIKE.  
 FT NON TER 117  
 FT SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1EF7 CRC64;  
 Query Match 64.5%; Score 385; DB 1; Length 117;  
 Best Local Similarity 79.2%; Pred. No. 1,7e-32;  
 Matches 76; Conservative 8; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 OVQLVSGAEVKKPKSSVYKSCAKSGTSSHAISWVROAPGQGLWMDIIPILGTGNY 60  
 DB 20 OVQLVSGAEVKKPKSSVYKSCAKSGTSSHAISWVROAPGQGLWMDIIPILGTGNY 79  
 QY 61 AOKFOGRTITADESTAYMELSTLTSDETAIVYCC 96  
 DB 80 AOKFOGRTITADESTAYMELSSLRSDTAIFYC 115

## RESULT 3

HV4B\_MOUSE STANDARD; PRT; 138 AA.  
 ID HV4B\_MOUSE  
 AC P03960;  
 DT 23-OCT-1986 (Rel. 02, Created)  
 DT 23-OCT-1986 (Rel. 02, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region TEPC 1017 precursor.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_Taxid=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84248078; PubMed=6429663;  
 RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Muehlinke J.F.,  
 RA Tucker P.W.;  
 RT "Illegitimate recombination generates a class switch from C mu to C  
 delta in an Igd-secreting plasmacytoma.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).  
 RL PIR; A02033; HVMS7.  
 DR HSSP; P01810; 2PBJ.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.  
 FT DOMAIN 21 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 128 138 FRAMEWORK-4.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON TER 138  
 FT SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 62.6%; Score 373.5; DB 1; Length 138;  
 Best Local Similarity 58.8%; Pred. No. 3.1e-31;  
 Matches 70; Conservative 21; Mismatches 23; Indels 5; Gaps 1;

QY 1 OVQLVSGAEVKKPKSSVYKSCAKSGTSSHAISWVROAPGQGLWMDIIPILGTGNY 60  
 DB 20 OVQLVSGAEVKKPKSSVYKSCAKSGTSSHAISWVROAPGQGLWMDIIPILGTGNY 79  
 QY 61 AOKFOGRTITADESTAYMELSTLTSDETAIVYCC-----LDWFIYWGQTMVTSS 114  
 DB 80 NEKFGKATLVDSKSSAYMQLSLTPEFAVYCCASDGYDVFYWGQTLVTFSA 138

## RESULT 4

HV1G\_HUMAN STANDARD; PRT; 117 AA.  
 ID HV1G\_HUMAN  
 AC P23083;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-I region V35 precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_Taxid=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88296408; PubMed=2841108;  
 RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,  
 RA Ohno H., Fukuhara S., Honjo T.;  
 RT "Dispersed localization of D segments in the human immunoglobulin  
 heavy-chain locus.";  
 RL EMBO J. 7:1047-1051(1988).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC -----  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 6.1121 Seconds

(Without alignment)  
877.119 Million cell updates/sec

Title: US-09-674-752-51

Perfect score: 597

Sequence: 1 QVQLVDSGAEVKKPGSSVKV.....YCELMFRTMGCTMTYSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 430.5 | 72.1        | 117    | 1  | HV1A_HUMAN  |
| 2          | 385   | 64.5        | 117    | 1  | HV1B_HUMAN  |
| 3          | 373.5 | 62.6        | 138    | 1  | HV48_MOUSE  |
| 4          | 371   | 62.1        | 117    | 1  | HV1G_HUMAN  |
| 5          | 371   | 62.1        | 147    | 1  | HV1C_HUMAN  |
| 6          | 369   | 61.8        | 114    | 1  | HV00_MOUSE  |
| 7          | 367.5 | 61.6        | 117    | 1  | HV12_MOUSE  |
| 8          | 363.5 | 60.9        | 117    | 1  | HV13_MOUSE  |
| 9          | 362.5 | 60.7        | 140    | 1  | HV02_MOUSE  |
| 10         | 356.5 | 59.7        | 120    | 1  | HV03_MOUSE  |
| 11         | 353   | 59.1        | 120    | 1  | HV50_MOUSE  |
| 12         | 352   | 59.0        | 139    | 1  | HV07_MOUSE  |
| 13         | 351   | 58.8        | 118    | 1  | HV51_MOUSE  |
| 14         | 346   | 58.0        | 124    | 1  | HV1E_HUMAN  |
| 15         | 345.5 | 57.9        | 121    | 1  | HV01_MOUSE  |
| 16         | 342   | 57.3        | 137    | 1  | HV11_MOUSE  |
| 17         | 334.5 | 56.0        | 125    | 1  | HV1P_HUMAN  |
| 18         | 333   | 55.8        | 124    | 1  | HV1D_HUMAN  |
| 19         | 331   | 55.4        | 117    | 1  | HV06_MOUSE  |
| 20         | 326   | 54.6        | 117    | 1  | HV05_MOUSE  |
| 21         | 326   | 54.6        | 117    | 1  | HV52_MOUSE  |
| 22         | 316.5 | 53.0        | 117    | 1  | HV04_MOUSE  |
| 23         | 316.5 | 53.0        | 116    | 1  | HV15_MOUSE  |
| 24         | 315   | 52.8        | 114    | 1  | HV3B_HUMAN  |
| 25         | 312   | 52.3        | 117    | 1  | HV09_MOUSE  |
| 26         | 312   | 52.3        | 117    | 1  | HV49_MOUSE  |
| 27         | 309   | 51.8        | 117    | 1  | HV14_MOUSE  |
| 28         | 304   | 50.9        | 112    | 1  | HV10_MOUSE  |
| 29         | 299   | 50.1        | 122    | 1  | HV3G_HUMAN  |
| 30         | 298   | 49.9        | 119    | 1  | HV40_MOUSE  |
| 31         | 295.5 | 49.5        | 119    | 1  | HV31_HUMAN  |
| 32         | 295   | 49.4        | 119    | 1  | HV37_MOUSE  |
| 33         | 294   | 49.2        | 119    | 1  | HV38_MOUSE  |

|    |       |      |     |   |            |                    |
|----|-------|------|-----|---|------------|--------------------|
| 34 | 293.5 | 49.2 | 115 | 1 | HV3D_HUMAN | P01765 homo sapien |
| 35 | 292   | 48.9 | 114 | 1 | HV01_CANFA | P01784 canis fam1  |
| 36 | 291.5 | 48.8 | 121 | 1 | HV3J_HUMAN | P01771 homo sapien |
| 37 | 291.5 | 48.8 | 142 | 1 | HV01_RAT   | P01805 rattus norv |
| 38 | 289   | 48.4 | 120 | 1 | HV1H_HUMAN | P04421 homo sapien |
| 39 | 286   | 47.9 | 119 | 1 | HV3P_HUMAN | P01777 homo sapien |
| 40 | 285.5 | 47.8 | 117 | 1 | HV42_MOUSE | P01812 mus musculu |
| 41 | 284.5 | 47.7 | 117 | 1 | HV41_MOUSE | P01811 mus musculu |
| 42 | 284   | 47.6 | 122 | 1 | HV3H_HUMAN | P01769 homo sapien |
| 43 | 283.5 | 47.5 | 115 | 1 | HV3J_MOUSE | P01801 mus musculu |
| 44 | 283.5 | 47.5 | 115 | 1 | HV3F_HUMAN | P01767 homo sapien |
| 45 | 283.5 | 47.5 | 117 | 1 | HV02_CANFA | P01785 canis fam1  |

## ALIGNMENTS

### RESULT 1

ID HV1A\_HUMAN STANDARD; PRT; 117 AA.

AC P01742;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V-I region EU.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxId=9606;

RN [1]

RP SEQUENCE.

RA MEDLINE=71064024; PubMed=5489771;

RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,

RA Maxdel M.J., Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino

acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";

RL Biochemistry 9:3161-3170(1970).

RN [2]

RP DISULFIDE BOND.

RX MEDLINE=71064027; PubMed=4923144;

RA "The covalent structure of a human gamma G-immunoglobulin. X.

RT Intrachain disulfide bonds.";

RL Biochemistry 9:3188-3196(1970).

CC -I- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS

MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.

CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR, A90563; GHEU.

DR HSSP; P01772; 2F84.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; P:antigen binding activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR003106; Ig\_1Ike.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_V.

DR Pfam; PF00047; Ig\_1.

DR SMART; SM00406; IGV\_1.

DR PROSITE; PS50835; IG\_LIKE; 1.

KW Immunoglobulin V region; Pyroglutamate carboxylic acid.

FT DOMAIN 1 112 IG-LIKE.

FT MOD\_RES 1 1 PYROLIDONE CARBOXYLIC ACID.

FT NON\_TER 22 96

FT SEQUENCE 117 AA; 12472 MW; 99060ADAEED52818 CRC64;

Query Match 72.1%; Score 430.5; DB 1; Length 117;

Best Local Similarity 75.4%; Pred. No. 4e-37;

Matches 89; Conservative 8; Mismatches 16; Indels 5; Gaps 2;

QY 1 QVQLVDSGAEVKKPGSSVKASGTFSSNAISVVRQAPGQGLEPMGDIPIIGTGY 60

DB 1 QVQLVDSGAEVKKPGSSVKASGTFSSNAISVVRQAPGQGLEPMGDIPIIGTGY 60





Db 61 AOKFGQRTVITADKSTAYMELSLRSEDTAVYCAKAGNDIYWGSTRSDAFDIWGQ 120

QY 107 GTMTVTSS 114  
:|||||  
Db 121 GTMTVTSS 128

RESULT 6  
C33548  
Ig heavy chain V-1 region (783) - human

C/Species: Homo sapiens (man)

C/Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996

C/Accession: C33548

R/Klpps, T.J.; Tomhave, E.; Pratt, L.F.; Duffly, S.; Chen, P.P.; Carson, D.A.

Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989

A/Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr

A/Reference number: A33548; MUID:8935575; PMID:2503826

A/Accession: C33548

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A/Molecule type: DNA

A/Residues: 1-133 <RIP>

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 504.5; DB 2; Length 133;

Best Local Similarity 76.7%; Pred. No. 1.4e-38;

Matches 102; Conservative 5; Mismatches 7; Indels 19; Gaps 2;

QY 1 QVQLVQSGAEVKKPKSSVKVSCKASGCTFSSHAISWVRQAPQGLEWMDIPIILGTGNY 60  
1 QVQLVQSGAEVKKPKSSVKVSCKASGCTFSSVAISWVRQAPQGLEWMDIPIFGTANY 60  
Db 1 QVQLVQSGAEVKKPKSSVKVSCKASGCTFSSVAISWVRQAPQGLEWMDIPIFGTANY 60  
QY 61 AOKFGQRTVITADESTAYMELSLRSEDTAVYCAKAGILGIPYSSGWPNSDYIYCGM 120  
:|||||  
Db 61 AOKFGQRTVITADESTAYMELSLRSEDTAVYCAKAGILGIPYSSGWPNSDYIYCGM 120

QY 103 -IWGGTMTVTSS 114  
:|||||  
Db 121 DVMGGGTTVTSS 133

RESULT 7  
S14683

Ig mu chain precursor, membrane-bound (clone 201) - human

C/Species: Homo sapiens (man)

C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999

C/Accession: S14683; S08047

R/Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.

Nucleic Acids Res. 18, 4278, 1990

A/Title: Complete nucleotide sequence of the membrane form of the human Igm heavy chain.

A/Reference number: S14683; MUID:90332450; PMID:2115996

A/Accession: S14683

A/Molecule type: mRNA

A/Residues: 1-627 <FRI>

A/Cross-references: EMBL:X17115; NID:933450; PIDN:CAA34971.1; PID:933451

C/Suprafamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: immunoglobulin, membrane protein

F/15-627/Domain: signal sequence #status predicted <SIG>

F/16-627/Product: Ig mu chain #status predicted <NAT>

F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 504.5; DB 2; Length 627;

Best Local Similarity 76.7%; Pred. No. 6.6e-38;

Matches 102; Conservative 5; Mismatches 7; Indels 19; Gaps 2;

QY 1 QVQLVQSGAEVKKPKSSVKVSCKASGCTFSSHAISWVRQAPQGLEWMDIPIILGTGNY 60  
1 QVQLVQSGAEVKKPKSSVKVSCKASGCTFSSVAISWVRQAPQGLEWMDIPIFGTANY 79  
Db 20 QVQLVQSGAEVKKPKSSVKVSCKASGCTFSSVAISWVRQAPQGLEWMDIPIFGTANY 79  
QY 61 AOKFGQRTVITADESTAYMELSLRSEDTAVYCAKAGILGIPYSSGWPNSDYIYCGM 102  
:|||||

Db 80 AOKFGQRTVITADESTAYMELSLRSEDTAVYCAKAGILGIPYSSGWPNSDYIYCGM 139

QY 103 -IWGGTMTVTSS 114  
:|||||  
Db 140 DVMGGGTTVTSS 152

RESULT 8  
PH0953  
Ig heavy chain V region (G6+ CLU-SIC) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

C/Accession: PH0953

R/Martin, T.; Duffly, S.F.; Carson, D.A.; Klpps, T.J.

J. Exp. Med. 175, 983-991, 1992

A/Title: Evidence for somatic selection of natural autoantibodies.

A/Reference number: PH0953; MUID:92202880; PMID:1552291

A/Accession: PH0953

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-135 <MAR>

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-30/Region: framework 1

F/15-98/Domain: immunoglobulin homology <IMM>

F/31-35/Region: complementarity-determining 1

F/36-50/Region: complementarity-determining 2

F/51-67/Region: complementarity-determining 3

F/68-98/Region: framework 3

F/99-123/Region: complementarity-determining 3

Query Match 84.3%; Score 503.5; DB 2; Length 135;

Best Local Similarity 77.8%; Pred. No. 1.8e-38;

Matches 105; Conservative 2; Mismatches 7; Indels 21; Gaps 2;

QY 1 QVQLVQSGAEVKKPKSSVKVSCKASGCTFSSHAISWVRQAPQGLEWMDIPIILGTGNY 60  
1 QVQLVQSGAEVKKPKSSVKVSCKASGCTFSSVAISWVRQAPQGLEWMDIPIFGTANY 60  
Db 1 QVQLVQSGAEVKKPKSSVKVSCKASGCTFSSVAISWVRQAPQGLEWMDIPIFGTANY 60  
QY 61 AOKFGQRTVITADESTAYMELSLRSEDTAVYCAKAGILGIPYSSGWPNSDYIYCGM 99  
:|||||  
Db 61 AOKFGQRTVITADESTAYMELSLRSEDTAVYCAKAGILGIPYSSGWPNSDYIYCGM 120

QY 100 WFIWGGTMTVTSS 114  
:|||||  
Db 121 AFDIMGPGTMTVTSS 135

RESULT 9  
S46394  
Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000

C/Accession: S46394

R/Figini, M.; Marke, J.D.; Winter, G.; Griffiths, A.D.

J. Mol. Biol. 239, 68-78, 1994

A/Title: In vitro assembly of repertoire of antibody chains on the surface of phage by

A/Reference number: S46394; MUID:94254092; PMID:8196048

A/Accession: S46394

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-132 <FIG>

A/Cross-references: EMBL:Z31681; NID:9509788; PIDN:CAA83486.1; PID:91335147

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 502; DB 2; Length 132;

Best Local Similarity 77.3%; Pred. No. 2.4e-38;

Matches 102; Conservative 7; Mismatches 5; Indels 18; Gaps 3;

QY 1 QVQLVQSGAEVKKPKSSVKVSCKASGCTFSSHAISWVRQAPQGLEWMDIPIILGTGNY 60  
1 QVQLVQSGAEVKKPKSSVKVSCKASGCTFSSVAISWVRQAPQGLEWMDIPIFGTANY 60  
Db 20 QVQLVQSGAEVKKPKSSVKVSCKASGCTFSSVAISWVRQAPQGLEWMDIPIFGTANY 79  
QY 61 AOKFGQRTVITADESTAYMELSLRSEDTAVYCAKAGILGIPYSSGWPNSDYIYCGM 102  
:|||||

C/Keywords: heterotetramer; immunoglobulin  
F:1-30/Region: framework 1  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:36-50/Region: framework 2  
F:51-67/Region: complementarity-determining 2  
F:68-98/Region: framework 3  
F:99-107/Region: complementarity-determining 3

Query Match 86.0%; Score 513.5; DB 2; Length 119;  
Best Local Similarity 84.9%; Pred. No. 1.9e-39;  
Matches 101; Conservative 5; Mismatches 8; Indels 5; Gaps 1;

1 OVOLVSGAEVKKPGSSSVKVCCKASGGTFSSHAISWVQAPOGGLBWMGDIIPILGTGNY 60  
1 OVOLVSGAEVKKPGSSSVKVCCKASGGTFSSHAISWVQAPOGGLBWMGDIIPILGTANY 60  
1 OVOLVSGAEVKKPGSSSVKVCCKASGGTFSSHAISWVQAPOGGLBWMGDIIPILGTANY 60  
61 AOKFGGRVTITADESTSTAYMELSTLTSEDTAVYYC-----IMGGITWTVSS 114  
61 AOKFGGRVTITADESTSTAYMELSTLTSEDTAVYYCARGYVYGGMDVWGQTTVTWSS 119

Db 61 AOKFGGRVTITADESTSTAYMELSTLTSEDTAVYYCARGYVYGGMDVWGQTTVTWSS 119

RESULT 3  
PH0957  
Ig heavy chain V region (G6+ CLL-BRA) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C/Accession: PH0957  
R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A/Title: Evidence for somatic selection of natural autoantibodies.  
A/Reference number: PH0952; MUID:92202880; PMID:1552291  
A/Accession: PH0957  
A/Status: nucleic acid sequence not shown  
A/Molecule type: DNA  
A/Residues: 1-125 <MAR>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:1-30/Region: framework 1  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:36-50/Region: framework 2  
F:51-67/Region: complementarity-determining 2  
F:68-98/Region: framework 3  
F:99-113/Region: complementarity-determining 3

Query Match 85.5%; Score 510.5; DB 2; Length 125;  
Best Local Similarity 80.8%; Pred. No. 3.8e-39;  
Matches 101; Conservative 5; Mismatches 8; Indels 11; Gaps 1;

1 OVOLVSGAEVKKPGSSSVKVCCKASGGTFSSHAISWVQAPOGGLBWMGDIIPILGTGNY 60  
1 OVOLVSGAEVKKPGSSSVKVCCKASGGTFSSHAISWVQAPOGGLBWMGDIIPILGTANY 60  
61 AOKFGGRVTITADESTSTAYMELSTLTSEDTAVYYC-----PFYIWGQTM 109  
61 AOKFGGRVTITADESTSTAYMELSTLTSEDTAVYYC-----PFYIWGQTM 120

Db 61 AOKFGGRVTITADESTSTAYMELSTLTSEDTAVYYC-----PFYIWGQTM 120

Qy 110 TVWSS 114  
111  
112  
121 VTWSS 125

Db 121 VTWSS 125

RESULT 4  
A33548  
Ig heavy chain V-1 region (NEI) - human  
C/Species: Homo sapiens (man)  
C/Date: 17-Jan-1990 #sequence\_revision 17-Jan-1990 #text\_change 16-Aug-1996  
C/Accession: A33548; PH0956  
R/Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.  
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989  
A/Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr  
A/Reference number: A33548; MUID:89345575; PMID:2503826

A/Accession: A33548  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-129 <RIP>  
R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A/Title: Evidence for somatic selection of natural autoantibodies.  
A/Reference number: PH0952; MUID:92202880; PMID:1552291  
A/Accession: PH0956  
A/Status: nucleic acid sequence not shown  
A/Molecule type: DNA  
A/Residues: 1-129 <MAR>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:1-30/Region: framework 1  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:36-50/Region: framework 2  
F:51-67/Region: complementarity-determining 2  
F:68-98/Region: framework 3  
F:99-117/Region: complementarity-determining 3

Query Match 85.2%; Score 508.5; DB 2; Length 129;  
Best Local Similarity 79.8%; Pred. No. 6e-39;  
Matches 103; Conservative 3; Mismatches 8; Indels 15; Gaps 1;

1 OVOLVSGAEVKKPGSSSVKVCCKASGGTFSSHAISWVQAPOGGLBWMGDIIPILGTGNY 60  
1 OVOLVSGAEVKKPGSSSVKVCCKASGGTFSSHAISWVQAPOGGLBWMGDIIPILGTANY 60  
1 OVOLVSGAEVKKPGSSSVKVCCKASGGTFSSHAISWVQAPOGGLBWMGDIIPILGTANY 60  
61 AOKFGGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDWFIYWG 105  
61 AOKFGGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDWFIYWG 120

Db 61 AOKFGGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDWFIYWG 120

Qy 106 QGTWTVSS 114  
111  
112  
121 QGTWTVSS 129

Db 121 QGTWTVSS 129

RESULT 5  
PH0952  
Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
C/Accession: PH0952  
R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.  
J. Exp. Med. 175, 983-991, 1992  
A/Title: Evidence for somatic selection of natural autoantibodies.  
A/Reference number: PH0952; MUID:92202880; PMID:1552291  
A/Accession: PH0952  
A/Status: nucleic acid sequence not shown  
A/Molecule type: DNA  
A/Residues: 1-128 <MAR>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:1-30/Region: framework 1  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:36-50/Region: framework 2  
F:51-67/Region: complementarity-determining 2  
F:68-98/Region: framework 3  
F:99-116/Region: complementarity-determining 3

Query Match 84.9%; Score 507; DB 2; Length 128;  
Best Local Similarity 80.5%; Pred. No. 8.1e-39;  
Matches 103; Conservative 3; Mismatches 8; Indels 14; Gaps 1;

1 OVOLVSGAEVKKPGSSSVKVCCKASGGTFSSHAISWVQAPOGGLBWMGDIIPILGTGNY 60  
1 OVOLVSGAEVKKPGSSSVKVCCKASGGTFSSHAISWVQAPOGGLBWMGDIIPILGTANY 60  
1 OVOLVSGAEVKKPGSSSVKVCCKASGGTFSSHAISWVQAPOGGLBWMGDIIPILGTANY 60  
61 AOKFGGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDWFIYWG 106  
61 AOKFGGRVTITADESTSTAYMELSTLTSEDTAVYYC-----ELDWFIYWG 120

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 ; Search time 10.9277 Seconds  
(without alignments)  
1003.251 Million cell updates/sec

Title: US-09-674-752-51

Perfect score: 597  
Sequence: 1 QVQLVQSGAEVKKPGSSSVKRV.....YCELDMPYIMGGTMTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:.\*  
1: p1r1:.\*  
2: p1r2:.\*  
3: p1r3:.\*  
4: p1r4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 516   | 86.4        | 116    | 2 PH0959 | Ig heavy chain V r |
| 2          | 513.5 | 86.0        | 119    | 2 PH0961 | Ig heavy chain V r |
| 3          | 510.5 | 85.5        | 125    | 2 PH0957 | Ig heavy chain V r |
| 4          | 508.5 | 85.2        | 129    | 2 A33548 | Ig heavy chain V-1 |
| 5          | 507   | 84.9        | 128    | 2 PH0952 | Ig heavy chain V r |
| 6          | 504.5 | 84.5        | 133    | 2 C33548 | Ig heavy chain V-1 |
| 7          | 504.5 | 84.5        | 627    | 2 S14683 | Ig mu chain precut |
| 8          | 503.5 | 84.3        | 135    | 2 PH0953 | Ig heavy chain V r |
| 9          | 502   | 84.1        | 132    | 2 S46394 | Ig heavy chain V r |
| 10         | 501   | 83.9        | 120    | 2 PH0962 | Ig heavy chain V r |
| 11         | 501   | 83.9        | 132    | 2 PH0954 | Ig heavy chain V r |
| 12         | 498   | 83.4        | 122    | 2 PH0958 | Ig heavy chain V r |
| 13         | 495.5 | 83.0        | 127    | 2 PH0955 | Ig heavy chain V r |
| 14         | 493   | 82.6        | 126    | 2 B33548 | Ig heavy chain V-1 |
| 15         | 493   | 82.6        | 136    | 2 PH0960 | Ig heavy chain V r |
| 16         | 472   | 79.1        | 135    | 2 B32274 | Ig heavy chain V r |
| 17         | 465   | 77.9        | 116    | 2 S36261 | Ig heavy chain V r |
| 18         | 462   | 77.4        | 98     | 2 S26915 | Ig heavy chain V r |
| 19         | 462   | 77.4        | 116    | 2 S31698 | Ig heavy chain pre |
| 20         | 462   | 77.4        | 123    | 2 S44108 | Ig heavy chain V-D |
| 21         | 458   | 76.7        | 98     | 2 S24680 | Ig heavy chain V1  |
| 22         | 457.5 | 76.6        | 113    | 2 PH1653 | Ig heavy chain V r |
| 23         | 456.5 | 76.5        | 109    | 2 PH1671 | Ig heavy chain V r |
| 24         | 454   | 76.0        | 108    | 2 PH1664 | Ig heavy chain V r |
| 25         | 453   | 75.9        | 119    | 2 S44106 | Ig heavy chain V-D |
| 26         | 451   | 75.5        | 98     | 2 S46463 | Ig heavy chain V1  |
| 27         | 443   | 74.2        | 97     | 2 PH0870 | Ig heavy chain V r |
| 28         | 438.5 | 73.5        | 121    | 2 A49590 | Ig heavy chain V r |
| 29         | 436   | 73.0        | 171    | 2 S23623 | Ig heavy chain V r |

|    |       |      |     |          |                    |
|----|-------|------|-----|----------|--------------------|
| 30 | 432.5 | 72.4 | 122 | 2 C49590 | Ig heavy chain V r |
| 31 | 432   | 72.4 | 118 | 2 S36265 | Ig heavy chain V r |
| 32 | 430.5 | 72.1 | 117 | 1 G1H9E  | Ig heavy chain V-1 |
| 33 | 428.5 | 71.8 | 122 | 2 B49590 | Ig heavy chain V r |
| 34 | 424   | 71.0 | 116 | 2 S31667 | Ig heavy chain V r |
| 35 | 422   | 70.7 | 136 | 2 S31600 | Ig heavy chain V r |
| 36 | 419.5 | 70.3 | 122 | 2 S36271 | Ig heavy chain V r |
| 37 | 418.5 | 70.1 | 123 | 2 D33548 | Ig heavy chain V-1 |
| 38 | 417.5 | 69.9 | 129 | 2 S36260 | Ig heavy chain V r |
| 39 | 416.5 | 69.8 | 142 | 2 A32483 | Ig heavy chain V r |
| 40 | 415   | 69.5 | 98  | 2 A30523 | Ig heavy chain V-1 |
| 41 | 415   | 69.5 | 135 | 2 S49510 | anti-Sm antibody V |
| 42 | 414   | 69.3 | 124 | 2 S19665 | Ig heavy chain V r |
| 43 | 407.5 | 68.3 | 129 | 2 S46393 | Ig heavy chain V r |
| 44 | 406   | 68.0 | 119 | 2 P49590 | Ig heavy chain V r |
| 45 | 399.5 | 66.9 | 160 | 2 PL0105 | anti-PR2 erythrocy |

## ALIGNMENTS

### RESULT 1

PH0959  
Ig heavy chain V region (G6+ T-L26) - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

C:Accession: PH0959  
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

A:Title: Evidence for somatic selection of natural autoantibodies.  
A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0959  
A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-116 <MAR>  
A:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1

F:36-50/Region: framework 2  
F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3  
F:99-104/Region: complementarity-determining 3

Query Match 86.4%; Score 516; DB 2; Length 116;  
Best Local Similarity 87.9%; Pred. No. 1,1e-39;

Matches 102; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 QVQLVQSGAEVKKPGSSSVKSCAKSGCTFSSHAISWVQAPOGLEWNGDIIPILGQNY 60  
DB 1 QVQLVQSGAEVKKPGSSSVKSCAKSGCTFSSVAISWVQAPOGLEWNGDIIPILGQNY 60

QY 61 AOKFGKRVITITDESTSTAYMELSTLTSEDTAVYICEL--DMFYWGQGTMTVSS 114  
DB 61 AOKFGKRVITITDESTSTAYMELSLRSDTAIVYCARGDWDFWGGQGTMTVSS 116

### RESULT 2

PH0961  
Ig heavy chain V region (G6+ T-L33) - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996

C:Accession: PH0961  
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

A:Title: Evidence for somatic selection of natural autoantibodies.  
A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0961  
A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-119 <MAR>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology





MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934.373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-07-934-373C-4

Query Match 67.4%; Score 443.5; DB 2; Length 120;  
Best Local Similarity 70.4%; Pred. No. 2.9e-37;  
Matches 88; Conservative 14; Mismatches 18; Indels 5; Gaps 2;

QY 1 EVOLVKSQGLVYKPGSGSLRLSCAAGFTFRRYDIHMVYRQTPKGLWVSSISGNGNYIDY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCAAGFTFSDIYAMSWVRQAPGKLEWAVISENSDITY 60

QY 61 ADSVKGRTISRDNANNVYLYQNNSLRAEDMAVYFCARDGTFGSAAATRAFDINGRTM 120  
DB 61 ADSVKGRTISRDDSKNTLYLYQNNSLRAEDTAIVYTCARDR---GCAVSY--FDVVGQGITL 115

QY 121 VTVSS 125  
DB 116 VTVSS 120

RESULT 14  
US-08-437-642B-4  
Sequence 4, Application US/08437642B  
Patent No. 6054297  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/437.642B  
FILING DATE: 09-May-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/934373  
FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-437-642B-4

Query Match 67.4%; Score 443.5; DB 3; Length 120;  
Best Local Similarity 70.4%; Pred. No. 2.9e-37;  
Matches 88; Conservative 14; Mismatches 18; Indels 5; Gaps 2;

QY 1 EVOLVKSQGLVYKPGSGSLRLSCAAGFTFRRYDIHMVYRQTPKGLWVSSISGNGNYIDY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCAAGFTFSDIYAMSWVRQAPGKLEWAVISENSDITY 60

QY 61 ADSVKGRTISRDNANNVYLYQNNSLRAEDMAVYFCARDGTFGSAAATRAFDINGRTM 120  
DB 61 ADSVKGRTISRDDSKNTLYLYQNNSLRAEDTAIVYTCARDR---GCAVSY--FDVVGQGITL 115

QY 121 VTVSS 125  
DB 116 VTVSS 120

RESULT 15  
US-08-146-206C-4  
Sequence 4, Application US/08146206C  
Patent No. 6407213  
GENERAL INFORMATION:  
APPLICANT: Carter, Paul J.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Method for Making Humanized Antibodies  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146.206C  
FILING DATE: 17-No. 6407213-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P1  
TELECOMMUNICATION INFORMATION:



```

? APPLICANT: Siegel, Donald L.
? TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY
? TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
? FILE REFERENCE: 09596-4202
? CURRENT APPLICATION NUMBER: US/09/240,274
? EARLIER FILING DATE: 1999-01-29
? EARLIER APPLICATION NUMBER: 60/081,380
? EARLIER FILING DATE: 1998-04-10
? EARLIER APPLICATION NUMBER: 60/028,550
? EARLIER FILING DATE: 1996-10-11
? NUMBER OF SEQ. ID NOS: 224
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 144
? LENGTH: 126
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: anti-Rh(D) antibody clone SH24
? US-09-240-274-144

```

```
Query Match      68.0%; Score 447.5; DB 3; Length : ;
Best Local Similarity 68.3%; Pred. No. 1.2e-37;
Matches 86; Conservative 15; Mismatches 24; Indels 1; Gaps 1.
```

[illegible]

|    |     |        |     |
|----|-----|--------|-----|
| QY | 120 | MVTVSS | 125 |
|    |     |        |     |
| Db | 121 | MVTVSS | 126 |

RESULT 9  
US-09-240-274-150  
; Sequence 150, Application US/09240274

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[illegible]

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|----|-----|--------|-----|
| Qy | 120 | MVTVSS | 125 |
|    |     |        |     |
| Db | 121 | MVTVSS | 126 |

RESULT 10  
US-08-428-197-1  
; Sequence 1, Application US/08428197  
; Patent No. 5851438  
; GENERAL INFORMATION:  
; INVENTOR: STEPHEN J. CHEN  
; ATTORNEY: STEPHEN J. CHEN

1 TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF  
2 TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED  
3 TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERNATANT AND CONJUGATES  
4 THEREOF  
5 NUMBER OF SEQUENCES: 51  
6 CORRESPONDENCE ADDRESS:  
7 ADDRESSEE: Spensley Horn Judas & Lubitz  
8 STREET: 1880 Century Park East - Suite 500  
9 CITY: Los Angeles  
10 STATE: California  
11 COUNTRY: USA  
12 ZIP: 90067  
13  
14 COMPUTER READABLE FORM:  
15 MEDIUM TYPE: floppy disk  
16 COMPUTER: IBM PC compatible  
17 OPERATING SYSTEM: PC-DOS/MS-DOS  
18 SOFTWARE: PatentIn Release #1.0, Version #1.25  
19 CURRENT APPLICATION DATA:  
20 APPLICATION NUMBER: US/08/428,197  
21 FILING DATE: 08/01/90

```

: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/10555
: FILING DATE: 29-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Howells, Stacy L.
: REGISTRATION NUMBER: 34,842
: REFERENCE/DOCKET NUMBER: PD-2630
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 455-5100
: TELEFAX: (619) 455-5110
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 125 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: IMMEDIATE SOURCE:
: CLONE: 18/2
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: 1..125
: US-08-428-197-1

```

|         | Query Match      | Score                                                       | DB #               | Length  |
|---------|------------------|-------------------------------------------------------------|--------------------|---------|
| Beet    | Local Similarity | 67.2%                                                       | Pred. No. 2,26-37/ |         |
| Matches | 84; Conservative | 16; Mismatches                                              | 25; Indels         | 0; Gaps |
| QY      | 1                | EVQLVGGSGLVPGGSLRLCSAASGFFPRRDIMHWYKOTPGKLEWVSSTISCGNTIDY   | 60                 |         |
| DB      | 1                | EVQLVGGSGGLVQPGSLRLCSAASGFFTSYAMSWYQAQKLEWVSATISGSGSTYY     | 60                 |         |
| QY      | 61               | ADSVKRFPTISRDNANVYVLOMNSLRAPEDMAVYFCARDGITFQSAATRAFDIWGNGTM | 120                |         |
| DB      | 61               | ADSVKRFPTISRDNSKNTLYVLOMNSLRAPEDVAVYCTGQVLYVGGSGSYNFDWGGSTL | 120                |         |

|    |     |       |     |
|----|-----|-------|-----|
| Qy | 121 | VTVSS | 125 |
|    |     |       |     |
| Db | 121 | VTVSS | 125 |



```

:
: APPLICANT: Fendly, Brian M.
: APPLICANT: Gurney, Austin L.
: TITLE OF INVENTION: Agonist Antibodies
: FILE REFERENCE: P0979
: CURRENT APPLICATION NUMBER: US/08/918,148A
: CURRENT FILING DATE: 1997-08-25
: NUMBER OF SEQ ID NOS: 79
: SEQ ID NO 75
: LENGTH: 245
: TYPE: PRT
: ORGANISM: artificial
US-08-918-148-75

```

|                       |       |              |         |            |    |        |    |      |   |
|-----------------------|-------|--------------|---------|------------|----|--------|----|------|---|
| Query Match           | 70.0% | Score        | 460.5   | DB         | 4  | Length | 2  | 5    |   |
| Best Local Similarity | 72.7% | Pred. No.    | 1.4e-38 |            |    |        |    |      |   |
| Matches               | 93    | Conservative | 8       | Mismatches | 14 | Indels | 13 | Gaps | 2 |

```

QY 1 EVLVYSGEGLVYRPGGSLRISCASGFTFRYRDIMWRQTPGKGLEWVS 15SGGNTIDY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 EVOLVDSGGGLVYRPGGSLRISCASGFTTSDYIMNIMQAPGKGLEWVS 15SSGGNTIYY 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ADSVKGRFTTIRDNANNVVYLQNNSSLRADMAVYFCARDGITFGSAAW 15--AFDIWGR 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 ADSVKGRFTTIRKNSKQTLTYLQNNSSLRADTDVYTCAR-----W 15EDAFDIWQ 112
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 118 GTMVTWSS 125
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 113 GTMVTWSS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 3  
US-09-240-274-27  
; Sequence 27, Application US/09240274

|                          |        |                  |           |            |
|--------------------------|--------|------------------|-----------|------------|
| Query Match              | 69.9%  | Score 460;       | DB 3;     | Length 127 |
| Best Local Similarity    | 70.3%; | Pred. No. 7e-39; |           |            |
| Matches 90; Conservative | 11;    | Mismatches 23;   | Indels 4; | Gaps 2     |

|    |     |                                                 |                 |
|----|-----|-------------------------------------------------|-----------------|
| Oy | 1   | EVLVYKSGEGILVMPGSLRLTASCAAGFTPRRDIMHWOTPKGLIEW; | [SSCGANTIDY 60  |
|    |     |                                                 |                 |
|    |     | : : : :                                         | :               |
| Dd | 1   | EVQLLEGGGGLVMPGSSLRLSCAAGFTSSVSMHWVAQAPKGLEW;   | [SNSNTIYY 60    |
|    |     |                                                 |                 |
| Oy | 61  | ADSKRGFTISPNANNVYLWNLSLRADMVAVCARDGTIFGSAAIT    | --RAFDIMGR 117  |
|    |     |                                                 |                 |
|    |     | : : : :                                         | :               |
| Dd | 61  | ADAVKAGFTISRDKANSLYLONNSLRADMVAITCARDSR--TSNPLR | %SDGDHDYWGQ 119 |
|    |     |                                                 |                 |
| Oy | 118 | GTMVTASS 125                                    |                 |
|    |     |                                                 |                 |
| Dd | 120 | GTVIVASS 127                                    |                 |
|    |     |                                                 |                 |

## RESULT 4

US-08-665-202-30  
; Sequence 30, Application US/08665202  
; Patent No. 5977322

TITLE OF INVENTION: Tumor Antigens  
 NUMBER OF SEQUENCES: 141  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA

|                       |                 |               |          |            |
|-----------------------|-----------------|---------------|----------|------------|
| Query Match           | 69.3%           | Score 456     | DB 2     | length 123 |
| Best Local Similarity | 72.0%           | Pred. No.     | 1.7e-38  |            |
| Matches 90            | Conservative 14 | Mismatches 19 | Indels 2 | Gaps 1     |

```

QY      1 EVOLYKSGBELVKPGSLRLSCAASGFTFRRYDTHMVRQTFKGLIEWVSLSSGGRIDY 60
      :
Db      1 QVQLVDSGGGLVQPGGSLRLSCAASGFTFSSSYEMWNRQAQGLKEWVSYISSGGTIYY 60
QY      61 ADSYKRFITSRDNNANVYLLQMSLRPAEDMAVYECARDGTFISGSAATWRAFDWGRGTM 120
      :
Db      61 ADSYKRGFTISRDNNAKNSLYLQMSLRPAEDTAVYICARD--LGYSYGYVGLDWGGGTL 118
QY      121 VTVSS 125
      : : : : :
Db      119 VTVSS 123

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```

RESULT 5
US-09-315-574-30
: Sequence 30, Application US/09315574
: Patent No. 6512097
: GENERAL INFORMATION:
: APPLICANT: Marks, James D.
: TITLE OF INVENTION: No. 6512097a1 High Affinity Human Antibodies co
: TITLE OF INVENTION: Tumor Antigens

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 30, 2003, 10:47:45 ; Search time 12.692 Seconds  
(without alignments)  
416,677 Million cell updates/sec

Title: US-09-674-752-49

Perfect score: 658

Sequence: 1 EVOLVSGEGLVKGPGSLRL.....ATWRAFDWGRGTMV VSS 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued\_PatentB\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/6CTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to give a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                         |
|------------|-------|-------------|--------|----|-------------------------------------|
| 1          | 467.5 | 71.0        | 245    | 4  | US-08-918-148-78 Sequ. 78, Appl.    |
| 2          | 460.5 | 70.0        | 245    | 4  | US-08-918-148-75 Sequ. 75, Appl.    |
| 3          | 460   | 69.9        | 127    | 3  | US-09-240-274-27 Sequ. 27, Appl.    |
| 4          | 456   | 69.3        | 123    | 2  | US-08-665-202-30 Sequ. 30, Appl.    |
| 5          | 456   | 69.3        | 123    | 4  | US-09-315-574-30 Sequ. 30, Appl.    |
| 6          | 448   | 68.1        | 121    | 3  | US-09-202-181-4 Sequ. 4, Appl.      |
| 7          | 447.5 | 68.0        | 126    | 3  | US-09-240-274-10 Sequ. 10, Appl.    |
| 8          | 447.5 | 68.0        | 126    | 3  | US-09-240-274-144 Sequ. 144, Appl.  |
| 9          | 447.5 | 68.0        | 126    | 3  | US-09-240-274-150 Sequ. 150, Appl.  |
| 10         | 445   | 67.6        | 125    | 2  | US-08-428-197-1 Sequ. 1, Appl.      |
| 11         | 445   | 67.6        | 125    | 5  | PCT-US93-10555-1 Sequ. 32, Appl.    |
| 12         | 444.5 | 67.6        | 109    | 2  | US-08-379-057-32 Sequ. 32, Appl.    |
| 13         | 443.5 | 67.4        | 120    | 2  | US-07-934-373C-4 Sequ. 4, Appl.     |
| 14         | 443.5 | 67.4        | 120    | 3  | US-08-437-642B-4 Sequ. 4, Appl.     |
| 15         | 443.5 | 67.4        | 120    | 4  | US-08-146-206C-4 Sequ. 4, Appl.     |
| 16         | 442.5 | 67.2        | 135    | 3  | US-08-579-378A-20 Sequ. 20, Appl.   |
| 17         | 442.5 | 67.2        | 443    | 5  | PCT-US86-13152-4 Sequ. 4, Appl.     |
| 18         | 442   | 67.2        | 117    | 4  | US-09-025-769B-24 Sequ. 24, Appl.   |
| 19         | 442   | 67.2        | 120    | 1  | US-07-942-245-35 Sequ. 35, Appl.    |
| 20         | 442   | 67.2        | 125    | 3  | US-09-240-274-24 Sequ. 24, Appl.    |
| 21         | 442   | 67.2        | 131    | 3  | US-09-240-274-28 Sequ. 28, Appl.    |
| 22         | 441   | 67.0        | 125    | 3  | US-09-240-274-9 Sequ. 9, Appl.      |
| 23         | 441   | 67.0        | 249    | 4  | US-10-039-785-53 Sequ. 53, Appl.    |
| 24         | 440.5 | 66.9        | 120    | 4  | US-09-025-769B-38 Sequ. 38, Appl.   |
| 25         | 440.5 | 66.9        | 120    | 4  | US-09-025-769B-63 Sequ. 63, Appl.   |
| 26         | 440.5 | 66.9        | 140    | 3  | US-08-983-607-32 Sequ. 32, Appl.    |
| 27         | 440.5 | 66.9        | 281    | 4  | US-09-025-769B-178 Sequ. 178, Appl. |

|    |       |      |     |   |                                      |
|----|-------|------|-----|---|--------------------------------------|
| 28 | 439.5 | 66.8 | 124 | 4 | US-09-425-638A-49 Sequence 49, Appl. |
| 29 | 439.5 | 66.8 | 124 | 4 | US-09-543-004-49 Sequence 49, Appl.  |
| 30 | 439.5 | 66.8 | 139 | 1 | US-08-129-930B-96 Sequence 96, Appl. |
| 31 | 439.5 | 66.8 | 139 | 4 | US-08-134-346A-51 Sequence 51, Appl. |
| 32 | 439.5 | 66.8 | 139 | 4 | US-08-976-288A-96 Sequence 96, Appl. |
| 33 | 439.5 | 66.8 | 245 | 4 | US-08-918-148-76 Sequence 76, Appl.  |
| 34 | 439   | 66.7 | 125 | 3 | US-09-240-274-151 Sequence 151, App  |
| 35 | 438   | 66.6 | 121 | 3 | US-08-599-226-2 Sequence 2, Appl.    |
| 36 | 438   | 66.6 | 121 | 3 | US-09-125-098-2 Sequence 2, Appl.    |
| 37 | 438   | 66.6 | 121 | 4 | US-09-540-018-2 Sequence 2, Appl.    |
| 38 | 438   | 66.6 | 127 | 3 | US-09-240-274-19 Sequence 19, Appl.  |
| 39 | 437.5 | 66.5 | 312 | 4 | US-09-079-029-10 Sequence 10, Appl.  |
| 40 | 437   | 66.4 | 113 | 3 | US-08-974-899-6 Sequence 6, Appl.    |
| 41 | 435.5 | 66.2 | 124 | 3 | US-08-983-607-47 Sequence 47, Appl.  |
| 42 | 435   | 66.1 | 125 | 1 | US-08-478-039-99 Sequence 99, Appl.  |
| 43 | 435   | 66.1 | 125 | 1 | US-08-476-349A-99 Sequence 99, Appl. |
| 44 | 434.5 | 66.0 | 120 | 2 | US-08-958-201-10 Sequence 10, Appl.  |
| 45 | 434.5 | 66.0 | 124 | 4 | US-09-425-638A-54 Sequence 54, Appl. |

#### ALIGNMENTS

```
RESULT 1
US-08-918-148-78
; Sequence 78, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 78
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; NAME/KEY: unknown
; LOCATION: 208
; OTHER INFORMATION: unknown amino acid
US-08-918-148-78

Query Match      71.0%, Score 467.5; DB 4; Length 245;
Best Local Similarity 74.4%; Pred. No. 2.7e-39;
Matches 93; Conservative 11; Mismatches 14; Indels 7; Gaps 2;

QY      1 EVOLVSGEGLVKGPGSLRLSCAASGFTFRYYDHWVROTGKGLIEWSSISGANYIDY 60
       3 QVQLVSSGSGVLRPGGSLRLSCAASGFTFSNNMWRQAQKGLIEWSSISSTSYLY 62
       61 ADVVSGRTISRDNANNVYLVQNSLRADMAVYFCARDGTIFGSAATWRAFDWGRGTM 120
       63 ADVVSGRTISRDNANKSLVQNSLRADTAIVYICARDR---GST---GMDWGRGTL 115
QY      121 VTVSS 125
       116 VTVSS 120
Db

RESULT 2
US-08-918-148-75
; Sequence 75, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
```

/ PRIOR FILING DATE: 2001-05-25  
/ NUMBER OF SEQ ID NOS: 3239  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 2040  
/ LENGTH: 237  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-09-880-748-2040

Query Match 70.3%; Score 462.5; DB 11; Length 237;

Best Local Similarity 72.8%; Pred. No. 3,6e-36; Mismatches 12; Indels 11; Gaps 1;  
Matches 91; Conservative 11; Mismatches 12; Indels 11; Gaps 1;

|    |     |                                                             |     |
|----|-----|-------------------------------------------------------------|-----|
| Qy | 1   | EVQLVKGSGGLVPGGSLRLSCAASGFTFERRDYDIHWVROTPGKGLHWYSISGGNYIDY | 60  |
| Db | 1   | QVQLVQSGGGLVPGGSLRLSCAASGFTFSYEMHWVROAPGKGLHWYSISGGSTIYY    | 60  |
| Qy | 61  | ADSVKGRFTISRDNANNTVLTQNSLRADMAVYFCARDGTFGSAATWRAFDIWRGSTM   | 120 |
| Db | 61  | ADSVKGRFTISRDNANKLLYLQNSLRADTAAYVYCARDYT-----DYGKRGTL       | 109 |
| Qy | 121 | VTWSS                                                       | 125 |
| Db | 110 | VTWSS                                                       | 114 |

Search completed: December 30, 2003, 11:45:25  
Job time : 27.8075 secs



```

; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1179
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
; OS-09-880-748-1179

```

| Query Match | Similarity | 70.7%                                                       | Score 465         | DB 11    | Length 250 |
|-------------|------------|-------------------------------------------------------------|-------------------|----------|------------|
| Best Local  | Similarity | 71.7%                                                       | Pred. No. 3.5e-36 |          |            |
| Matches     | 91         | Conservative 12                                             | Mismatches 22     | Indels 2 | Gaps 1     |
| Qy          | 1          | EVOLVKSGEGLVYKCGSLRLSCAASGFPRFRYDIHVMVQTEPGKLEWSSISSGGNTYD  | 60                |          |            |
|             |            | :     :     :     :     :     :     :     :     :     :     |                   |          |            |
| Db          | 1          | EVOLVETGGGLVYKCGSLRLSCAASGFSSSYEMVMVQAQKGLIEWSYISSGGSTIYY   | 60                |          |            |
|             |            | :     :     :     :     :     :     :     :     :           |                   |          |            |
| Qy          | 61         | ADSVKGRFTISRDNANNVYLQNNSLRAEDNAVYFCARDG--TIFGSAATRAPDIMG    | 118               |          |            |
|             |            | :     :     :     :     :     :     :     :     :           |                   |          |            |
| Db          | 61         | ADSVKGRFTISRDNANNSLYLQNNSLRAEDNAVYCTTDGYDILITGVSYVYGMVDWGRG | 120               |          |            |
|             |            | :     :     :     :     :     :     :     :     :           |                   |          |            |
| Qy          | 119        | TMVTVSS                                                     | 125               |          |            |
|             |            | :                                                           |                   |          |            |
| Db          | 121        | TLVTVSS                                                     | 127               |          |            |

```

RESULT 13
US-09-880-748-1937
; Sequence 1937, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OR INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCES: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1937
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
; IS-09-880-748-1937

```

|                       |                                                          |                                                               |            |             |
|-----------------------|----------------------------------------------------------|---------------------------------------------------------------|------------|-------------|
| Query Match           | 70.4%                                                    | Score 463;                                                    | DB 11;     | Length 241; |
| Best Local Similarity | 75.0%;                                                   | Pred. No. 5.1e-36;                                            |            |             |
| Matches               | 93; Conservative                                         | 8; Mismatches                                                 | 15; Indels | 8; Gaps     |
| QY                    | 2                                                        | VOLVKSGEGLVKPGGSLRLSCAASGFTTRRRYDIHWNRQTPEKSGLEWSSISSGGNYIDYA | 61         |             |
|                       |                                                          |                                                               |            |             |
| 2                     | VOLVOSGGGLVKSGGSLRLSCAASGFTTRYSANMWRAPCKGLEWSSISSSSIIYYA | 61                                                            |            |             |
|                       |                                                          |                                                               |            |             |

[illegible]

```

RESULT 14
US-09-880-748-2019
; Sequence 2019, Application US/09860748
; Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OR INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIORITY APPLICATION NUMBER: 60/212,210
PRIORITY FILING DATE: 2000-06-15
PRIORITY APPLICATION NUMBER: 60/240,816
PRIORITY FILING DATE: 2000-10-17
PRIORITY APPLICATION NUMBER: 60/276,248
PRIORITY FILING DATE: 2001-03-16
PRIORITY APPLICATION NUMBER: 60/277,379
PRIORITY FILING DATE: 2001-03-21
PRIORITY APPLICATION NUMBER: 60/293,499
PRIORITY FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2019
LENGTH: 217
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-2019

```

```

Query Match:          70.3%; Score 462.5; DB: 11; Length 237;
Best Local Similarity 73.6%; Pred.No. 5.6e-36f
Matches    92; Conservative     9; Mismatches   13; Indels    11; Gaps      1

QY      1 EVQLVDSGEGLVTPGGSLRLSCAASGFTPRRYDIDHWRTIPGKGLEWSSISSGGNYIDY 60
       :|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1 QVQLVSGGGGLVTPGGSLRLSCAASGFTFSSEYENMWVRQAPEGKLEWVSIVSSSGTITY 60
       ||::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      61 ADSVKGRFTISDNANNVYLQMNSLRAEEDMAVYFCARDGTIFCSAAITRAPIWGRTM 120
       :|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      61 ADSVKGRFTISRDKAKNSLYLQMNSLRAEDEVAVYYCARDIT-----DYMGRTM 109
       :|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      121 VTVSS 125
       |||||
Db      110 VTVSS 114
       |||||

RESULT 15
US-09-880-748-2040
? Sequence 2040, Application US/09880748
? Publication No. US20030059937A1
? GENERAL INFORMATION:
? APPLICANT: Ruben et al.
? TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
? FILE REFERENCE: PFS23
? CURRENT APPLICATION NUMBER: US/09/880,748
? CURRENT FILING DATE: 2001-06-15
? PRIOR APPLICATION NUMBER: 60/212,210
? PRIOR FILING DATE: 2000-06-15
? PRIOR APPLICATION NUMBER: 60/240,816
? PRIOR FILING DATE: 2000-10-17
? PRIOR APPLICATION NUMBER: 60/276,248
? PRIOR FILING DATE: 2001-03-16
? PRIOR APPLICATION NUMBER: 60/277,379
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/293,499

```

|    |     |          |     |
|----|-----|----------|-----|
| Qy | 116 | GRGTMVTS | 124 |
|    |     | : :      |     |
| Db | 121 | GKGLTVTS | 129 |

RESULT 9  
US-09-88

; Sequence 883, Application US/09880/48  
 ; Publication No. US20030059937A1  
 ; GENERAL INFORMATION:

APPLICANT: RUDEN et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blyss  
FILE REFERENCE: PF523

;  
; CURRENT APPLICATION NUMBER: 05/09/88  
;  
; CURRENT FILING DATE: 2001-06-15  
;  
; PRIOR APPLICATION NUMBER: 60/212,210

;  
PRIOR FILING DATE: 2000-06-15  
;  
PRIOR APPLICATION NUMBER: 60/240,816  
;  
PRIOR FILING DATE: 2000-10-17  
;

;  
; PRIOR APPLICATION NUMBER: 60/276,248  
;  
; PRIOR FILING DATE: 2001-03-16  
;  
; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING  
; PRIOR APPLIC  
; PRIOR FILING

```

; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver.
; SEQ ID NO 883

```

```

; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
;

```

|                   |                                        |
|-------------------|----------------------------------------|
| US-09-880-748-883 |                                        |
| Query Match       | 71.2%; Score 468.5; DB 11; Length 250; |

Best Local Similarity 75.8%; Pred. No. 1.6e-36;  
Matches 94; Conservative 9; Mismatches 20; Indels 1; Gaps 1

Cy 2 VOLVSGEGLVKPGSLRLSCAASGTFRRDHWROTPKGLEWWSISSGNVIDYA 61  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 2 VOLVSGGGIVPPGSLRLSCAASGTFRRYSMMNWRQAPKGLEWWSISSGN-1YYA 60

62 DSVKGRFTTGRDNANNVYLQMSLRAEDMAVYFCARDGTIFGSAATWRAPIWGRGTMV 121

|    |                     |
|----|---------------------|
| Db | 61 DSVRGFTISRDNKSVY |
| Ov | 122 TVSS 125        |

ORGANISM: homo sapiens  
US-10-041-860-270

|                       |                  |                    |           |             |
|-----------------------|------------------|--------------------|-----------|-------------|
| Query Match           | 71.0%;           | Score 467.5;       | DB 12;    | Length 126; |
| Best Local Similarity | 74.6%;           | Pred. No. 9.7e-37; |           |             |
| Matches 94;           | Conservative 10; | Mismatches 21;     | Indels 1; | Gaps 1.     |

```

09      1  EVOLVKSSEGLVFKPGSLRLSCAASGFTFRRYDIIHVRQTPGKLEWSSISSGQNYIDY  60
      2  |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
      3  1  EVOLVKSSEGLVFKPGSLRLSCAASGFTFRRYDIIHVRQTPGKLEWSSISSGQNYIDY  60
      4  |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

```

DB IRVLLVESGGGLVFPQGSIRLKLCLAAAGFPRKIINQUMVKAFQAGQIDRMVSSIDSSDDN... 50

QY 61 ADGVKGRFTISRNANNVYLOMSLRADMAVYFCARDGTI-FGSAATWRAPDIWGRGT 119

Db 61 AD5VKGRFTT

|    |     |        |     |
|----|-----|--------|-----|
| QY | 120 | MVTWSS | 125 |
|    |     | ::::   |     |
| Db | 121 | VLTWSS | 126 |

## RESULT 11

US-09-880-748-1764  
; Sequence 1764, Application US/09880748  
; Publication No. US20030059937A1

```

; GENERAL INFORMATION:
;
; APPLICANT: Ruben et al.
;
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

```

```

; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15

```

;; PRIOR APPLICATION NUMBER: 60/212,210  
;; PRIOR FILING DATE: 2000-06-15  
;; PRIOR APPLICATION NUMBER: 60/240,816

;; PRIOR FILING DATE: 2000-10  
;; PRIOR APPLICATION NUMBER:  
;; PRIOR FILING DATE: 2001-03

;; PRIOR APPLICATION NUMBER:  
;; PRIOR FILING DATE: 2001-03  
;; PRIOR APPLICATION NUMBER:

PRIOR FILING DATE: 2001-05-25  
 NUMBER OF SEQ ID NOS: 3239  
 SOFTWARE: PatentIn Ver. 2.0

```

: SEQ ID NO 1764
:
: LENGTH: 247
:
: TYPE: PRT
:

```

```
/ CURRENT FILING DATE: 2002-01-07
/ NUMBER OF SEQ ID NOS: 377
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13
/ LENGTH: 126
/ TYPE: PRF
/ ORGANISM: homo sapiens
US-10-041-860-13

Query Match
Best Local Similarity 71.7%; Score 471.5; DB 12; Length 126;
Matches 95; Conservative 9; Mismatches 21; Indels 1; Gaps 1;

QY 1 EVOLVSGGLVPGGSLRLSCAASGFTFRRIYDIHWRTQPGKLEWVSSISSGNYIDY 60
Db 1 EVOLVSGGGLVPGGSLRLSCAASGFTFRYNNMWRQAPGKLEWVSSISSSSNIYY 60
QY 61 ADSVKGRFTISRDNANNNVYLQNNSLRAEDMAVYFCARDGTI-FGSAATWRAPDIWGRGT 119
Db 61 ADSVKGRFTISRDNANNNVYLQNNSLRAEDTAVYVCARDIMITFGIIASFYFDYWGQGT 120
QY 120 MVTWSS 125
Db 121 LVTWSS 126

RESULT 6
US-10-041-860-208
/ Sequence 208, Application US/10041860
/ Publication No. US20030157109A1
/ GENERAL INFORMATION:
/ APPLICANT: Corvalan, Jose R.F.
/ APPLICANT: Jia, Xiao-Chi
/ APPLICANT: Feng, Xiao
/ APPLICANT: Yang, Xiao-Peng
/ APPLICANT: Chen, Francine
/ APPLICANT: Gazit, Gad
/ APPLICANT: Weber, Richard
/ APPLICANT: Bezabeh, Biniam
/ TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
/ FILE REFERENCE: THEREOF
/ CURRENT APPLICATION NUMBER: US/10/041,860
/ CURRENT FILING DATE: 2002-01-07
/ NUMBER OF SEQ ID NOS: 377
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 208
/ LENGTH: 126
/ TYPE: PRF
/ ORGANISM: homo sapiens
US-10-041-860-208

Query Match
Best Local Similarity 71.7%; Score 471.5; DB 12; Length 126;
Matches 95; Conservative 9; Mismatches 21; Indels 1; Gaps 1;

QY 1 EVOLVSGGLVPGGSLRLSCAASGFTFRRIYDIHWRTQPGKLEWVSSISSGNYIDY 60
Db 1 EVOLVSGGGLVPGGSLRLSCAASGFTFRYNNMWRQAPGKLEWVSSISSSSNIYY 60
QY 61 ADSVKGRFTISRDNANNNVYLQNNSLRAEDMAVYFCARDGTI-FGSAATWRAPDIWGRGT 119
Db 61 ADSVKGRFTISRDNANNNVYLQNNSLRAEDTAVYVCARDIMITFGIIASFYFDYWGQGT 120
QY 120 MVTWSS 125
Db 121 LVTWSS 126

RESULT 7
US-10-091-300-31
/ Sequence 31, Application US/10091300
/ Publication No. US20030108545A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Rockwell, Patricia
/ APPLICANT: Goldstein, Neil I.
/ TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
/ FILE REFERENCE: 11245/46211
/ CURRENT APPLICATION NUMBER: US/10/091,300
/ CURRENT FILING DATE: 2002-03-04
/ NUMBER OF SEQ ID NOS: 85
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 31
/ LENGTH: 116
/ TYPE: PRF
/ ORGANISM: Human
US-10-091-300-31

Query Match
Best Local Similarity 71.5%; Score 470.5; DB 15; Length 116;
Matches 94; Conservative 8; Mismatches 14; Indels 9; Gaps 1;

QY 1 EVOLVSGGLVPGGSLRLSCAASGFTFRRIYDIHWRTQPGKLEWVSSISSGNYIDY 60
Db 1 EVOLVSGGGLVPGGSLRLSCAASGFTFSYMMWRQAPGKLEWVSSISSSSYIYY 60
QY 61 ADSVKGRFTISRDNANNNVYLQNNSLRAEDMAVYFCARDGTIFGSAATWRAPDIWGRGT 120
Db 61 ADSVKGRFTISRDNANNNVYLQNNSLRAEDTAVYVCARD-----VTDAFDIWGQGT 111
QY 121 VTWSS 125
Db 112 VTWSS 116

RESULT 8
US-09-880-748-1318
/ Sequence 1318, Application US/09880748
/ Publication No. US2003005937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunoselectively Bind BlyS
/ FILE REFERENCE: PFS23
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ CURRENT FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1318
/ LENGTH: 256
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-09-880-748-1318

Query Match
Best Local Similarity 71.4%; Score 469.5; DB 11; Length 256;
Matches 93; Conservative 11; Mismatches 20; Indels 5; Gaps 2;

QY 1 EVOLVSGGLVPGGSLRLSCAASGFTFRRIYDIHWRTQPGKLEWVSSISSGNYIDY 60
Db 1 EVOLVSGGGLVPGGSLRLSCAASGFTFSYMMWRQAPGKLEWVSSISSSSYIYY 60
QY 61 ADSVKGRFTISRDNANNNVYLQNNSLRAEDMAVYFCARD-GTIFGSAATWR-----AFDIW 115
Db 61 ADSVKGRFTISRDNANNNVYLQNNSLRAEDTAVYVCARDLGSFYDILTALRLNENYGMQDW 120
```

Db 61 ADVKGRFTISRDNKNSLYLQMSLRAEDTAIVYVCARGHYDILGYFG-----FDY 113  
Qy 115 WGRGTMVTSS 125  
Db 114 WGRGTLVTSS 124

RESULT 2  
US-10-091-300-24  
; Sequence 24, Application US/10091300  
; Publication No. US20030108545A1  
; GENERAL INFORMATION:  
; APPLICANT: Rockwell, Patricia  
; APPLICANT: Goldstein, Neil I.  
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth with a Vascular  
; TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist  
; FILE REFERENCE: 11245/46211  
; CURRENT APPLICATION NUMBER: US/10/091,300  
; CURRENT FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 24  
; LENGTH: 116  
; TYPE: PRT  
; ORGANISM: Human  
US-10-091-300-24

Query Match 72.3%; Score 475.5; DB 15; Length 116;  
Best Local Similarity 76.0%; Pred. No. 1,6e-37;  
Matches 95; Conservative 7; Mismatches 14; Indels 9; Gaps 1;

Qy 1 EVOLVKSSEGLVYKPGSLRLSCAASGFTPRRYDIHWVROTQPKGLEWVSSISGGNYIDY 60  
Db 1 EVOLVQSGGGLVYKPGSLRLSCAASGFTSSYSNMWVQAQPKGLEWVSSISGGSYIYY 60  
Qy 61 ADVKGRFTISRDNANNVYLYQMSLRAEDMAVYFCARDGTFGSAATWRAFDIWRGTM 120  
Db 61 ADVKGRFTISRDNKNSLYLQMSLRAEDTAIVYVCAR-----VTDARFDIWRGTM 111

Qy 121 VTVSS 125  
Db 112 VTVSS 116

RESULT 3  
US-10-150-475A-6  
; Sequence 6, Application US/10150475A  
; Publication No. US20030103985A1  
; GENERAL INFORMATION:  
; APPLICANT: Adolf, G. et al.  
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunocjugates  
; FILE REFERENCE: 1/1211  
; CURRENT APPLICATION NUMBER: US/10/150,475A  
; CURRENT FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: US 60/307,451  
; PRIOR FILING DATE: 2001-07-24  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Humanised  
; OTHER INFORMATION: Murine Antibody BiWA 4 Heavy Chain SEQ ID NO: 6  
US-10-150-475A-6

Query Match 71.8%; Score 472.5; DB 15; Length 444;  
Best Local Similarity 73.6%; Pred. No. 1,3e-36;  
Matches 92; Conservative 8; Mismatches 14; Indels 11; Gaps 1;

Qy 1 EVOLVKSSEGLVYKPGSLRLSCAASGFTPRRYDIHWVROTQPKGLEWVSSISGGNYIDY 60  
Db 1 EVOLVKSSEGLVYKPGSLRLSCAASGFTPRRYDIHWVROTQPKGLEWVSSISGGNYIDY 60

Db 1 EVOLVKSSEGLVYKPGSLRLSCAASGFTSSYSNMWVQAQPKGLEWVSSISGGSYIYY 60  
Qy 61 ADVKGRFTISRDNANNVYLYQMSLRAEDMAVYFCARDGTFGSAATWRAFDIWRGTM 120  
Db 61 LDSIKGRFTISRDNKNSLYLQMSLRAEDTAIVYVCAROG-----LDYWRGHTL 109  
Qy 121 VTVSS 125  
Db 110 VTVSS 114

RESULT 4  
US-09-880-748-913  
; Sequence 913, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PFE523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 913  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-913

Query Match 71.7%; Score 472; DB 11; Length 248;  
Best Local Similarity 72.0%; Pred. No. 7,5e-37;  
Matches 90; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

Qy 1 EVOLVKSSEGLVYKPGSLRLSCAASGFTPRRYDIHWVROTQPKGLEWVSSISGGNYIDY 60  
Db 1 EVOLVKSSEGLVYKPGSLRLSCAASGFTSSYSNMWVQAQPKGLEWVSSISNRSYIYY 60  
Qy 61 ADVKGRFTISRDNANNVYLYQMSLRAEDMAVYFCARDGTFGSAATWRAFDIWRGTM 120  
Db 61 ADVKGRFTISRDNKNSLYLQMSLRAEDTAIVYVCAREGRDILGYVYGLDVWGQGLT 120  
Qy 121 VTVSS 125  
Db 121 VTVSS 125

RESULT 5  
US-10-041-860-13  
; Sequence 13, Application US/10041860  
; Publication No. US20030157109A1  
; GENERAL INFORMATION:  
; APPLICANT: Corvalan, Jose R.F.  
; APPLICANT: Jia, Xiao-Chi  
; APPLICANT: Peng, Xiao  
; APPLICANT: Yang, Xiao-Dong  
; APPLICANT: Chen, Francine  
; APPLICANT: Gazit, Gadi  
; APPLICANT: Weber, Richard  
; APPLICANT: Bezebel, Binayam  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USBS  
; FILE REFERENCE: ABGENIX-051A  
; CURRENT APPLICATION NUMBER: US/10/041,860



XX 22-FEB-2001; 2001WO-JP01298.  
PF  
XX 22-FEB-2000; 2000JP-0050543.  
PR  
XX  
XX  
PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.  
XX  
PI Kuroiawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M,  
PI Okuno Y, Shiraki K;  
XX  
XX WPI; 2001-565420/63.  
DR N-PSDB; AAA47732.  
XX  
XX Producing gene libraries and antibody libraries, involves selecting a  
PT light chain that binds to a heavy chain product to produce a functional  
PT formation, and producing a gene library of the light chain variable  
PT regions -  
XX  
PS Examples: p 168-169; 181pp; Japanese.  
XX  
XX The invention relates to producing gene libraries, comprising  
CC immunoglobulin light and heavy variable region. The method involves  
CC selecting light chain that binds with the heavy chain product to produce  
CC a functional conformation, producing a gene library comprising a  
CC collection of these light chain variable genes, and combining with gene  
CC library of heavy chain variable genes. The method is used for production  
CC of gene and antibody libraries.  
XX  
SQ Sequence 119 AA;  
  
Query Match 70.9%; Score 466.5; DB 22; Length 119;  
Best Local Similarity 70.3%; Pred. No. 1e-35;  
Matches 90; Conservative 12; Mismatches 13; Indels 13; Gaps 2;  
  
QY 1 EVQLVKGSGEGLVPRGSGLRISCAASGTFPRRDYHWVROTPRGKLEWSSISGSGNYIDY 60  
DB 1 EVQLVESGGGSLVPRGSGLRISCAASGTFPRYGMNWRQAPGKLEWSSISGSGTYIH 60  
QY 61 ADSVKGRFTISRDNANNVYLIQNNSLRAEDMAVYFCARDGTIFGSAATWR---AFDING 116  
DB 61 SDSVKGRFTYSRDNANNSLFLNENSLRAEDTAIYYCARD-----WESHETALDYWG 111  
QY 117 RGTMTVTS 124  
DB 112 QGTLVTVS 119

Search completed: December 30, 2003, 10:54:36  
Job time : 41.2945 secs



CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.

XX Sequence 256 AA;

Query Match 71.4%; Score 469.5; DB 23; Length 256;  
 Best Local Similarity 72.1%; Pred. No. 1.5e-35;  
 Matches 93; Conservative 11; Mismatches 20; Indels 5; Gaps 2;

1 EVQLVSGEGLVPGGSLRLSCAASGFTPRRIYDIHWYRQPGKLEWVSSISGGNYIDY 60  
 1 EVQLVSGGGLVPGGSLRLSCAASGFTPRSYSMNWYRQAPGKLEWVSSISGGNYIDY 60

61 ADSVKGRTISRDNANNVYLYQNSLRAEDMAVYFCARD-GTIFGSAATWR---AFDIW 115  
 61 ADSVKGRTISRDNANKSVLYLQNSLRAEDTAVYVCARDLGSFYDILTLRLNMGDW 120

116 GRTGMYTVS 124  
 121 GKGTLVTVS 129

RESULT 12

ABP44872 ID ABP44872 standard; Protein; 250 AA.

AC ABP44872;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 883.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;  
 XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
 XX immunosuppressive; immunostimulant; immunomodulatory; antitumoral;  
 XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

XX MO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX MPI, 2002-114799/15.

XX Antibodies against B lymphocyte stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 XX Claim 1; Page 1455-1456; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytotatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antitumoral and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.

XX Sequence 250 AA;

Query Match 71.2%; Score 468.5; DB 23; Length 250;  
 Best Local Similarity 75.8%; Pred. No. 1.5e-35;  
 Matches 94; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

2 VOLVYSGEGLVPGGSLRLSCAASGFTPRRIYDIHWYRQPGKLEWVSSISGGNYIDY 61  
 2 VOLVYSGGGLVPGGSLRLSCAASGFTPRSYSMNWYRQAPGKLEWVSSISGGN-IYYA 60

62 DSVKGRFTISRDNANNVYLYQNSLRAEDMAVYFCARDGTIFGSAATWRAPDIWGRGTW 121  
 61 DSVKGRFTISRDNANKSVLYLQNSLRAEDTAVYVCARDSDYDILTLGRGYTFYWGKTLV 120

122 TVSS 125  
 121 TVSS 124

RESULT 13

AA06717 ID AA06717 standard; Protein; 245 AA.

AC AA06717;

DT 17-JUN-1999 (first entry)

DE Antibody 12B5 single chain Fv (scFv) fragment.

XX Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;  
 XX megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;  
 XX bone marrow hypoplasia; disseminated intravascular coagulation; anemia;  
 XX myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour; MDS; CDR;  
 XX neuromuscular; muscular dystrophy; complementarity determining region.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 208 /note= "unspecified"

PN MO9910494-A2.

PD 04-MAR-1999.

PP 21-AUG-1998; 98WO-US17364.

PR 25-AUG-1997; 97US-0918148.

PA (GETH ) GENENTECH INC.

PI Adams CW, Carter PJ, Fendly BM, Gurney AL;

XX MPI, 1999-204666/17.



CC expresses VEGFR. It is also useful for inhibiting growth of colon tumour  
 CC or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.  
 CC It is preferably useful for treating subjects with both solid tumours,  
 CC preferably high vascular tumours and non-solid tumours. The inhibition  
 CC or reduction of tumour growth includes prevention or inhibition of the  
 CC progression of tumour, including cancerous and non-cancerous tumours,  
 CC where the progression of tumours includes the invasiveness, metastasis,  
 CC recurrence and increase in size of the tumour. The present sequence is  
 CC human KDR (VEGFR-2) Fab antibody heavy chain protein.

XX Sequence 116 AA:

Query Match 71.5%; Score 470.5; DB 23; Length 116;  
 Best Local Similarity 75.2%; Pred. No. 4.3e-36;  
 Matches 94; Conservative 8; Mismatches 14; Indels 9; Gaps 1;

QY 1 EVQLVSGSGGVKPGGSLRLSCAASGFTPRRYDIIHWKOTPKGLIEWSSISGNYIDY 60  
 DB 1 EVQLVSGSGGVKPGGSLRLSCAASGFTPRRYDIIHWKOTPKGLIEWSSISGNYIDY 60  
 QY 61 ADSVKGRTISRDNANNNVYVYQNNSLRAEDMAVYFCARDGTIFGSAATWRADFIMGRGTM 120  
 DB 61 ADSVKGRTISRDNANNNVYVYQNNSLRAEDMAVYFCARDGTIFGSAATWRADFIMGRGTM 111  
 QY 121 VTSS 125  
 DB 112 VTSS 116

RESULT 10

ABJ26766  
 ID ABJ26766 standard; Protein; 116 AA.

XX ABJ26766;

AC 01-MAY-2003 (first entry)

DE VEGF binding related protein SEQ ID No 83.

XX Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;

KW leukaemia cell; vascular endothelial growth factor; tumour;

XX bispecific antigen-binding protein; human.

OS Homo sapiens.

PN WO2003002144-A1.

PD 09-JAN-2003.

PF 26-JUN-2002; 2002WO-US20332.

XX 26-JUN-2001; 2001US-301299P.

XX (IMCL-) IMCLONE SYSTEMS INC.

PI Zhu Z;

XX WPI; 2003-201468/19.

DR N-PSDB; ABT3330.

XX New bispecific antibodies having antigen-binding sites specific for a

PT first vascular endothelial growth factor (VEGF) receptor and for a

PT second VEGF receptor, useful for inhibiting migration of leukemia

PT cells, or for treating tumors -

XX Claim 15; Page 74; 98pp; English.

XX The invention relates to a novel antibody having a first antigen binding

CC and migration of leukaemia cells. The antibodies are useful for treating  
 CC tumours and for in vivo or in vitro for investigative and diagnostic  
 CC methods. This sequence represents a human protein relating to the  
 CC bispecific antibodies that bind to the VEGF receptors of the invention.

XX Sequence 116 AA:

Query Match 71.5%; Score 470.5; DB 24; Length 116;  
 Best Local Similarity 75.2%; Pred. No. 4.3e-36;  
 Matches 94; Conservative 8; Mismatches 14; Indels 9; Gaps 1;

QY 1 EVQLVSGSGGVKPGGSLRLSCAASGFTPRRYDIIHWKOTPKGLIEWSSISGNYIDY 60  
 DB 1 EVQLVSGSGGVKPGGSLRLSCAASGFTPRRYDIIHWKOTPKGLIEWSSISGNYIDY 60  
 QY 61 ADSVKGRTISRDNANNNVYVYQNNSLRAEDMAVYFCARDGTIFGSAATWRADFIMGRGTM 120  
 DB 61 ADSVKGRTISRDNANNNVYVYQNNSLRAEDMAVYFCARDGTIFGSAATWRADFIMGRGTM 111  
 QY 121 VTSS 125  
 DB 112 VTSS 116

RESULT 11

ABP45307  
 ID ABP45307 standard; Protein; 256 AA.

XX ABP45307;

AC 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1318.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

KW tumour necrosis factor; B cell proliferation; B cell differentiation;

KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

XX 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX Antibodies against B lymphocyte Stimulating polypeptides, useful for

PT the diagnosis and treatment of cancers and immune disorders -

XX Claim 1; Page 1975-1976; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to

CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the

CC tumour necrosis factor (TNF) super family and induces B cell

CC proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to

XX Sequence 444 AA;  
 Query Match 71.8%; Score 472.5; DB 24; Length 444;  
 Best Local Similarity 73.6%; Pred. No. 1.2e-35; Indels 11; Gaps 1;  
 Matches 92; Conservative 8; Mismatches 14; Indels 11; Gaps 1;  
 QY 1 EVQVLSGEGLVPGGSLRLSCAASGFTFRRIYDIHWVROTPGKLEWVSISSGGVYIDY 60  
 DB 1 EVQVLSGEGLVPGGSLRLSCAASGFTFSIDYMWVROTPGKLEWVSISSGGVYIDY 60  
 QY 61 ADSVKGRFTISRDNANNVYLYQNSLRPAEDMAVYFCARDGTIFGSAATRAPDIWGRGTM 120  
 DB 61 LDSIKGRFTISRDNANKSLYLYQNSLRPAEDTAVYVCAROG-----LDYWGRTL 109  
 QY 121 VTVSS 125  
 DB 110 VTVSS 114  
 RESULT 8  
 ID ABP44902 standard; Protein: 248 AA.  
 AC ABP44902;  
 DT 19-AUG-2002 (first entry)  
 XX Human BlyS binding scFv SEQ ID 913.  
 DE Human BlyS binding scFv SEQ ID 913.  
 BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 tumour necrosis factor; B cell proliferation; B cell differentiation;  
 immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 common variable immunodeficiency; acquired immunodeficiency syndrome.  
 OS Homo sapiens.  
 PN MO200202641-A1.  
 PD 10-JAN-2002.  
 PF 15-JUN-2001; 2001MO-US19110.  
 PR 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 DR WPI; 2002-114799/15.  
 XX This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS  
 CC and so may be used to detect and quantitate the presence of BlyS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BlyS. They may also be

CC administered to treat diseases associated with aberrant BlyS expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.  
 XX Sequence 248 AA;  
 Query Match 71.7%; Score 472; DB 23; Length 248;  
 Best Local Similarity 72.0%; Pred. No. 7.1e-36; Indels 0; Gaps 0;  
 Matches 90; Conservative 14; Mismatches 21; Indels 0; Gaps 0;  
 QY 1 EVQVLSGEGLVPGGSLRLSCAASGFTFRRIYDIHWVROTPGKLEWVSISSGGVYIDY 60  
 DB 1 EVQVLSGEGLVPGGSLRLSCAASGFTFSIDYMWVROTPGKLEWVSISSGGVYIDY 60  
 QY 61 ADSVKGRFTISRDNANNVYLYQNSLRPAEDMAVYFCARDGTIFGSAATRAPDIWGRGTM 120  
 DB 61 ADSVKGRFTISRDNANKVLYLYQNSLRPAEDTAVYVCARGRDILTVYYGLDVMGRTL 120  
 QY 121 VTVSS 125  
 DB 121 VTVSS 125  
 RESULT 9  
 ID AAE28873 standard; Protein: 116 AA.  
 AC AAE28873;  
 DT 27-DEC-2002 (first entry)  
 XX Human KDR (VEGFR-2) Fab heavy chain (VH) protein from D2H2 clone.  
 DE Human KDR (VEGFR-2) Fab heavy chain (VH) protein from D2H2 clone.  
 BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 tumour necrosis factor; B cell proliferation; B cell differentiation;  
 immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 common variable immunodeficiency; acquired immunodeficiency syndrome.  
 OS Homo sapiens.  
 PN MO200270008-A1.  
 PD 12-SEP-2002.  
 PR 04-MAR-2002; 2002MO-US06762.  
 PR 02-MAR-2001; 2001US-0798689.  
 PA (IMCL-) IMCLONE SYSTEMS INC.  
 PA (ROCK/) ROCKWELL P.  
 PA (GOLD/) GOLDSTEIN N I.  
 DR WPI; 2002-691738/74.  
 DR N-PSDB; AAD46234.  
 XX Inhibiting tumor growth in humans involves administering vascular  
 CC endothelial growth factor receptor antagonists in combination with  
 CC radiation, chemotherapeutic agents, or epidermal growth factor receptor  
 CC antagonists -  
 PS Example 12; Page 127; 151pp; English.  
 CC The invention relates to a method of inhibiting tumour growth which  
 CC involves administering, vascular endothelial growth factor receptor  
 CC (VEGFR) antagonists in combination with radiation, chemotherapeutic  
 CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method  
 CC is useful for inhibiting tumour growth in a human, where the tumour (e.g.  
 CC tumour of the breast, heart, lung, small intestine, colon, spleen, bone,  
 CC kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,  
 CC bone marrow, blood, thymus, uterus, testicles, cervix or liver) over

CC The invention relates to a novel antibody having a first antigen binding  
 CC site specific for a first vascular endothelial growth factor (VEGF)  
 CC receptor and a second antigen-binding site specific for a second VEGF  
 CC receptor. The bispecific antigen-binding proteins block activation of the  
 CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
 CC cellular functions such as mitogenesis of vascular endothelial cells  
 CC and migration of leukemia cells. The antibodies are useful for treating  
 CC tumors and for in vivo or in vitro for investigative and diagnostic  
 CC methods. This sequence represents a human protein relating to the  
 CC bispecific antibodies that bind to the VEGF receptors of the invention.

XX Sequence 116 AA;

Query Match 72.3%; Score 475.5; DB 24; Length 116;  
 Best Local Similarity 76.0%; Pred. No. 1.5e-36;  
 Matches 95; Conservative 7; Mismatches 14; Indels 9; Gaps 1;

QY 1 EVQLVKGSGEGLVKGSGSLRLSCAASGFFPRRDIMHWRTQPKGLEWVSISGSGNYIDY 60  
 DB 1 EVQLVQSGGGLVKGSGSLRLSCAASGFTPSYSMWVRQAPGKLEWVSISSSSYIYY 60  
 QY 61 ADSVKGRTISRDNANNVYLOMNSLRADMAVYFCARDGTIFGSAATWRARFDINGRTM 120  
 DB 61 ADSVKGRTISRDNANNVYLOMNSLRADDTAVYTCAR-----VTDARFDINGRTM 111

QY 121 VTWSS 125  
 DB 112 VTWSS 116

RESULT 6  
 AAE34873  
 ID AAE34873 standard; Protein; 114 AA.

XX AAE34873;

DT 28-MAY-2003 (first entry)

XX B1W48 antibody heavy chain variable region.

XX B1W48 antibody; heavy chain variable region; light chain variable region;  
 XX VH; VL; CD44v6; medicament; cancer; antibody therapy.

OS Unidentified.

XX MO200294879-A1.

XX 28-NOV-2002.

PF 17-MAY-2002; 2002WO-BP05467.

XX 18-MAY-2001; 2001EP-0112237.

PR 26-SEP-2001; 2001US-325147P.

XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.

PA (BOEH ) BOEHRINGER INGELHEIM PHARM INC.

PI Adolf G. Ostermann E, Patzelt E, Sproll M, Heider K, Miglietta JJ;

XX Van Dongen AAMS;

DR N-PSDB; AAD53209.

XX New antibodies specific for an epitope coded by the variant exon of the  
 PT CD44 gene, useful for treating cancer, including non-small cell lung,  
 PT breast, head and neck, ovarian and lung cancer -

XX Claim 1; Column 43; 78pp; English.

XX The present invention relates to novel antibody molecules comprising a  
 CC variable region of the heavy (VH) and/or light chain (VL) of CD44v6  
 CC specific humanised antibody called B1W48 and B1W44. Sequences of the  
 CC invention are useful for manufacturing a medicament and for treating

CC cancer including colorectum, non-small cell lung, breast, head and neck,  
 CC ovarian, lung, bladder, pancreatic cancer or metastatic cancers of the  
 CC brain. They are also useful in antibody therapy. The present sequence  
 CC is B1W48 antibody heavy chain variable region. This sequence is used  
 CC in the exemplification of the invention.

XX Sequence 114 AA;

Query Match 71.8%; Score 472.5; DB 24; Length 114;  
 Best Local Similarity 73.6%; Pred. No. 2.7e-36;  
 Matches 92; Conservative 8; Mismatches 14; Indels 11; Gaps 1;

QY 1 EVQLVKGSGEGLVKGSGSLRLSCAASGFFPRRDIMHWRTQPKGLEWVSISGSGNYIDY 60  
 DB 1 EVQLVQSGGGLVKGSGSLRLSCAASGFTPSYDMWVRQAPGKLEWVSISGSGSYIYY 60  
 QY 61 ADSVKGRTISRDNANNVYLOMNSLRADMAVYFCARDGTIFGSAATWRARFDINGRTM 120  
 DB 61 LDSIKGRTISRDNANNVYLOMNSLRADDTAVYTCARQ-----LDYWGRTTL 109

QY 121 VTWSS 125  
 DB 110 VTWSS 114

RESULT 7  
 AAE34876  
 ID AAE34876 standard; Protein; 444 AA.

XX AAE34876;

DT 28-MAY-2003 (first entry)

XX B1W44/8 antibody heavy chain mature protein.

XX B1W48 antibody; heavy chain variable region; light chain variable region;  
 XX VH; VL; CD44v6; medicament; cancer; antibody therapy.

OS Unidentified.

XX MO200294879-A1.

XX 28-NOV-2002.

PF 17-MAY-2002; 2002WO-BP05467.

XX 18-MAY-2001; 2001EP-0112237.

PR 26-SEP-2001; 2001US-325147P.

XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.

PA (BOEH ) BOEHRINGER INGELHEIM PHARM INC.

PI Adolf G. Ostermann E, Patzelt E, Sproll M, Heider K, Miglietta JJ;

XX Van Dongen AAMS;

DR N-PSDB; AAD53212, AAD53215.

XX New antibodies specific for an epitope coded by the variant exon of the  
 PT CD44 gene, useful for treating cancer, including non-small cell lung,  
 PT breast, head and neck, ovarian and lung cancer -

XX Claim 24; Column 44; 78pp; English.

XX The present invention relates to novel antibody molecules comprising a  
 CC variable region of the heavy (VH) and/or light chain (VL) of CD44v6  
 CC specific humanised antibody called B1W48 and B1W44. Sequences of the  
 CC invention are useful for manufacturing a medicament and for treating  
 CC cancer including colorectum, non-small cell lung, breast, head and neck,  
 CC ovarian, lung, bladder, pancreatic cancer or metastatic cancers of the  
 CC brain. They are also useful in antibody therapy. The present sequence  
 CC is B1W44/8 antibody heavy chain mature protein. This sequence is used  
 CC in the exemplification of the invention.



PT treatment of hemophilia A patients with these antibodies -  
XX  
PS Example 8; Fig 9E; 61pp; English.  
CC This invention describes a novel polynucleotide (1) (and complements and  
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence  
CC coding for a human antibody with factor VIII specificity which has  
CC hemostatic activity. (1) is useful a primer or probe for detecting the  
CC presence of inhibitory antibodies directed against factor VIII. The  
CC polypeptides of the invention and the antibodies generated from them  
CC are useful in compositions for neutralizing factor VIII inhibiting  
CC antibodies in hemophilia A patients. This sequence represents a fragment  
CC of the human factor VIII antibody heavy chain variable region protein B04  
CC which is used in the method of the invention.  
XX  
SQ Sequence 125 AA;  
Query Match 100.0%; Score 658; DB 21; Length 125;  
Best Local Similarity 100.0%; Pred. No. 2.1e-53;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EVOLVKSGBGLVPGGSLRLSCAASGFTPRRDIHWVROTPGKLEWVSISGNYIDY 60  
DB 1 EVOLVKSGBGLVPGGSLRLSCAASGFTPRRDIHWVROTPGKLEWVSISGNYIDY 60  
QY 61 ADSVKGRFTISRDNANNNVYLQWNSLRADMAVYFCARDGTIFGSAATWRAFDIWRGTM 120  
DB 61 ADSVKGRFTISRDNANNNVYLQWNSLRADMAVYFCARDGTIFGSAATWRAFDIWRGTM 120  
QY 121 VTVSS 125  
DB 121 VTVSS 125  
RESULT 2  
AAV50965 standard; Protein; 126 AA.  
XX  
AC AAV50965;  
XX  
DT 23-MAR-2000 (first entry)  
XX  
DE Human FVIII antibody A3-C1 scFv heavy chain protein B04.  
XX  
KM Human, heavy chain; antibody; factor VIII; hemostatic;  
KM hemophilia A; scFv; A3-C1.  
XX  
OS Homo sapiens.  
XX  
PN WO9558680-A2.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 59WO-NL00285.  
XX  
PR 08-MAY-1998; 98EP-0201543.  
XX  
PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.  
PI Voorberg JJ, Van Den Brink EN, Turenhout EAM;  
DR WPI; 2000-053102/04.  
XX  
PT New polynucleotide, polypeptide and antibody useful for diagnosing the  
PT presence of neutralizing antibodies against factor VIII and for  
PT treatment of hemophilia A patients with these antibodies -  
XX  
PS Example 8; Fig 9A; 61pp; English.  
CC This invention describes a novel polynucleotide (1) (and complements and  
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence  
CC coding for a human antibody with factor VIII specificity which has  
CC hemostatic activity. (1) is useful a primer or probe for detecting the

CC presence of inhibitory antibodies directed against factor VIII. The  
CC polypeptides of the invention and the antibodies generated from them  
CC are useful in compositions for neutralizing factor VIII inhibiting  
CC antibodies in hemophilia A patients. This sequence represents the human  
CC factor VIII antibody A3-C1 specific scFv protein B04 which is used  
CC in the method of the invention.  
XX  
SQ Sequence 126 AA;  
Query Match 100.0%; Score 658; DB 21; Length 126;  
Best Local Similarity 100.0%; Pred. No. 2.1e-53;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EVOLVKSGBGLVPGGSLRLSCAASGFTPRRDIHWVROTPGKLEWVSISGNYIDY 60  
DB 1 EVOLVKSGBGLVPGGSLRLSCAASGFTPRRDIHWVROTPGKLEWVSISGNYIDY 60  
QY 61 ADSVKGRFTISRDNANNNVYLQWNSLRADMAVYFCARDGTIFGSAATWRAFDIWRGTM 120  
DB 61 ADSVKGRFTISRDNANNNVYLQWNSLRADMAVYFCARDGTIFGSAATWRAFDIWRGTM 120  
QY 121 VTVSS 125  
DB 121 VTVSS 125  
RESULT 3  
ABP45351 standard; Protein; 252 AA.  
XX  
AC ABP45351;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human Blys binding scFv SEQ ID 1362.  
XX  
KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200202641-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 15-JUN-2001; 2001WO-US19110.  
XX  
PR 16-JUN-2000; 2000US-212210P.  
XX  
PR 17-OCT-2000; 2000US-240816P.  
XX  
PR 16-MAR-2001; 2001US-276248P.  
XX  
PR 21-MAR-2001; 2001US-277379P.  
XX  
PR 25-MAY-2001; 2001US-293499P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
DR WPI; 2002-114799/15.  
XX  
PT Antibodies against B lymphocyte Stimulating polypeptides, useful for  
PT the diagnosis and treatment of cancers and immune disorders -  
XX  
PS Claim 1; Page 2028-2029; 3148pp; English.  
CC This invention describes novel antibodies that immunospecifically bind to  
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have



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ID Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 23, Last annotation update)
DE Single chain Fv (Fragment).
OS Homo sapiens (Human).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBT_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme: Isolation from a
RL human synthetic phage display library and characterization."
DR EMBL; AB049915; BAB16829.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 112 AA; 12243 MW; 24PIA45EC3B84788 CRC64;

Query Match 62.1%; Score 408.5; DB 4; Length 112;
Best Local Similarity 66.9%; Pred. No. 1.1e-34;
Matches 81; Conservative 10; Mismatches 21; Indels 9; Gaps 1;

Qy 1 EVOLKSGEGLYKPGSLRLSCAAGFTFRRYDIHVVROTPEGKLEWSSISGGNYIDY 60
Db 1 EVQLVESGGGVVQPGKSLRLSCAAGFTFYDDYGMGVVQAPGKGLWVSGINMGSTGY 60

Qy 61 ADSVKGRTISRDNANVVYLOMNSLRADMAVYFCARDGTIFGSNATWRAPDIWGRGTM 120
Db 61 ADSVKGRTISRDNANVVYLOMNSLRADMTAVYTCAR-----RRYALDYWGQGTLL 111

Qy 121 V 121
Db 112 V 112

RESULT 15
Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBT_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.

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DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 62.0%; Score 408; DB 4; Length 116;
Best Local Similarity 65.3%; Pred. No. 1.3e-34;
Matches 81; Conservative 13; Mismatches 22; Indels 8; Gaps 1;

Qy 2 VOLVKSGEGLYKPGSLRLSCAAGFTFRRYDIHVVROTPEGKLEWSSISGGNYIDYA 61
Db 1 EVQLVESGGGVVQPGKSLRLSCAAGFTFSYAMHWVQAPGKGLWVAVISYDSNKTYY 60

Qy 62 DSVKGRFTISRDNANVVYLOMNSLRADMAVYFCARDGTIFGSNATWRAPDIWGRGTMV 121
Db 61 DSVKGRFTISRDNANVVYLOMNSLRADMTAVYTCAGGGGL-----GLGYWGQGTLLV 112

Qy 122 TVSS 125
Db 113 TVSS 116

```

Search completed: December 30, 2003, 11:01:09  
 Job time : 31.463 secs

09UL84  
ID 09UL84 PRELIMINARY; PRT; 122 AA.  
AC 09UL84;  
DT 01-MAY-2000 (TEMBLrel. 13, Created)  
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=961934;  
RW X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetuses".  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035030; AAD56266.1; -.  
DR HSSP; P01772; 2FB4.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON TER 1  
FT NON TER 122  
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;  
  
Query Match 63.9%; Score 420.5; DB 4; Length 122;  
Best Local Similarity 66.1%; Pred. No. 7.1e-36;  
Matches 84; Conservative 17; Mismatches 19; Indels 7; Gaps 2;  
  
QY 1 EVOLVSGGLVPGGSLRLSCAASGTFRRYDIHWROTGPGLRWSSISGSGNYIDY 60  
DB 1 EVOLVSGGGLVPGGSLRLSCAASGTFRRYDIHWROTGPGLRWSSISGSGNYIDY 60  
QY 61 ADSVKGRFTISRDNANVVYLYQNSLRADMAVYFCARD--GTIFGSAATWRAFDIWRG 118  
DB 61 ADSVKGRFTISRDNANVVYLYQNSLRADMAVYFCARD--GTIFGSAATWRAFDIWRG 118  
QY 119 TMTVSS 125  
DB 116 TLVTSS 122  
  
RESULT 12  
Q91205 PRELIMINARY; PRT; 473 AA.  
AC Q91205;  
DT 01-DEC-2001 (TEMBLrel. 19, Created)  
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
DE Hypothetical 51.9 kDa protein.  
GN AU044919.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RU Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC010327; AA010327.1; -.  
DR MGD; MGI:214967; AU044919.  
DR InterPro; IPR000345; CytC\_heme\_bind.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig; 3.  
DR

DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00190; CYTOCHROME C; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;  
  
Query Match 63.6%; Score 418.5; DB 11; Length 473;  
Best Local Similarity 65.1%; Pred. No. 6.4e-35;  
Matches 82; Conservative 14; Mismatches 21; Indels 9; Gaps 2;  
  
QY 1 EVOLVSGGLVPGGSLRLSCAASGTFRRYDIHWROTGPGLRWSSISGSGNYIDY 60  
DB 20 EVOLVSGGGLVPGGSLRLSCAASGTFRRYDIHWROTGPGLRWSSISGSGNYIDY 79  
QY 61 ADSVKGRFTISRDNANVVYLYQNSLRADMAVYFCARDGTIFGSAATW--RAFDIWRG 119  
DB 80 ADSVKGRFTISRDNANVVYLYQNSLRADMAVYFCARDGTIFGSAATW--RAFDIWRG 131  
QY 120 TMTVSS 125  
DB 132 TLVTSS 137  
  
RESULT 13  
Q920E7 PRELIMINARY; PRT; 119 AA.  
AC Q920E7;  
DT 01-DEC-2001 (TEMBLrel. 19, Created)  
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
DE Pterin-mimicking anti-idiotypic heavy chain variable region  
DE (fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Atkin J.D., Iape A., Jennings I.G., Horaltis O., Cotton R.G.H.;  
RT "Definition of the idiotype of Pterin-mimicking Antibodies Expressed  
in Mammalian Cells".  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307937; AA09421.1; -.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON TER 1  
FT NON TER 119  
SQ SEQUENCE 119 AA; 13025 MW; F6B90404381CA7C CRC64;  
  
Query Match 63.5%; Score 418; DB 11; Length 119;  
Best Local Similarity 63.6%; Pred. No. 1.2e-35;  
Matches 82; Conservative 17; Mismatches 16; Indels 14; Gaps 2;  
  
QY 1 EVOLVSGGLVPGGSLRLSCAASGTFRRYDIHWROTGPGLRWSSISGSGNYIDY 60  
DB 1 EVOLVSGGGLVPGGSLRLSCAASGTFRRYDIHWROTGPGLRWSSISGSGNYIDY 60  
QY 61 ADSVKGRFTISRDNANVVYLYQNSLRADMAVYFCARDGTIFGSAATWRAFDI---NG 116  
DB 61 ADSVKGRFTISRDNANVVYLYQNSLRADMAVYFCARDGTIFGSAATWRAFDI---NG 116  
QY 117 RGTMTVSS 125  
DB 111 QGTLVTSSA 119  
  
RESULT 14  
Q9HCCI



## RESULT 8

Q9NSK4 PRELIMINARY; PRT; 499 AA.  
 ID O9NSK4  
 AC O9NSK4  
 DT 01-OCT-2002 (TREMblrel. 22, Created)  
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxId=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RA Struhsberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC032249; AAH32249.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-CL.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 4.  
 DR SMART; SM00409; IG; 4.  
 DR SMART; SM00407; IGL1; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 4.  
 DR PROSITE; PSS0290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;  
 Query Match 65.2%; Score 428; DB 4; Length 499;  
 Best Local Similarity 66.9%; Pred. No. 5.6e-36;  
 Matches 85; Conservative 13; Mismatches 27; Indels 2; Gaps 1;  
 QY 1 EVOLVSGEGLVPGGSLRLSCAASGFTFRRIYDIHWVROTPGKLEWSSISSGGNYIDY 60  
 DB 20 EVQLVESGGGVVPRGSLRLSCISGFTFDGSGAVVRQAPGKLEWSSISSGGNYIDY 79  
 QY 61 ADSVKGRTISRDNANNVYLOMNSLRADMAVYFCARDGTFGSAATWRAFDIWRG 118  
 DB 80 ADSVKGRTISRDNANNVYLOMNSLRADMAVYFCARDGTFGSAATWRAFDIWRG 139  
 QY 119 TWTYVSS 125  
 DB 140 TWTYVSS 146  
 RESULT 9  
 ID O99KA4 PRELIMINARY; PRT; 487 AA.  
 AC O99KA4  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Hypothetical 52.6 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_TaxId=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RA Struhsberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC004786; AAH04786.1; -.  
 DR HSSP; P01810; 2FBJ.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 4.  
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PSS0835; IG\_LIKE; 4.  
 DR PROSITE; PSS0290; IG\_MHC; 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB33077B CRC64;

Query Match 64.7%; Score 425.5; DB 11; Length 487;  
 Best Local Similarity 65.4%; Pred. No. 1.2e-35;  
 Matches 83; Conservative 18; Mismatches 21; Indels 5; Gaps 2;

QY 1 EVOLVSGEGLVPGGSLRLSCAASGFTFRRIYDIHWVROTPGKLEWSSISSGGNYIDY 60  
 DB 20 EVQLVESGGGVVPRGSLRLSCISGFTFDGSGAVVRQAPGKLEWSSISSGGNYIDY 79  
 QY 61 ADSVKGRTISRDNANNVYLOMNSLRADMAVYFCARDGTFGSAATWRAFDIWRG 118  
 DB 80 PDVVGRTISRDNANNVYLOMNSLRADMAVYFCARDGTFGSAATWRAFDIWRG 136  
 QY 119 TWTYVSS 125  
 DB 137 TWTYVSS 143  
 RESULT 10  
 ID Q9UL90 PRELIMINARY; PRT; 113 AA.  
 AC Q9UL90  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region (fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxId=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalie N.N., Berney S.M., Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035024; AAD56260.1; -.  
 DR HSSP; P01772; 2FBJ.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 64.6%; Score 425; DB 4; Length 113;  
 Best Local Similarity 66.4%; Pred. No. 2.2e-36;  
 Matches 83; Conservative 13; Mismatches 17; Indels 12; Gaps 1;

QY 1 EVOLVSGEGLVPGGSLRLSCAASGFTFRRIYDIHWVROTPGKLEWSSISSGGNYIDY 60  
 DB 1 EVQLVESGGGVVPRGSLRLSCISGFTFDGSGAVVRQAPGKLEWSSISSGGNYIDY 79  
 QY 61 ADSVKGRTISRDNANNVYLOMNSLRADMAVYFCARDGTFGSAATWRAFDIWRG 120  
 DB 61 ADSVKGRTISRDNANNVYLOMNSLRADMAVYFCARDGTFGSAATWRAFDIWRG 108  
 QY 121 VTVSS 125  
 DB 109 VTVSS 113  
 RESULT 11



Qy 121 VTSS 125  
 |||||  
 Db 137 VTSS 141

## RESULT 2

Q9UL91

PRELIMINARY; PRT; 118 AA.

AC Q9UL91: PRELIMINARY; PRT; 118 AA.  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxId=9606;  
 [1]  
 RX MEDLINE=98277139; PubMed=9614934;  
 WU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;  
 "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
 RL EMBL: AF035023; AAD56259.1; -.  
 DR HSP; P01772; 2F84.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 118  
 SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 67.7%; Score 445.5; DB 4; Length 118;  
 Best Local Similarity 74.4%; Pred. No. 1.7e-38;  
 Matches 92; Conservative 9; Mismatches 16; Indels 7; Gaps 2;

Qy 1 EVOLVSGGLVPGSLRLSCAAGFTFRRIYDIHWRTQPGKLEWVSISGGNYIDY 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1 EVOLVSGGGLVPGSLRLSCAAGFTFRRIYDIHWRTQPGKLEWVSISGGNYIDY 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 61 ADSVKGRTISRDNANNVYLQNSLRADMAVYFCARDGTIFGSAATWRAPDIWGRGM 120  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 61 ADSVKGRTISRDNANNVYLQNSLRADMAVYFCARDGTIFGSAATWRAPDIWGRGM 113  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 121 VTSS 124  
 |||||  
 Db 114 VTSS 117

## RESULT 3

Q96K68

PRELIMINARY; PRT; 494 AA.

AC Q96K68: PRELIMINARY; PRT; 494 AA.  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Hypothetical protein FLJ14473.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxId=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RA Itoigai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shitatori A., Sudo H.,

RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi M., Chiba Y., Ienida S., Murakawa K., Ono Y., Takiguchi S.,  
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuo Y.,  
 RA Niimura K., Iwayanagi T.;  
 RT "NEO human cDNA sequencing project";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK027379; BAB55072.1; -.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_4.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AB5A84C0E CRC64;

Query Match 67.1%; Score 441.5; DB 4; Length 494;  
 Best Local Similarity 70.4%; Pred. No. 2.8e-37;  
 Matches 88; Conservative 11; Mismatches 23; Indels 3; Gaps 1;

Qy 1 EVOLVSGGLVPGSLRLSCAAGFTFRRIYDIHWRTQPGKLEWVSISGGNYIDY 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 20 EVOLVSGGGLVPGSLRLSCAAGFTFRRIYDIHWRTQPGKLEWVSISGGNYIDY 79  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 61 ADSVKGRTISRDNANNVYLQNSLRADMAVYFCARDGTIFGSAATWRAPDIWGRGM 120  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 80 RDSVKGRTISRDNANNVYLQNSLRADMAVYFCARDGTIFGSAATWRAPDIWGRGM 136  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 121 VTSS 125  
 |||||  
 Db 137 VTSS 141

## RESULT 4

Q96BB9

PRELIMINARY; PRT; 597 AA.

AC Q96BB9: PRELIMINARY; PRT; 597 AA.  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxId=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=B-cell;  
 RC Straussberg R.;  
 RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC015760; AAH15760.1; -.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_5.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 5.  
 DR PROSITE: PS00290; IG\_MHC; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 597 AA; 65039 MW; 4FCNA3AD8ECE263D9 CRC64;

Query Match 66.7%; Score 439; DB 4; Length 597;  
 Best Local Similarity 66.4%; Pred. No. 5.5e-37;  
 Matches 83; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

Qy 1 EVOLVSGGLVPGSLRLSCAAGFTFRRIYDIHWRTQPGKLEWVSISGGNYIDY 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 20 EVOLVSGGGLVPGSLRLSCAAGFTFRRIYDIHWRTQPGKLEWVSISGGNYIDY 79  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Qy 61 ADSVKGRTISRDNANNVYLQNSLRADMAVYFCARDGTIFGSAATWRAPDIWGRGM 120  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: December 30, 2003, 10:46:19 ; Search time 30.463 Seconds  
(without alignments)  
1058.876 Million cell updates/sec

Title: US-09-674-752-49

Perfect score: 1 EVOLVSGSGVLKPGGSLRL.....AATWRAFDIWRGTMVTWSS 125

Sequence: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPTRMBL\_23:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mmc:\*  
9: sp\_organelle:\*  
10: sp\_phase:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeophages:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 475.5 | 72.3        | 471    | 4     | Q8TC77      |
| 2          | 445.5 | 67.1        | 494    | 4     | Q9UL91      |
| 3          | 441.5 | 67.1        | 494    | 4     | Q96K68      |
| 4          | 439   | 66.7        | 597    | 4     | Q96BB9      |
| 5          | 438.5 | 66.6        | 613    | 4     | Q8WUK1      |
| 6          | 438   | 66.6        | 121    | 4     | Q9UL71      |
| 7          | 434.5 | 66.0        | 573    | 4     | Q8WU38      |
| 8          | 429   | 65.2        | 499    | 4     | Q8NSK4      |
| 9          | 425.5 | 64.7        | 487    | 11    | Q99KA4      |
| 10         | 425   | 64.6        | 113    | 4     | Q9UL90      |
| 11         | 420.5 | 63.9        | 122    | 4     | Q9UL84      |
| 12         | 418.5 | 63.6        | 473    | 11    | Q91205      |
| 13         | 418   | 63.5        | 119    | 11    | Q92087      |
| 14         | 408.5 | 62.1        | 112    | 4     | Q9HCC1      |
| 15         | 408   | 62.0        | 116    | 4     | Q9UL93      |
| 16         | 407   | 61.9        | 493    | 4     | Q8NCL6      |

|    |       |      |     |    |        |
|----|-------|------|-----|----|--------|
| 17 | 406.5 | 61.8 | 147 | 4  | Q9Y509 |
| 18 | 402.5 | 61.2 | 118 | 4  | Q9UL72 |
| 19 | 392   | 59.6 | 479 | 11 | Q91WPS |
| 20 | 383   | 58.2 | 131 | 4  | Q9UL88 |
| 21 | 382   | 58.1 | 486 | 11 | Q91207 |
| 22 | 380.5 | 57.8 | 469 | 11 | Q8R3V9 |
| 23 | 379   | 57.6 | 480 | 11 | Q91XEL |
| 24 | 363.5 | 55.2 | 457 | 11 | Q9R1A4 |
| 25 | 362   | 55.0 | 521 | 4  | Q8N4Y9 |
| 26 | 360.5 | 54.8 | 124 | 6  | Q9N0M4 |
| 27 | 360   | 54.7 | 95  | 4  | Q9ULB6 |
| 28 | 357.5 | 54.3 | 124 | 6  | Q9N0M6 |
| 29 | 357.5 | 54.3 | 288 | 11 | Q90YF0 |
| 30 | 356.5 | 54.2 | 484 | 11 | Q8VEA0 |
| 31 | 352   | 53.5 | 104 | 4  | Q9UL87 |
| 32 | 350   | 53.2 | 112 | 4  | Q9UGP3 |
| 33 | 348.5 | 53.0 | 124 | 4  | Q9UL92 |
| 34 | 342   | 52.0 | 125 | 4  | Q9UL95 |
| 35 | 328.5 | 49.9 | 159 | 4  | Q96QSO |
| 36 | 324   | 49.2 | 142 | 11 | Q924Q1 |
| 37 | 320   | 48.6 | 473 | 11 | Q9D8L4 |
| 38 | 318   | 48.3 | 614 | 4  | Q96GA6 |
| 39 | 316   | 48.0 | 119 | 4  | Q9UL94 |
| 40 | 315   | 47.9 | 481 | 11 | Q91WT1 |
| 41 | 314   | 47.7 | 147 | 11 | Q925S3 |
| 42 | 314   | 47.7 | 497 | 4  | Q8WY24 |
| 43 | 313.5 | 47.6 | 613 | 11 | Q8VCX7 |
| 44 | 313   | 47.6 | 168 | 11 | Q8VDC9 |
| 45 | 309   | 47.0 | 117 | 11 | Q9QXEX |

## ALIGNMENTS

|                                                              |              |                                                             |                                      |
|--------------------------------------------------------------|--------------|-------------------------------------------------------------|--------------------------------------|
| Q8TC77                                                       | PRELIMINARY; | PRT;                                                        | 471 AA.                              |
| AC Q8TC77;                                                   |              |                                                             |                                      |
| DT 01-JUN-2002 (TREMBLrel. 21, Created)                      |              |                                                             |                                      |
| DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)         |              |                                                             |                                      |
| DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)       |              |                                                             |                                      |
| DS Hypothetical protein.                                     |              |                                                             |                                      |
| OS Homo sapiens (Human).                                     |              |                                                             |                                      |
| OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;   |              |                                                             |                                      |
| OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. |              |                                                             |                                      |
| OX NCBI_Taxid=9606;                                          |              |                                                             |                                      |
| RN [1]                                                       |              |                                                             |                                      |
| RP SEQUENCE FROM N.A.                                        |              |                                                             |                                      |
| RC TISSUE=Spleen;                                            |              |                                                             |                                      |
| RA Strauberg R.;                                             |              |                                                             |                                      |
| RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.   |              |                                                             |                                      |
| DR EMBL: BC024289; AAI24289.1; -                             |              |                                                             |                                      |
| DR InterPro: IPR007110; IG_Like.                             |              |                                                             |                                      |
| DR InterPro: IPR003006; IG_MHC.                              |              |                                                             |                                      |
| DR InterPro: IPR003596; IG_V.                                |              |                                                             |                                      |
| DR Pfam: PF00047; IG; 4.                                     |              |                                                             |                                      |
| DR SMART: SM00406; IG; 1.                                    |              |                                                             |                                      |
| DR PROSITE: PSS0835; IG_LIKE; 4.                             |              |                                                             |                                      |
| DR PROSITE: PSS00290; IG_MHC; 2.                             |              |                                                             |                                      |
| KW Hypothetical protein.                                     |              |                                                             |                                      |
| SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;        |              |                                                             |                                      |
| Query Match                                                  | 72.3%;       | Score 475.5;                                                | DB 4; Length 471;                    |
| Best Local Similarity                                        | 74.4%;       | Pred. No. 7.9e-41;                                          |                                      |
| Matches                                                      | 93;          | Conservative                                                | 11; Mismatches 18; Indels 3; Gaps 1; |
| QY                                                           | 1            | EVOLVSGSGVLKPGGSLRLSCAAGTFRRIYIHWRQTPGKGLVWSSISGANYDY 60    |                                      |
| DB                                                           | 20           | EVOLVSGSGVLKPGGSLRLSCAAGTFRFSSYMNWYRQAPGKGLVWSSISYIY 79     |                                      |
| QY                                                           | 61           | ADVYKGRFTISRNNKVVYLVQNSLRAPDMAYVFCARDITIGSATWRAFDIWRGTM 120 |                                      |
| DB                                                           | 80           | ADVYKGRFTISRNNKVVYLVQNSLRAPDMAYVFCARDITIGSATWRAFDIWRGTM 136 |                                      |



DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG LIKE; 1.  
 KM Immunoglobulin V region: Signal; 3D-structure.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.  
 FT DOMAIN 20 >117 IG-LIKE.  
 FT NON\_TER 117 117  
 SO SEQUENCE 117 AA; 12582 MW; E826733FLA3GB0F1 CRC64;  
 Query Match 58.4%; Score 384; DB 1; Length 117;  
 Best Local Similarity 74.5%; Pred. No. 6e-33;  
 Matches 73; Conservative 9; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 EVQLVSGEGLVPGGSLRLISCAASGFTPRRDYDHWROTQPGKLEWVSSISGCAITYD 60  
 DB 20 EVQLVSGGGLVPGGSLRLISCAASGFTFSYAMSWRAQPGKLEWVAISGSGSTYY 79  
 QY 61 ADSVKGFTISRDNANVYLYQNNSLRAEDMAVYFCAR 98  
 DB 80 GDSVKGFTISRDNANVYLYQNNSLRAEDTAIYCAK 117  
 RESULT 14  
 HV20 MOUSE STANDARD; PRT; 122 AA.  
 ID HV20\_MOUSE  
 AC P01759;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region M603.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8019926; PubMed=6769593;  
 RA Early P., Huang H., Davis M., Calame K., Hood L.;  
 RT "An immunoglobulin heavy chain variable region gene is generated from  
 three segments of DNA: VH, D and JH.";  
 RL Cell 19:981-992(1980).  
 RN [2]  
 RP SEQUENCE OF 1-120.  
 RX MEDLINE=75017346; PubMed=4213527;  
 RA Rudikoff S., Potter M.;  
 RT "Variable region sequence of the heavy chain from a phosphorylcholine  
 binding myeloma protein.";  
 RL Biochemistry 13:4033-4038(1974).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF FAB FRAGMENT.  
 RX MEDLINE=75065510; PubMed=4530984;  
 RA Segal D.M., Padlan E.A., Cohen G.H., Rudikoff S., Potter M.,  
 RA Davies D.R.;  
 RT "The three-dimensional structure of a phosphorylcholine-binding mouse  
 immunoglobulin Fab and the nature of the antigen binding site.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 71:4298-4302(1974).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
 BINDS PHOSPHORYLCHOLINE.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC PIR: B90795; AVMS63.  
 DR PDB; 1MCP; 15-JUL-92.  
 DR PDB; 2MCP; 15-JUL-92.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG LIKE; 1.  
 DR Immunoglobulin V region; 3D-structure.  
 KW DOMAIN 1 121 IG-LIKE.

FT SITE 33 33 H-BOND WITH THE PHOSPHATE GROUP OF PHOS-  
 FT SITE 52 52 PHORYLCHOLINE.  
 FT STRAND 3 7 H-BOND WITH THE PHOSPHATE GROUP OF PHOS-  
 FT STRAND 11 12 PHORYLCHOLINE.  
 FT STRAND 14 15  
 FT STRAND 17 25  
 FT STRAND 30 31  
 FT STRAND 33 39  
 FT TURN 41 42  
 FT STRAND 46 50  
 FT TURN 54 55  
 FT STRAND 61 61  
 FT TURN 64 69  
 FT STRAND 70 75  
 FT TURN 76 79  
 FT STRAND 80 86  
 FT HELIX 90 92  
 FT STRAND 94 103  
 FT STRAND 107 112  
 FT STRAND 116 120  
 FT NON\_TER 122 122  
 SO SEQUENCE 122 AA; 13626 MW; BA2C864438B64F0F CRC64;  
 Query Match 58.1%; Score 382.5; DB 1; Length 122;  
 Best Local Similarity 59.8%; Pred. No. 8.9e-33;  
 Matches 76; Conservative 22; Mismatches 22; Indels 7; Gaps 4;  
 QY 1 EVQLVSGEGLVPGGSLRLISCAASGFTPRRDYDHWROTQPGKLEWVSSISGCAITYD 58  
 DB 1 EVQLVSGGGLVPGGSLRLISCAASGFTFSYAMSWRAQPGKLEWVAISGSGSTYY 60  
 QY 59 DYADSVKGFTISRDNANVYLYQNNSLRAEDMAVYFCARDGTFSSAATWRAFDIWRG 118  
 DB 61 EYASVKGFTISRDNANVYLYQNNSLRAEDTAIYCAK--YGS--TW-YFDVWAG 115  
 QY 119 TWYTVSS 125  
 DB 116 TWYTVSS 122  
 RESULT 15  
 HV01 CANPA STANDARD; PRT; 114 AA.  
 ID HV01\_CANPA  
 AC P01754;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region GOM.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=77242268; PubMed=407924;  
 RA Wasserman R.L., Capra J.D.;  
 RT "Primary structure of the variable regions of two canine  
 immunoglobulin heavy chains.";  
 RL Biochemistry 16:3160-3168(1977).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC PIR: A02067; AYDCGM.  
 DR HSSP; P01772; 2FB4.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG LIKE; 1.  
 DR Immunoglobulin V region.  
 KW DOMAIN 1 112 IG-LIKE.

```

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region BJT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN (1)
RP MEDLINE=78137069; PubMed=416441;
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
RT IGA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02050; AZHUBU.
DR HSSP: P01789; 1MCP.
DR GO: GO:000576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DC64 CRC64;

Query Match 58.8%; Score 387; DB 1; Length 115;
Best Local Similarity 62.4%; Pred. No. 2,9e-33;
Matches 78; Conservative 16; Mismatches 21; Indels 10; Gaps 2;

QY 1 EVQLVSGEGLVPGGSLRLSCAASGFTPRRDIMHTQPGKLEWVSISGCAVYDY 60
DB 1 EVQLVSGGGLVPGGSLRLSCAASGFTVBSHSMWYRQAPGVALZVWSAIVGGITY-Y 59
QY 61 ADSVKGFTISRDNANVYVLTQNSLRADMAVYFCARPGTIGSATWRAFDIWRGTM 120
DB 60 ADSVKGFTISRDSRBTYVLTQNSLRADPTAVYTCARD-----LAARLFGKGT 110
QY 121 VTWSS 125
DB 111 VTWSS 115

RESULT 12
HV3E HUMAN STANDARD; PRT; 120 AA.
ID P01765;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region BRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN (1)
RP MEDLINE=77117674; PubMed=65324;
RA Capra J.D., Hopper J.E.;
RT "Comparative studies on monocytic IgM lambda and IgG kappa from an
RT individual patient. II. The complete amino acid sequence of the VH
RT region of the IgM paraprotein.";
RL Immunohistochemistry 13:995-999(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE
CC SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM

```

```

CC TYPE.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02049; M3HUBW.
DR HSSP: P01772; 2P84.
DR GO: GO:000576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG-LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13227 MW; D3F0428F7C2BE6410 CRC64;

Query Match 58.8%; Score 387; DB 1; Length 120;
Best Local Similarity 61.2%; Pred. No. 3e-33;
Matches 79; Conservative 18; Mismatches 14; Indels 18; Gaps 4;

QY 1 EVQLVSGEGLVPGGSLRLSCAASGFTPRRDIMHTQPGKLEWVSISGCAVYDY 60
DB 1 EVQLVSGGGLVPGGSLRLSCAASGFTFSYNNMVRQVTKGLEWVAIGTAGDQY-Y 59
QY 61 ADSVKGFTISRDNANVYVLTQNSLRADMAVYFCAR-----DGTI---FGSATWRA 111
DB 60 ADSVKGFTISRDSRBTYVLTQNSLRADPTAVYTCARSPVLDVDMKLYYYGS----- 113
QY 112 PDWRGTM 120
DB 114 --VWGQGT 120

RESULT 13
HV3C HUMAN STANDARD; PRT; 117 AA.
ID P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN (1)
RP MEDLINE=81101090; PubMed=6450418;
RA Matthyseens G., Rablitz T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00236; AA053516.1; --
CC EMBL: M35415; AA058735.1; --
CC PIR: A02047; H3HUB2.
CC PDB: 1HOU; 23-DEC-99.
CC Genew: HGNC:5545; IGHV0.
DR GO: GO:000576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE, AND DISULFIDE BONDS.  
 RX MEDLINE=83289131; PubMed=6884994;  
 RA Schmidt W.E., Jung H.-D., Palm W., Hillebrand N.;  
 RT "Three-dimensional structure determination of antibodies. Primary  
 structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=81072295; PubMed=7441755.  
 RA Marguerat M., Deisenhofer J., Huber R., Palm W.;  
 RT "Crystallographic refinement and atomic models of the intact  
 immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A  
 resolution.";  
 RL J. Mol. Biol. 141:369-391(1980).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02055; GHUKL.  
 DR PDB; 2FB4; 12-JUL-89.  
 DR PDB; 2IG2; 12-JUL-89.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; IgV; 1.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.  
 FT DOMAIN 1 112 IG-LIKE.  
 FT MOD\_RES 1 1  
 FT DISULFID 22 96  
 FT DISULFID 105 110  
 FT STRAND 3 7  
 FT STRAND 11 12  
 FT TURN 14 15  
 FT STRAND 18 25  
 FT STRAND 29 31  
 FT HELIX 34 39  
 FT TURN 41 42  
 FT STRAND 45 51  
 FT TURN 53 54  
 FT STRAND 58 60  
 FT STRAND 62 64  
 FT HELIX 65 65  
 FT STRAND 66 67  
 FT TURN 68 73  
 FT TURN 74 77  
 FT STRAND 78 83  
 FT STRAND 88 90  
 FT HELIX 92 99  
 FT STRAND 106 106  
 FT TURN 107 108  
 FT STRAND 109 109  
 FT STRAND 113 116  
 FT STRAND 120 124  
 FT NON\_TER 126 126  
 SQ SEQUENCE 126 AA; 13718 MW; EAD71B52B16F8776 CRC64;  
 Query Match 60.1%; Score 395.5; DB 1; Length 126;  
 Best Local Similarity 63.5%; Pred. No. 4.2e-34;  
 Matches 80; Conservative 17; Mismatches 28; Indels 1; Gaps 1;  
 QY 1 EVQLVKGSGEGLVPRGSGLRISCAASGFTFRRYDIHWVROTGPKGLEWVSISGSGNYIDY 60  
 DQ 1 QVQLVDSGGGVVQGRSLRISCSGSGFTFSYAMVWRQAGKGLRWVAITLWDGSDQHY 60  
 QY 61 ADSVKGRTISRDNANVYVLYQNSLRAEDMAVYFCARDGTI-FGSAATWRAFDIWRGT 119  
 DB 61 ADSVKGRTISRDNANVYVLYQNSLRAEDMAVYFCARDGTI-FGSAATWRAFDIWRGT 120

QY 120 MVTYSS 125  
 DQ 121 PVTYSS 126  
 RESULT 10  
 HV3U HUMAN STANDARD; PRT; 120 AA.  
 ID HV3U HUMAN  
 AC P01782;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE 1g heavy chain V-II1 region DOB.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=80020921; PubMed=114209;  
 RA Steiner L.A., Garcia Pardo A., Margolies M.N.;  
 RT "Amino acid sequence of the heavy-chain variable region of the  
 RT crystallizable human myeloma protein Dob.";  
 RL Biochemistry 18:4068-4080(1979).  
 RN [2]  
 RP CRYSTALLIZATION.  
 RX MEDLINE=80020920; PubMed=114208;  
 RA Steiner L.A., Lopes A.D.;  
 RT "The crystallizable human myeloma protein Dob has a hinge-region  
 RT deletion.";  
 RL Biochemistry 18:4054-4067(1979).  
 CC -1- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE  
 CC HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN  
 CC DISULFIDE BONDS.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A90431; GHUBD.  
 DR HSBP; P01772; 2FB4.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 112 IG-LIKE.  
 FT NON\_TER 120 120  
 SQ SEQUENCE 120 AA; 13440 MW; 880DE307C4B2627 CRC64;  
 Query Match 59.7%; Score 392.5; DB 1; Length 120;  
 Best Local Similarity 63.2%; Pred. No. 8.1e-34;  
 Matches 79; Conservative 15; Mismatches 26; Indels 5; Gaps 3;  
 QY 1 EVQLVKGSGEGLVPRGSGLRISCAASGFTFRRYDIHWVROTGPKGLEWVSISGSGNYIDY 60  
 DQ 1 EVQLVDSGGGVVQGRSLRISCSGSGFTFSYAMVWRQAGKGLRWVAITLWDGSDQHY 60  
 QY 61 ADSVKGRTISRDNANVYVLYQNSLRAEDMAVYFCARDGTI-FGSAATWRAFDIWRGT 120  
 DB 61 ADSVKGRTISRDNANVYVLYQNSLRAEDMAVYFCARDGTI-FGSAATWRAFDIWRGT 120  
 QY 121 VTYSS 125  
 DQ 121 VTYSS 120  
 RESULT 11  
 HV3F HUMAN STANDARD; PRT; 115 AA.  
 ID HV3F HUMAN  
 AC P01767;





RT "The rule of antibody structure. The primary structure of a  
 RT monoclonal IgG1 immunoglobulin (myeloma protein Nle). III. The  
 RT cytoelectric peptides of the H-chain, alignment of the tryptic  
 RT peptides and discussion of the complete structure."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).  
 RN [2]  
 RP DISULFIDE BOND.  
 CC MEDLINE=77070267; PubMed=1002129;  
 RA Decker L., Schwarz J., Reicher W., Hilschmann N.;  
 RA "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nle). I: Purification and  
 RT characterization of the protein, the L- and H-chains, the  
 RT cyanogen bromide cleavage products, and the disulfide bridges."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540 (1976).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
 CC PROTEIN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR HSSP; P01772; 2FB4.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KM Immunoglobulin V region; Pyroliidone carboxylic acid.  
 FT MOD\_RES 1 112 IG-LIKE.  
 FT DISULFID 22 96 PYROLIDONE CARBOXYLIC ACID.  
 FT NON\_TER 119 119  
 SQ SEQUENCE 119 AA; 13242 MW; C96335AGE5SE165B CRC64;  
 Query Match 61.2%; Score 403; DB 1; Length 119;  
 Best Local Similarity 63.8%; Pred. No. 6,6e-35;  
 Matches 81; Conservative 15; Mismatches 21; Indels 10; Gaps 2;  
 QY 1 EVOLVSGEGLVKPGSLRLSCAASGFTFRRIYDIHWRTPGKLEWSSISGNYIDY 60  
 ID HV3B\_HUMAN STANDARD; PRT; 114 AA.  
 AC P01763;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region WEA.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=63273707; PubMed=6410398;  
 RA Goni F., Frangione B.;  
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM  
 RT (protein WEA) with antibody activity against 3,4-pyruvylated  
 RT galactose in Klebsiella polysaccharides K30 and K33."  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY

CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH  
 CC WALDENSTROM'S MACROGLOBULINEMIA.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02046; M3HWE.  
 DR HSSP; P01772; 2FB4.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KM Immunoglobulin V region; Pyroliidone carboxylic acid.  
 FT MOD\_RES 1 112 IG-LIKE.  
 FT NON\_TER 114 114 PYROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;  
 Query Match 60.9%; Score 400.5; DB 1; Length 114;  
 Best Local Similarity 64.0%; Pred. No. 1.1e-34;  
 Matches 80; Conservative 16; Mismatches 18; Indels 11; Gaps 2;  
 QY 1 EVOLVSGEGLVKPGSLRLSCAASGFTFRRIYDIHWRTPGKLEWSSISGNYIDY 60  
 ID HV3B\_HUMAN STANDARD; PRT; 121 AA.  
 AC P01771;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region HIL.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=79124695; PubMed=420800;  
 RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;  
 RT "Amino acid sequence of the VH region of human myeloma  
 RT cytoimmunoglobulin IgG H11."  
 RL Biochemistry 18:553-560 (1979).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
 CC PROTEIN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02054; GIHDL.  
 DR HSSP; P01772; 2FB4.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KM Immunoglobulin V region; Pyroliidone carboxylic acid.  
 FT MOD\_RES 1 112 IG-LIKE.  
 FT NON\_TER 1 112 PYROLIDONE CARBOXYLIC ACID.



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## OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 6.70187 Seconds

(Without alignments)  
877.119 Million cell updates/sec

Title: US-09-674-752-49

Perfect score: 658  
Sequence: 1 EVQLVKGSGGLVKGSGSLRL.....AATWRAFDIWRGCTMTVSS 125Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 438.5 | 66.6        | 122    | 1  | HV3G_HUMAN  |
| 2          | 408.5 | 62.1        | 136    | 1  | HV16_MOUSE  |
| 3          | 406.5 | 61.8        | 122    | 1  | HV3H_HUMAN  |
| 4          | 403   | 61.2        | 119    | 1  | HV3I_HUMAN  |
| 5          | 400.5 | 60.9        | 114    | 1  | HV3B_HUMAN  |
| 6          | 400   | 60.8        | 121    | 1  | HV3J_HUMAN  |
| 7          | 398.5 | 60.6        | 122    | 1  | HV3A_HUMAN  |
| 8          | 397.5 | 60.4        | 116    | 1  | HV3T_HUMAN  |
| 9          | 395.5 | 60.1        | 126    | 1  | HV3K_HUMAN  |
| 10         | 392.5 | 59.7        | 120    | 1  | HV3U_HUMAN  |
| 11         | 387   | 58.8        | 115    | 1  | HV3F_HUMAN  |
| 12         | 387   | 58.8        | 120    | 1  | HV3E_HUMAN  |
| 13         | 384   | 58.4        | 117    | 1  | HV3C_HUMAN  |
| 14         | 382.5 | 58.1        | 122    | 1  | HV20_MOUSE  |
| 15         | 379.5 | 57.7        | 114    | 1  | HV01_CANPA  |
| 16         | 379   | 57.6        | 98     | 1  | HV57_MOUSE  |
| 17         | 377   | 57.3        | 123    | 1  | HV18_MOUSE  |
| 18         | 376.5 | 57.2        | 119    | 1  | HV38_MOUSE  |
| 19         | 375   | 57.0        | 117    | 1  | HV58_MOUSE  |
| 20         | 374   | 56.8        | 115    | 1  | HV3D_HUMAN  |
| 21         | 374   | 56.8        | 123    | 1  | HV25_MOUSE  |
| 22         | 373.5 | 56.8        | 97     | 1  | HV56_MOUSE  |
| 23         | 373   | 56.7        | 123    | 1  | HV19_MOUSE  |
| 24         | 372.5 | 56.6        | 122    | 1  | HV21_MOUSE  |
| 25         | 372   | 56.5        | 117    | 1  | HV55_MOUSE  |
| 26         | 371   | 56.4        | 123    | 1  | HV23_MOUSE  |
| 27         | 370   | 56.2        | 123    | 1  | HV22_MOUSE  |
| 28         | 370   | 56.2        | 144    | 1  | HV26_MOUSE  |
| 29         | 369.5 | 56.2        | 116    | 1  | HV05_CARAU  |
| 30         | 369   | 56.1        | 123    | 1  | HV24_MOUSE  |
| 31         | 367   | 55.8        | 117    | 1  | HV02_CANPA  |
| 32         | 362.5 | 55.1        | 119    | 1  | HV37_MOUSE  |
| 33         | 362   | 55.0        | 117    | 1  | HV17_MOUSE  |

|    |       |      |     |   |            |
|----|-------|------|-----|---|------------|
| 34 | 360.5 | 54.8 | 119 | 1 | HV2N_HUMAN |
| 35 | 359.5 | 54.6 | 119 | 1 | HV3P_HUMAN |
| 36 | 359   | 54.6 | 119 | 1 | HV3L_HUMAN |
| 37 | 358.5 | 54.5 | 119 | 1 | HV3M_HUMAN |
| 38 | 358   | 54.4 | 116 | 1 | HV3R_HUMAN |
| 39 | 356   | 54.1 | 117 | 1 | HV54_MOUSE |
| 40 | 356   | 54.1 | 118 | 1 | HV39_MOUSE |
| 41 | 355   | 54.0 | 115 | 1 | HV32_MOUSE |
| 42 | 355   | 54.0 | 117 | 1 | HV59_MOUSE |
| 43 | 355   | 54.0 | 142 | 1 | HV01_RAT   |
| 44 | 353   | 53.6 | 113 | 1 | HV30_MOUSE |
| 45 | 351.5 | 53.4 | 111 | 1 | HV35_MOUSE |

## ALIGNMENTS

## RESULT 1

ID HV3G\_HUMAN STANDARD; PRT; 122 AA.  
AC P01768;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V-II region CAM.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Buthera; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE.  
RX MEDLINE=61013859; PubMed=6774332;  
RA Lehman D.W., Putnam F.W.;  
RT "Amino acid sequence of the variable region of a human mu chain:  
location of a possible JH segment";  
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243 (1980).  
CC -I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A  
CC PATIENT WITH MACROGLOBULINEMIA.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR HSSP; P01772; 2FB4.  
DR GO; GO:000576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG\_1.  
DR SMART; SM00406; IgV\_1.  
DR PROSITE; PS50835; IG\_LIKE\_1.  
KM Immunoglobulin V region; Pyroglutamate carboxylic acid.  
FT DOMAIN 1 112 IG-LIKE.  
FT MOD\_RBS 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252P1C2 CRC64;

Query Match 66.6%; Score 438.5; DB 1; Length 122;  
Best Local Similarity 65.6%; Pred. No. 1.4e-38;  
Matches 82; Conservative 21; Mismatches 19; Indels 3; Gaps 1;

|    |     |                                                              |
|----|-----|--------------------------------------------------------------|
| Qy | 1   | EVQLVKGSGGLVKGSGSLRLSCAASGFTPRRQDIHWVRQTPGKLEWVSISGGNYIDY 60 |
| Db | 1   | QVELVSSGGVAVZPGRSLRLSCAASGFTPSNYAMHWVRQPGKLEWVAIVSYBGBKYY 60 |
| Qy | 61  | ADSVKGRFTISRNANVVYLQNSLRADMAVYFCARDCITIGSAAATRAPDIMGRTM 120  |
| Db | 61  | ABSVDKRFITSRDSSKRTYLQNSLRABTAVYCARDPILYGB--YDAFNYMGQTL 117   |
| Qy | 121 | VTVSS 125                                                    |
| Db | 118 | VTVSS 122                                                    |

**C/Keywords:** heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>

| Query Match      | 67.88; | Score 446; | DB 2; | Length 121; |
|------------------|--------|------------|-------|-------------|
| PostgreSQL: 100% | 100%   | 100%       | 100%  | 100%        |

Matches 87; Conservative 13; Mismatches 21; Indels 4; Gaps 1;

**Dy**

1 EVQLVDSGEGLVKPGSRLRSCAASGFTFRRYDLMHWRTQPKGLEWSSISGGNTDY 60  
         :  
         :  
         :  
         :  
         :  
         :  
         :  
         :  
         :  
         :  
         :  
         :  
         :  
         :  
         :  
         :  
         :  
         :  
         :  
         :  
         :

**Db**

1 QVLVESGGGVQPGRSLRISCASAGFTFSSYAMHWVRQAPEGLEWAVVISDGSKYY 60

[illegible]

**RESULT 15**

**C36005**

Ig heavy chain V region (30p1) - human

C;Species: Homo sapiens (man)

```
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C;Accession: C26005
```

C;Accession: C36005

Kirschroeder Jr., H.W.; Wang, J.Y.  
Proc Natl Acad Sci U S A 87 6145-6150 1990

A: Title: Preferential utilization of conserved im  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A:Reference number: A36005; MUID:90349571; PMID:2117273

A;Accession: C36005

A;Status: preliminary

A; molecule type: mRNA

A;Residues: 1-119 &lt;SCH&gt;

**A; Cross-references: GB:**

C; Superfamily: Immunoglobulin

**Keywords:** heterotetramer; immunoglobulin C; Key words: heterotetramer; immunoglobulin C; Key words: heterotetramer; immunoglobulin C

F;15-98/Domain: immunoglobulin homology <1

Query Match 67.68: Score 445.

| Query Match | Similarity | Score | DB | Length |
|-------------|------------|-------|----|--------|
| Beat Local  | 69.8%      | 445   | 2  | 119    |

Matched 88: Conservative 11: Mismatches 19: Indels 8: Gaps 2:  
 best local similarity 89.8%; Pred. NO. 1: 98-34;

```

Oy      1 EVQLVKGSGEGLVYPGGSLRLSCAASGFFRRYYDHWVRQTPGKGLIEWSSLSGGNYIDY 600
        |||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 EVQLVKGSGEGLVQPGGSLRLSCAASGFFRTSSYANSWVRQDPAKGLIEWSAISGGSGSTYY 600

```

Dy 61 ADSYKGRFTISRDNANNVYLQMSLRADMAVFPCARDGITFGSLATW-RAPDINRGRT 119  
| | | | | : | | | | | : | | | |  
Db 61 ADSYKGRFTISRDNANKTLVLQMSLRADDAVYYCAKD-----AGMGSGFDYWGGGT 113

Search completed: December 30, 2003, 11:03:19  
Job time : 11.9821 Secs

Query Match 68.1%; Score 448; DB 2; Length 119;  
 Best Local Similarity 69.6%; Pred. No. 1e-34;  
 Matches 87; Conservative 13; Mismatches 19; Indels 6; Gaps 1;

QY 1 EVOLVSGEGLVKPGSLRLSCAASGFTFRRYDIHWYRQTPGKLEWVSISGSGNYIDY 60  
 DB 1 EVOLVSGGGLVOPGSLRLSCAASGFTFSSYMSWVROAPGKLEWVSISGSGSTYY 60

QY 61 ADVKGRFTISRDNANVVYLQNNSLRAEDMAVYFCARDGTIFGSAATWRAFDWGRGT 120  
 DB 61 ADVKGRFTISRDNANVVYLQNNSLRAEDTAVYTCADKRLTGT-----FDYWGQGT 114

QY 121 VTVSS 125  
 DB 115 VTVSS 119

RESULT 11  
 Ig heavy chain - human  
 C/Species: Homo sapiens (man)  
 C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
 R/Accession: S31116  
 R/Author: F.M.; Timmer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
 Eur. J. Immunol. 22, 247-251, 1992  
 A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement  
 A/Reference number: S31104; MUID:92111633; PMID:1730252  
 A/Accession: S31116  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-118 <RBA>  
 A/Cross-references: EMBL:X62966  
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.0%; Score 447.5; DB 2; Length 118;  
 Best Local Similarity 72.0%; Pred. No. 1.1e-34;  
 Matches 90; Conservative 11; Mismatches 17; Indels 7; Gaps 2;

QY 1 EVOLVSGEGLVKPGSLRLSCAASGFTFRRYDIHWYRQTPGKLEWVSISGSGNYIDY 60  
 DB 1 QVOLVSGGGLVOPGSLRLSCAASGFTFSSYMSWVROAPGKLEWVSISGSGNKRY 60

QY 61 ADVKGRFTISRDNANVVYLQNNSLRAEDMAVYFCARDGTIFGSAATWRAFDWGRGT 120  
 DB 61 ADVKGRFTISRDNANVVYLQNNSLRAEDTAVYTCADG---GKA---AFDWMQGT 113

QY 121 VTVSS 125  
 DB 114 VTVSS 118

RESULT 12  
 Ig heavy chain V region - human  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996  
 R/Accession: S30532  
 R/Author: X.  
 submitted to the EMBL Data Library, October 1992  
 A/Reference number: S30520  
 A/Accession: S30532  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-123 <MAR>  
 A/Cross-references: EMBL:Z18318  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 67.9%; Score 447; DB 2; Length 123;  
 Best Local Similarity 72.2%; Pred. No. 1.3e-34;  
 Matches 91; Conservative 10; Mismatches 21; Indels 4; Gaps 3;

QY 1 EVOLVSGEGLVKPGSLRLSCAASGFTFRRYDIHWYRQTPGKLEWVSISGSGNYIDY 60  
 DB 1 EVOLVSGGGLVOPGSLRLSCAASGFTFDYAMHWROAPGKLEWVSISGSGTLYG 60

QY 61 ADVKGRFTISRDNANVVYLQNNSLRAEDMAVYFCARDGTIFGSAATWRAFDWGRGT 119  
 DB 61 ADVKGRFTISRDNANVVYLQNNSLRAEDTAVYTCADKRLTGT-----FDYWGQGT 117

QY 120 MVTSS 125  
 DB 118 MVTSS 123

RESULT 13  
 Ig heavy chain V region - human  
 C/Species: Homo sapiens (man)  
 C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
 R/Accession: S26786  
 R/Author: F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.  
 Eur. J. Immunol. 22, 241-245, 1992  
 A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam  
 A/Reference number: S26786; MUID:92111632; PMID:1730251  
 A/Accession: S26786  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-128 <MOR>  
 A/Cross-references: EMBL:X61014; MUID:932800; PIDN:CA44348.1; PID:91335129  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 67.9%; Score 446.5; DB 2; Length 128;  
 Best Local Similarity 69.5%; Pred. No. 1.5e-34;  
 Matches 91; Conservative 11; Mismatches 20; Indels 9; Gaps 3;

QY 1 EVOLVSGEGLVKPGSLRLSCAASGFTFRRYDIHWYRQTPGKLEWVSISGSGNYIDY 60  
 DB 1 QVOLVSGGGLVOPGSLRLSCAASGFTFDYMSWVROAPGKLEWVSISGSGSTYNY 60

QY 61 ADVKGRFTISRDNANVVYLQNNSLRAEDMAVYFCARDGTIFGSAATWRAFDWGRGT 114  
 DB 61 ADVKGRFTISRDNANVVYLQNNSLRAEDTAVYTCAR-GLYCSSTSCYIMSNM--FDP 117

QY 115 WGRGTMTVSS 125  
 DB 118 WGRGTMTVSS 128

RESULT 14  
 Ig heavy chain V region (M74) - human  
 C/Species: Homo sapiens (man)  
 C/Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Dec-1998  
 R/Accession: G36005  
 R/Author: Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
 A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
 A/Reference number: A36005; MUID:90349571; PMID:2117273  
 A/Accession: G36005  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-121 <SCH>  
 A/Cross-references: GB:M34031  
 C/Genetic8:  
 A/Genes: GDB:IGH@; IGHDI1  
 A/Cross-references: GDB:118731; OMIM:146910  
 A/Map position: 14q32.33-14q32.33  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology

|                       |        |                    |        |                |
|-----------------------|--------|--------------------|--------|----------------|
| Query Match           | 68.5%  | Score 451;         | DB 2;  | Length 125;    |
| Best Local Similarity | 71.2%; | Pred. No. 5.7e-35; |        |                |
| Matches               | 89;    | Conservative       | 10;    | Mismatches 26; |
|                       |        |                    | Indels | 0;             |
|                       |        |                    | Gaps   | 0;             |

```
QY      EVOLVYASGETLYVPGGSLTSCAASGFTRRADIMHWOTPGKGLIEWSSISGCGNIDY 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1 EVGLVSGGGGLVQPGGSLRISCASGFTSSYNNMHWQAQKGLIEWISYSSSSSTIIY 60

QY      ADSVKRFITISRDNNANNVYLLQNNSLPADMAVYFCADGTFISGSAATRAFDIWRGTM 120
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      61 ADSVKRFITISRDNNANSLYLQNNSLPADTAVYICARSRNYSDSGYSHYFDYWGGLT 120

QY      VTWYSS 125
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      121 VTWYSS 125
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

## RESULT 7

**S31105**  
Ig heavy chain (subclass IgM) - human (fragment)  
Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 23-Jul-1999  
C/Accession: S31105  
R/Radiophore, F.M.I.; Timmers, E.; Kentler, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar  
Eur. J. Immunol. 22, 247-251, 1992  
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement  
A/Reference number: S31104, MIMD:9211633, PMID:1730252  
A/Accession: S31105  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-118 <RAA>  
A/Cross-references: EMBL:X63081, NID:g32648, PIN:CAA44803.1, PID:g32649  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C/superfamily: immunoglobulin V region; immunoglobulin homology  
C/keywords: heterotetramer; immunoglobulin  
C/15-98/Domain: immunoglobulin homology <IMM>

|         |                                                                 |               |              |          |             |
|---------|-----------------------------------------------------------------|---------------|--------------|----------|-------------|
|         | Query Match                                                     | 68.3%         | Score 449.5; | DB 2;    | Length 118; |
|         | Best Local Similarity                                           | 73.6%         | Prod. No.    | 7.4e-35; |             |
| Matches | 92; Conservative                                                | 9; Mismatches | 17; Indels   | 7; Gaps  | 2;          |
| QY      | 1 EVQLVDSGSELVRPGSGLRISCAASGFTFRRYDIHWVTQTGGKLEWVSISSGSNYIDY    | 60            | :            | : :      | :           |
| Dd      | 1 QVOLVVSSGGGLVKRPGSLRLSCAASGFTFSDYMSWIROPCKGLEWVSIVSSSSTIYY    | 60            | :            | :        | :           |
| QY      | 61 ADSVKGRFTISRDNANNVLYIQNNSLRAEDMAYVFCAKDGTIRKSAAITWAAPFIWGRTM | 120           | :            | :        | :           |
| Dd      | 61 ADESVKRFTISRDNANKNSLYIQNNSLRAEPTATYYCA--CQLDD-----AFDIMGOGTM | 113           | :            | :        | :           |
| QY      | 121 VTTYS                                                       | 125           |              |          |             |
| Dd      | 114 VTTS                                                        | 118           |              |          |             |

|                       |        |                    |        |                |
|-----------------------|--------|--------------------|--------|----------------|
| Query Match           | 68.2%; | Score 449;         | DB 2;  | Length 121;    |
| Best Local Similarity | 72.8%; | Pred. No. 8.4e-35; |        |                |
| Matches               | 91;    | Conservative       | 10;    | Mismatches 20; |
|                       |        |                    | Indels | 4;             |
|                       |        |                    | Gaps   | 3;             |

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| QY | 1   | EVOLVKSGBEGLVYKKGSLRLTSCAASGCTFRFYDDHWMROTGKLELWSSLSGGNYIDY  | 60  |
| QY | 1   | EVOLVKSGBEGLVYKKGSLRLTSCAASGCTFRFYDDHWMROTGKLELWSSLSGGNYIDY  | 60  |
| Db | 1   | EVOLVBSGGGIVQGRSLRLTSCAASGCTFPDDYAHMHWROAKGKLEWVSGISMSNGSICG | 60  |
| QY | 61  | ADSVKGRFTISRDIANNVYLLQNNLSLAEDMAYVFCARDGTIPGSAATWRAFDIMGRGTM | 120 |
| QY | 61  | ADSVKGRFTISRDIANNVYLLQNNLSLAEDMAYVFCARDGTIPGSAATWRAFDIMGRGTM | 120 |
| Db | 61  | ADSVKGRFTISRDIANNVYLLQNNLSLAEDMAYVFCARD-VFMGSG--W-YFDLMGRGTL | 116 |
| QY | 121 | VTVSS                                                        | 125 |
| QY | 121 | VTVSS                                                        | 125 |
| Db | 117 | VTVSS                                                        | 121 |

## RESULT 9

Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 03-Mar-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31595  
R:Clisainer, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31595  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-128 <CUI>  
A:Cross-references: EMBL:Z14171; NID:g31007; PIDD:CA476540.1; PID:g31008  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
P:23-106/Domain: immunoglobulin homology <IMM>

|                       |       |                                                                |      |                                  |
|-----------------------|-------|----------------------------------------------------------------|------|----------------------------------|
| Query Match           | 68.2% | Score 448.5                                                    | DB 2 | Length 128                       |
| Best Local Similarity | 72.0% | Pred. No. 1e-34                                                |      |                                  |
| Matches               | 90    | Conservative                                                   | 9    | Mismatches 21; Indels 5; Gaps 1; |
| QY                    | 1     | EVQLVKGSGEGLVPFGSGLRLSCAASGFTFERRVDIHWVROTPGKGLIEWYSSISGGNYIDY | 60   |                                  |
|                       |       |                                                                |      |                                  |
|                       |       |                                                                |      |                                  |
| Db                    | 9     | EVQLVSGSGEGLVQGRSLRLSCAASGFTPDYIMHWYRAPKGLIEWYSSISNGSGTGY      | 68   |                                  |
|                       |       |                                                                |      |                                  |
|                       |       |                                                                |      |                                  |
| QY                    | 61    | ADSVKGRFTISRDNANNTVYLQWNSLRADDMAYVFCARDGTTFGSAATWRAFDIWRGSTM   | 120  |                                  |
|                       |       |                                                                |      |                                  |
|                       |       |                                                                |      |                                  |
| Db                    | 69    | ADSVKGRFTISRDNAAKSLYLQWNSLRADDTALYCAKD-----APGDHDAFDIWRGSTM    | 123  |                                  |
|                       |       |                                                                |      |                                  |
|                       |       |                                                                |      |                                  |
| QY                    | 121   | VTWSS                                                          | 125  |                                  |
|                       |       |                                                                |      |                                  |
|                       |       |                                                                |      |                                  |
| Db                    | 124   | VTWSS                                                          | 128  |                                  |

```

RESULT 10
S31108
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: S31108
R/Raaphorst, F.M.; Timmers, B.; Kenier, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A/Reference number: S31104; MUID:9211833; PMID:1730252
A/Accession: S31108
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-119 <RAA>
A/Cross-references: EMBL:X62956
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
C/115-98/Domain: immunoglobulin homology <Im>

```





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comphen Ltd.

# OM protein - protein search, using sw model

Run on: December 30, 2003, 10:47:09 ; Search time 11.9821 seconds  
(without alignments)  
1003.251 Million cell updates/sec

Title: US-09-674-752-49

Sequence: 1 EVQLVKGSGGLVPGGSLRL.....AATWPAFDIMWGRTVTVSS 125

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description               |
|------------|-------|-------------|--------|-------|---------------------------|
| 1          | 475.5 | 72.3        | 141    | 2     | S31669 Ig heavy chain V r |
| 2          | 467.5 | 71.0        | 128    | 2     | S26790 Ig heavy chain V r |
| 3          | 454   | 69.0        | 143    | 2     | S23624 Ig heavy chain V r |
| 4          | 452.5 | 68.8        | 145    | 2     | S11239 Ig heavy chain V r |
| 5          | 452   | 68.7        | 117    | 2     | S34012 Ig heavy chain V r |
| 6          | 451   | 68.5        | 125    | 2     | S30531 Ig heavy chain V r |
| 7          | 449.5 | 68.3        | 118    | 2     | S31105 Ig heavy chain V r |
| 8          | 449   | 68.2        | 121    | 2     | S31104 Ig heavy chain (bu |
| 9          | 448.5 | 68.1        | 128    | 2     | S31595 Ig heavy chain (bu |
| 10         | 448   | 68.1        | 119    | 2     | S31108 Ig heavy chain V r |
| 11         | 447.5 | 68.0        | 118    | 2     | S31116 Ig heavy chain - h |
| 12         | 447   | 67.9        | 123    | 2     | S30532 Ig heavy chain V r |
| 13         | 446.5 | 67.9        | 128    | 2     | S26786 Ig heavy chain V r |
| 14         | 446   | 67.8        | 121    | 2     | G36005 Ig heavy chain V r |
| 15         | 445   | 67.6        | 119    | 2     | G36005 Ig heavy chain V r |
| 16         | 445   | 67.6        | 127    | 2     | S19878 Ig heavy chain V r |
| 17         | 445   | 67.6        | 130    | 2     | I37783 Ig heavy chain V r |
| 18         | 444   | 67.5        | 138    | 2     | S31666 Ig variable region |
| 19         | 442.5 | 67.2        | 136    | 2     | S31587 Ig heavy chain V r |
| 20         | 442   | 67.2        | 121    | 2     | S31118 Ig heavy chain - h |
| 21         | 441.5 | 67.1        | 140    | 2     | S70442 Ig heavy chain pre |
| 22         | 441   | 67.0        | 119    | 2     | S31107 Ig heavy chain - h |
| 23         | 440.5 | 66.9        | 114    | 2     | S31120 Ig heavy chain - h |
| 24         | 440.5 | 66.9        | 122    | 2     | S31117 Ig heavy chain - h |
| 25         | 440   | 66.9        | 119    | 2     | F36005 Ig heavy chain V r |
| 26         | 440   | 66.9        | 121    | 2     | S19666 Ig heavy chain V r |
| 27         | 438.5 | 66.6        | 122    | 1     | M3HUM Ig heavy chain V-I  |
| 28         | 438.5 | 66.6        | 124    | 2     | S20782 Ig heavy chain V r |
| 29         | 438   | 66.6        | 120    | 2     | S36273 Ig heavy chain V r |

|    |       |      |     |   |                           |
|----|-------|------|-----|---|---------------------------|
| 30 | 438   | 66.6 | 123 | 2 | S26794 Ig heavy chain V r |
| 31 | 437.5 | 66.5 | 120 | 2 | S48798 Ig heavy chain V r |
| 32 | 437   | 66.4 | 123 | 2 | S31114 Ig heavy chain - h |
| 33 | 436.5 | 66.3 | 122 | 2 | S20772 Ig heavy chain V r |
| 34 | 436.5 | 66.3 | 147 | 2 | I37780 Ig variable region |
| 35 | 436   | 66.3 | 127 | 2 | S38489 Ig heavy chain - h |
| 36 | 436   | 66.3 | 134 | 2 | S31699 Ig heavy chain V r |
| 37 | 435   | 66.1 | 117 | 2 | S78486 Ig heavy chain V r |
| 38 | 435   | 66.1 | 140 | 2 | S31686 Ig heavy chain V r |
| 39 | 434   | 66.0 | 140 | 2 | S31588 Ig heavy chain V r |
| 40 | 433   | 65.8 | 139 | 2 | I37781 Ig heavy chain V r |
| 41 | 431.5 | 65.6 | 110 | 2 | PH1652 Ig variable region |
| 42 | 431.5 | 65.6 | 122 | 2 | S36005 Ig heavy chain V r |
| 43 | 431   | 65.5 | 119 | 2 | D36005 Ig heavy chain V r |
| 44 | 429   | 65.2 | 135 | 2 | S31598 Ig heavy chain V r |
| 45 | 428.5 | 65.1 | 114 | 2 | S46390 Ig heavy chain V r |

## ALIGNMENTS

### RESULT 1

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence\_reviseion 10-Nov-1995 #text\_change 23-Jul-1999

C/Accession: S31669

R/Cuisinier: A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31669

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-141 <CUI>

A/Cross-references: EMBL:Z14212; NID:g30959; PIDN:CA178581.1; PID:g30960

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

P/34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.3% Score 475.5; DB 2; Length 141;

Best Local Similarity 75.2% Pred. No. 3.4e-37;

Matches 94; Conservative 9; Mismatches 19; Indels 3; Gaps 1;

|    |     |                                                                  |  |
|----|-----|------------------------------------------------------------------|--|
| Qy | 1   | EVQLVKGSGGLVPGGSLRLCAASGFTPRRDYIMHWROTGPKGLEWVSISGANYDY 60       |  |
| Db | 20  | EVQLVESGGGLVPRGSLRLSCAASGFTFSISMMWRQAPKGLEWVSISSSSTIYY 79        |  |
| Qy | 61  | ADSVKGRFTISRDNANNTVLTQNSLRRAEDMAVYFCARDDTIFGSAATWPAFDIMGRGTM 120 |  |
| Db | 80  | ADSVKGRFTISRDAKNSLVLTQNSLRRAEDTAVYCARGHILGEGK---YFDLMGRGTL 136   |  |
| Qy | 121 | VTWSS 125                                                        |  |
| Db | 137 | VTWSS 141                                                        |  |

### RESULT 2

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence\_reviseion 13-Jan-1995 #text\_change 20-Jun-2000

C/Accession: S26790

R/Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.

Bur. J. Immunol. 22, 241-245, 1992

A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam

A/Reference number: S26786; MUID:92111632; PMID:1730251

A/Accession: S26790

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-128 <MOR>

A/Cross-references: EMBL:X61013; NID:g32798; PIDN:CA443347.1; PID:g1353128

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

Tue Dec 30 11:49:11 2003

us-09-674-752-46.rat

Page 7

Search completed: December 30, 2003, 11:05:35  
Job time : 12.2685 secs

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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D15
US-09-240-274-20

```

|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 76.8%;           | Score 477.5;       | DB 3;      | Length 125; |
| Best Local Similarity | 74.2%;           | Pred. No. 2.3e-40; |            |             |
| Matches 95;           | Conservative 10; | Mismatches 12;     | Indels 11; | Gaps 2      |

|    |     |                       |         |             |         |         |          |                |
|----|-----|-----------------------|---------|-------------|---------|---------|----------|----------------|
| QY | 1   | EVQLVSSGGGLVQPGKSLRLS | CVDSLT  | RTSSSGAHMNR | QAPAGLE | EWAVISY | GNDRKY   | 60             |
|    |     |                       |         |             |         |         |          |                |
| Db | 1   | EVQLTSSGGGVQPGKSLRLS  | CVSGSFT | FNNYGMHWR   | QAGKGL  | EWAVI   | WFGSNKY  | 60             |
|    |     |                       |         |             |         |         |          |                |
| QY | 61  | ADSVKRFPIISRNAKNTL    | YLQMSLT | TEEDTAVY    | CARDL   | ESNR    | -----    | EAALMGQ 112    |
|    |     |                       |         |             |         |         |          |                |
| Db | 61  | ADSVKRFPIISRNSQTL     | YLQMSLR | AEADIAVY    | ICAR    | ----    | ENQIKMSR | LYLYFFDMGQ 117 |
|    |     |                       |         |             |         |         |          |                |
| QY | 113 | GLTLVTVSS             | 120     |             |         |         |          |                |
| Db | 118 | GLTLVTVSS             | 125     |             |         |         |          |                |

RESULT 13  
US-09-240-274-21  
; Sequence 21, Application US/09240274

? PATENT NO. 6255455  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Siegel, Donald L.  
 ? TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS  
 ? TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
 ? FILE REFERENCE: 09596-4202  
 ? CURRENT APPLICATION NUMBER: US/09/240,274

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? SEQ ID NO 21
? LENGTH: 125
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: anti-Rh(D) chain Di6
US-09-240-274-21

```

|                       |                  |                    |            |             |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match           | 76.8%;           | Score 477.5;       | DB 3;      | Length 125; |
| Best Local Similarity | 74.2%;           | Pred. No. 2.3e-40; |            |             |
| Matches 95;           | Conservative 10; | Mismatches 12;     | Indels 11; | Gaps 2;     |

QY 1 EVGLVSSGGGLVQPGSLSTLSCVSDGLTFSSYGMHMRQAQAGAGLEWAVASYXNDKXY 60  
 QY 2 EVGLVSSGGGLVQPGSLSTLSCVSDGLTFSSYGMHMRQAQAGAGLEWAVASYXNDKXY 60  
 Db 1 EVGLTSSGGGVQPGSLSTLSCVSGFTFNNGHMRQAQKGLWAVAYMFGSNKXY 60  
 QY 61 ADSVKRFLAISDNACTYTLQMSLTTEPTAVYICADLTIESNIA-----EALMGQ 112  
 Db 61 ADSVKRFLTISRNSKNTLYLQMSLRAEDTAIVYICAR--ENQIKLSRYLYYFDYMG 117  
 QY 113 GILVTVSS 120  
 Db 118 GILVTVSS 125

RESULT 14  
US-09-240-274-22  
; Sequence 22, Application US/09240274

```

:
: Patent No. 6255455
:
: GENERAL INFORMATION:
:
: APPLICANT: Siegel, Donald L.
:
: TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
:
: TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
:
: FILE REFERENCE: 09596-4202

```

```

? CURRENT APPLICATION NUMBER: US/09/240,274
? CURRENT FILING DATE: 1999-01-29
? EARLIER APPLICATION NUMBER: 60/081,380
? EARLIER FILING DATE: 1998-04-10
? EARLIER APPLICATION NUMBER: 60/028,550
? EARLIER FILING DATE: 1996-10-11
? NUMBER OF SEQ ID NOS: 224
? SOFTWARE: Patentln Ver. 2.0
? SEQ ID NO 22
? LENGTH: 125
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: anti-rh(D) chain D17
? US-09-240-274-22

```

|                          |        |                    |            |             |
|--------------------------|--------|--------------------|------------|-------------|
| Query Match              | 76.8%; | Score 477.5;       | DB 3;      | Length 125; |
| Best Local Similarity    | 74.2%; | Pred. No. 2.3e-40; |            |             |
| Matches 95; Conservative | 10;    | Mismatches 12;     | Indels 11; | Gaps 2      |

[illegible]

RESULT 15  
US-09-240-274-24

Sequence 24, APPLICATION US/03240214  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D) -BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

```

1 FILEREFERENCE: 09596-4-202
2
3 CURRENT APPLICATION NUMBER: US/09/240,274
4
5 CURRENT FILING DATE: 1999-01-29
6
7 EARLIER APPLICATION NUMBER: 60/081,380
8
9 EARLIER FILING DATE: 1998-04-10
10
11 EARLIER APPLICATION NUMBER: 60/028,550
12
13 EARLIER FILING DATE: 1996-10-11
14
15 NUMBER OF SEQ ID NOS: 224
16
17 SOFTWARE: PatentIn Ver. 2.0

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```

; SEQ ID NO 24
; LENGTH: 125
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D20
US-05-240-274-24

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|                       |                  |                    |           |             |
|-----------------------|------------------|--------------------|-----------|-------------|
| Query Match           | 76.1%;           | Score 473.5;       | DB 3;     | Length 125; |
| Best Local Similarity | 73.6%;           | Pred. No. 5.6e-40; |           |             |
| Matches 92;           | Conservative 11; | Mismatches 17;     | Indels 5; | Gaps 1      |

QY 1 EVQLVESGGGLVQPGKSLRLSCTVDISGLTFSSYGMHWRAQAPGAELEWVAIVSYDGNKYY 60  
 |||||  
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 |||||  
 Db 1 EVQLVESGGGVVQPGKSLRLSCAASGFTFRTYGMHWRAQAPGLEWVAIVMPDGSNKYY 60  
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 QY 61 ADSVKGRAISRDNKNTLYLQNNSLTIEPTAVYYCAKDLIESNI-----AEALWGQGL 115  
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 Db 61 ADSVKGRTISRDNKNTLYLQNNSLPAEDTAVYYCARBEVGVGLMSRKEDYWGQGL 120  
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 QY 116 VTWSS 120  
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 |||||  
 Db 121 VTWSS 125

GENERAL INFORMATION:  
APPLICANT: Thompson, Julia E  
APPLICANT: Lennard, Simon N  
APPLICANT: Wilton, Alison J  
APPLICANT: Braddock, Peter SH  
APPLICANT: Du Fou, Sarah L  
APPLICANT: McCafferty, John G  
APPLICANT: Conroy, Louise A  
APPLICANT: Tempest, Philip R  
TITLE OF INVENTION: Specific binding members for TGFbeta1  
FILE REFERENCE: 28111/35620A  
CURRENT APPLICATION NUMBER: US/09/560,198A  
CURRENT FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/131,983  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 123  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-560-198A-4

Query Match 76.9%; Score 478.5; DB 4; Length 123;  
Best Local Similarity 78.0%; Pred. No. 1.8e-40;  
Matches 96; Conservative 5; Mismatches 19; Indels 3; Gaps 1;

QY 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60  
DB 1 EVOLVESGGGVOPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60  
QY 61 ADVKGRFAISRDNKNTLYLQNNSLTIEDTAVYVCAKDLIESNIA---AELMCGGLTYT 117  
DB 61 ADVKGRFTISRDNKNTLYLQNNSLRAEDTAVYVCAKDLIESNIA---AELMCGGLTYT 117  
QY 118 VSS 120  
DB 121 VSS 123

RESULT 10  
US-09-560-198A-10  
Sequence 10, Application US/09560198A  
Patent No. 6492497  
GENERAL INFORMATION:  
APPLICANT: Thompson, Julia E  
APPLICANT: Lennard, Simon N  
APPLICANT: Wilton, Alison J  
APPLICANT: Braddock, Peter SH  
APPLICANT: Du Fou, Sarah L  
APPLICANT: McCafferty, John G  
APPLICANT: Conroy, Louise A  
APPLICANT: Tempest, Philip R  
TITLE OF INVENTION: Specific binding members for TGFbeta1  
FILE REFERENCE: 28111/35620A  
CURRENT APPLICATION NUMBER: US/09/560,198A  
CURRENT FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/131,983  
PRIOR FILING DATE: 1999-04-30  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 123  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-560-198A-10

Query Match 76.8%; Score 477.5; DB 4; Length 123;  
Best Local Similarity 78.0%; Pred. No. 2.2e-40;  
Matches 96; Conservative 5; Mismatches 19; Indels 3; Gaps 1;  
QY 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60  
DB 1 EVOLVESGGGVOPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60

DB 1 QVOLVESGGGVOPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60  
QY 61 ADVKGRFAISRDNKNTLYLQNNSLTIEDTAVYVCAKDLIESNIA---AELMCGGLTYT 117  
DB 61 ADVKGRFTISRDNKNTLYLQNNSLRAEDTAVYVCAKDLIESNIA---AELMCGGLTYT 120  
QY 118 VSS 120  
DB 121 VSS 123

RESULT 11  
US-09-240-274-8  
Sequence 8, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 125  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain D01  
US-09-240-274-8

Query Match 76.8%; Score 477.5; DB 3; Length 125;  
Best Local Similarity 74.2%; Pred. No. 2.3e-40;  
Matches 95; Conservative 10; Mismatches 12; Indels 11; Gaps 2;

QY 1 EVOLVESGGGLVOPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60  
DB 1 EVOLVESGGGVOPGRSLRLSCVDSGLTFSSYGMHWVRQAPGAGLEWVAIVSYDNDKYY 60  
QY 61 ADVKGRFAISRDNKNTLYLQNNSLTIEDTAVYVCAKDLIESNIA---AELMCGGLTYT 112  
DB 61 ADVKGRFTISRDNKNTLYLQNNSLRAEDTAVYVCAKDLIESNIA---AELMCGGLTYT 117  
QY 113 GTLVTVSS 120  
DB 118 GTLVTVSS 125

RESULT 12  
US-09-240-274-20  
Sequence 20, Application US/09240274  
Patent No. 6255455  
GENERAL INFORMATION:  
APPLICANT: Siegel, Donald L.  
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
FILE REFERENCE: 09596-4202  
CURRENT APPLICATION NUMBER: US/09/240,274  
CURRENT FILING DATE: 1999-01-29  
EARLIER APPLICATION NUMBER: 60/081,380  
EARLIER FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 60/028,550  
EARLIER FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 224  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 20  
LENGTH: 125  
TYPE: PRT





## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/652,816A  
 FILING DATE: 23-MAY-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9125579.4  
 FILING DATE: 02-DEC-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9125579.8  
 FILING DATE: 02-DEC-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9206318.9  
 FILING DATE: 24-MAR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9206372.6  
 FILING DATE: 23-SEP-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9525004.9  
 FILING DATE: 07-DEC-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9610824.6  
 FILING DATE: 23-MAY-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/GB92/02240  
 FILING DATE: 02-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/244,597  
 FILING DATE: 01-JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: David W. Clough  
 REGISTRATION NUMBER: 36,107  
 REFERENCE/DOCKET INFORMATION:  
 TELEPHONE: 312-474-6300  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 123 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

US-08-652-816A-1

Query Match 82.5%; Score 492.5; DB 2; Length 123;

Best Local Similarity 79.7%; Pred. No. 1.2e-43;  
Matches 98; Conservative 8; Mismatches 8; Indels 9; Gaps 2;

QY 1 QVQLVSGAEVKKPKSSVSKVSCKASGTFSSHAISWVRQAPGQGLEWMGDIIPILGTQNY 60  
 DB 1 QVQLVSGAEVKKPKSSVSKVSCKASGTFSSNPINMLRQAPGQGLEWMGSIIPSGTANY 60  
 QY 61 AOKFGQRTITADSTSTAYMELSTLTSDDTAIVYC-----ELDMFY--IWGQGTMYT 111  
 DB 61 AOKFGQRLITADSTSTAYMELSLRSEDTAVYVCAGSHNYELYYIYMDVMWGQGTMYT 120  
 QY 112 VSS 114  
 DB 121 VSS 123

## RESULT 5

US-08-652-816A-6  
 Sequence 6, Application US/08652816A  
 Patent No. 5872215

## GENERAL INFORMATION:

APPLICANT: Osbourn, JK  
 APPLICANT: Allen, DJ  
 APPLICANT: McCaferrey, JG  
 TITLE OF INVENTION: Specific binding members, materials and  
 TITLE OF INVENTION: methods.  
 NUMBER OF SEQUENCES: 53

## CORRESPONDENCE ADDRESS:

ADDRESSSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 6300 Sears Tower, 233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States of America  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/652,816A  
 FILING DATE: 23-MAY-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9125579.4  
 FILING DATE: 02-DEC-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9125579.8  
 FILING DATE: 02-DEC-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9206318.9  
 FILING DATE: 24-MAR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9206372.6  
 FILING DATE: 23-SEP-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9525004.9  
 FILING DATE: 07-DEC-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9610824.6  
 FILING DATE: 23-MAY-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/GB92/02240  
 FILING DATE: 02-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/244,597  
 FILING DATE: 01-JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: David W. Clough  
 REGISTRATION NUMBER: 36,107  
 REFERENCE/DOCKET INFORMATION:  
 TELEPHONE: 312-474-6300  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 123 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

US-08-652-816A-6

Query Match 82.5%; Score 492.5; DB 2; Length 123;

Best Local Similarity 79.7%; Pred. No. 1.2e-43;  
Matches 98; Conservative 8; Mismatches 8; Indels 9; Gaps 2;

QY 1 QVQLVSGAEVKKPKSSVSKVSCKASGTFSSHAISWVRQAPGQGLEWMGDIIPILGTQNY 60  
 DB 1 QVQLVSGAEVKKPKSSVSKVSCKASGTFSSNPINMLRQAPGQGLEWMGSIIPSGTANY 60  
 QY 61 AOKFGQRTITADSTSTAYMELSTLTSDDTAIVYC-----ELDMFY--IWGQGTMYT 111  
 DB 61 AOKFGQRLITADSTSTAYMELSLRSEDTAVYVCAGSHNYELYYIYMDVMWGQGTMYT 120  
 QY 112 VSS 114  
 DB 121 VSS 123

## RESULT 6

US-08-652-816A-8  
 Sequence 8, Application US/08652816A  
 Patent No. 5872215

## GENERAL INFORMATION:

APPLICANT: Osbourn, JK  
APPLICANT: Allen, DJ  
APPLICANT: McCafferty, JG  
TITLE OF INVENTION: Specific binding members, materials and  
TITLE OF INVENTION: methods.  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,816A  
FILING DATE: 23-MAY-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.4  
FILING DATE: 02-DEC-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.8  
FILING DATE: 02-DEC-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9525004.9  
FILING DATE: 07-DEC-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02240  
FILING DATE: 02-DEC-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/244,597  
FILING DATE: 01-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33308  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-652-816A-8

Query Match 82.5%; Score 492.5; DB 2; Length 123;  
Best Local Similarity 79.7%; Pred. No. 1.2e-43;  
Matches 98; Conservative 8; Mismatches 8; Indels 9; Gaps 2;

QY 1 QVOLVSGAEVKKPGSSVSVKSCKASGCTFSSHAISWVRQAPQGLMWDIIPILGTGY 60  
DB 1 QVOLVSGAEVKKPGSSVSVKSCKASGCTFSSHAISWVRQAPQGLMWDIIPILGTGY 60  
QY 61 AGRFGRVITTADESTSTAYMELSTLSEPTAYYC-----ELDMFY--IMGOSTMYT 111  
DB 61 AGRFGRVITTADESTSTAYMELSTLSEPTAYYC-----ELDMFY--IMGOSTMYT 111  
QY 112 VSS 114  
DB 112 VSS 114  
QY 121 VSS 123  
DB 121 VSS 123

RESULT 7  
US-08-652-816A-9  
Sequence 9, Application US/08652816A  
Patent No. 5872215  
GENERAL INFORMATION:  
APPLICANT: Osbourn, JK  
APPLICANT: Allen, DJ  
APPLICANT: McCafferty, JG  
TITLE OF INVENTION: Specific binding members, materials and  
TITLE OF INVENTION: methods.  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,816A  
FILING DATE: 23-MAY-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.4  
FILING DATE: 02-DEC-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.8  
FILING DATE: 02-DEC-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9525004.9  
FILING DATE: 07-DEC-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02240  
FILING DATE: 02-DEC-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/244,597  
FILING DATE: 01-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33308  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-652-816A-9

Query Match 82.5%; Score 492.5; DB 2; Length 123;  
Best Local Similarity 79.7%; Pred. No. 1.2e-43;  
Matches 98; Conservative 8; Mismatches 8; Indels 9; Gaps 2;

QY 1 QVOLVSGAEVKKPGSSVSVKSCKASGCTFSSHAISWVRQAPQGLMWDIIPILGTGY 60  
DB 1 QVOLVSGAEVKKPGSSVSVKSCKASGCTFSSHAISWVRQAPQGLMWDIIPILGTGY 60  
QY 61 AGRFGRVITTADESTSTAYMELSTLSEPTAYYC-----ELDMFY--IMGOSTMYT 111  
DB 61 AGRFGRVITTADESTSTAYMELSTLSEPTAYYC-----ELDMFY--IMGOSTMYT 111  
QY 112 VSS 114  
DB 112 VSS 114  
QY 121 VSS 123  
DB 121 VSS 123



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; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-125-687-1
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```
Query Match      85.1%; Score 508; DB 15; Length 120;
Best Local Similarity 85.8%; Pred. No. 6,6e-43;
Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2;
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QY      1 QVQLVSGAEVKKPKSSVKVSCAKSGGTFFSSHAISWVROAPGQGLEWMGDIIPILGTNY 60
          |||
DB      1 QVQLVSGAEVKKPKSSVKVSCAKSGGTFFSSVAISWVROAPGQGLEWMGDIIPILGTNY 60
          |||
QY      61 AQKFGQKRVITTADESTSTAYMELSTLTSEPTAVYYCEL---DMFY---IWGQTMVTSS 114
          |||
DB      61 AQKFGQKRVITTADESTSTAYMELSLRSEDTAVYYCARWGIDGFYAMDYWGQGLVTVSS 120
          |||
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## RESULT 15

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US-09-880-748-1509
; Sequence 1509, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1509
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1509
```

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Query Match      84.9%; Score 507; DB 11; Length 253;
Best Local Similarity 79.7%; Pred. No. 1.9e-42;
Matches 102; Conservative 4; Mismatches 8; Indels 14; Gaps 1;
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QY      1 QVQLVSGAEVKKPKSSVKVSCAKSGGTFFSSHAISWVROAPGQGLEWMGDIIPILGTNY 60
          |||
DB      1 QVQLVSGAEVKKPKSSVKVSCAKSGGTFFSSVAISWVROAPGQGLEWMGDIIPILGTNY 60
          |||
QY      61 AQKFGQKRVITTADESTSTAYMELSTLTSEPTAVYYC-----ELDMFYIWGQ 106
          |||
DB      61 AQKFGQKRVITTADESTSTAYMELSLRSEDTAVYYCARWEGYDILTGYYPEGMFDPMGK 120
          |||
QY      107 GTMVTVSS 114
          |||
DB      121 GTMVTVSS 128
          |||
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Search completed: December 30, 2003, 11:45:25  
Job time : 24.4484 secs

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; Sequence 49, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-269-805-49

Query Match      86.1%; Score 514; DB 15; Length 120;
Best Local Similarity 86.7%; Pred. No. 1,7e-43;
Matches 104; Conservative 4; Mismatches 6; Indels 6; Gaps 3;

Qy      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTGNY 60
Db      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGRIIPILGTANY 60

Qy      61 AAKFGKRVTTTADDESTSTAYMELSTLTSEDTAVYCC--ELDM-FYI--WGQGTMTVYSS 114
Db      61 AAKFGKRVTTTADDESTSTAYMELSLRSEDTAVYCCATSRLEMLLYLDYGGQGLTVYSS 120

RESULT 11
US-10-308-817-191
; Sequence 191, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 191
; LENGTH: 119
; TYPE: PRT
; ORGANISM: human
; US-10-308-817-191

Query Match      86.0%; Score 513.5; DB 12; Length 119;
Best Local Similarity 84.9%; Pred. No. 1.9e-43;
Matches 101; Conservative 5; Mismatches 8; Indels 5; Gaps 1;

Qy      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTGNY 60
Db      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTANY 60

Qy      61 AAKFGKRVTTTADDESTSTAYMELSTLTSEDTAVYCCELDMFY----IMGQGTMTVYSS 114
Db      61 AAKFGKRVTTTADDESTSTAYMELSLRSEDTAVYCCAGGYYYIYMDYMGQGLTVYSS 119

RESULT 12
US-10-269-805-19
; Sequence 19, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
```

```
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-269-805-19

Query Match      85.7%; Score 511.5; DB 15; Length 121;
Best Local Similarity 85.1%; Pred. No. 3e-43;
Matches 103; Conservative 3; Mismatches 8; Indels 7; Gaps 1;

Qy      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTGNY 60
Db      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTANY 60

Qy      61 AAKFGKRVTTTADDESTSTAYMELSTLTSEDTAVYCCEL-----DWPYIMGQGTMTVYSS 113
Db      61 AAKFGKRVTTTADDESTSTAYMELSLRSEDTAVYCCARFESGYWGDAFDIMGQGTMTVYSS 120

Qy      114 S 114
Db      121 S 121

RESULT 13
US-10-025-687-1
; Sequence 1, Application US/10025687
; Publication No. US20020142255A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/025,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
; US-10-025-687-1

Query Match      85.1%; Score 508; DB 14; Length 120;
Best Local Similarity 85.8%; Pred. No. 6.6e-43;
Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2;

Qy      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTGNY 60
Db      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTANY 60

Qy      61 AAKFGKRVTTTADDESTSTAYMELSTLTSEDTAVYCCEL--DWPY----IMGQGTMTVYSS 114
Db      61 AAKFGKRVTTTADDESTSTAYMELSLRSEDTAVYCCARKGSDGYRNDYMGQGLTVYSS 120

RESULT 14
US-10-125-687-1
; Sequence 1, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/125,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent version 3.1
; SEQ ID NO 9
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-9

Query Match      86.7%; Score 517.5; DB 15; Length 121;
Best Local Similarity 86.0%; Pred. No. 7.7e-44;
Matches 104; Conservative 3; Mismatches 7; Indels 7; Gaps 1;

QY      1 QVQLVQSGAEVKKPKSSVKYSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTANY 60
DB      1 QVQLVQSGAEVKKPKSSVKYSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTANY 60
QY      61 AOKFGQGVTTITADSESTAYMELSTLTSEDPAVYYC-----ELDMFYIWGQGMVTVS 113
DB      61 AOKFGQGVTTITADSESTAYMELSLNSSEDTAVYYCAAFSPETDAFDIWDGQGMVTVS 120
QY      114 S 114
DB      121 S 121

RESULT 7
US-10-269-805-35
; Sequence 35, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent version 3.1
; SEQ ID NO 35
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-35

Query Match      86.5%; Score 516.5; DB 15; Length 125;
Best Local Similarity 83.2%; Pred. No. 1e-43;
Matches 104; Conservative 3; Mismatches 7; Indels 11; Gaps 1;

QY      1 QVQLVQSGAEVKKPKSSVKYSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTANY 60
DB      1 QVQLVQSGAEVKKPKSSVKYSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTANY 60
QY      61 AOKFGQGVTTITADSESTAYMELSTLTSEDPAVYYC-----LDMFYIWGQGMVTVS 109
DB      61 AOKFGQGVTTITADSESTAYMELSLNSSEDTAVYYCAAFSPETDAFDIWDGQGMVTVS 120
QY      110 VTSS 114
DB      121 VTSS 125

RESULT 8
US-09-976-118-2
; Sequence 2, Application US/09976118
; Patent No. US2002005803A1
; GENERAL INFORMATION:
; APPLICANT: Ratsch, Kevin Paul
; APPLICANT: Curjel, David T.
; APPLICANT: Bonner, James Allen
```

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; TITLE OF INVENTION: Human Anti-Epidermal Growth Factor Receptor
; FILE REFERENCE: D6355
; CURRENT APPLICATION NUMBER: US/09/976,118
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,353
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 270
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence of anti-EGFR ecfv
; OTHER INFORMATION: clone pSEX01-63
US-09-976-118-2

Query Match      86.4%; Score 516; DB 9; Length 270;
Best Local Similarity 81.7%; Pred. No. 2.6e-43;
Matches 103; Conservative 3; Mismatches 8; Indels 12; Gaps 1;

QY      1 QVQLVQSGAEVKKPKSSVKYSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTANY 60
DB      1 QVQLVQSGAEVKKPKSSVKYSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTANY 60
QY      61 AOKFGQGVTTITADSESTAYMELSTLTSEDPAVYYCELD-----WFIWQGMVT 108
DB      61 AOKFGQGVTTITADSESTAYMELSLNSSEDTAVYYCARDPDYSGSYRPFWDPMQGMVT 120
QY      109 MVTSS 114
DB      121 LVTVSS 126

RESULT 9
US-10-269-805-3
; Sequence 3, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patent version 3.1
; SEQ ID NO 3
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-3

Query Match      86.2%; Score 514.5; DB 15; Length 123;
Best Local Similarity 83.7%; Pred. No. 1.5e-43;
Matches 103; Conservative 4; Mismatches 7; Indels 9; Gaps 2;

QY      1 QVQLVQSGAEVKKPKSSVKYSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTANY 60
DB      1 QVQLVQSGAEVKKPKSSVKYSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTANY 60
QY      61 AOKFGQGVTTITADSESTAYMELSTLTSEDPAVYYC-----ELDM---FYIWQGMVT 111
DB      61 AOKFGQGVTTITADSESTAYMELSLNSSEDTAVYYCARGVGDPMISFPDYWGQGMVT 120
QY      112 VSS 114
DB      121 VSS 123

RESULT 10
US-10-269-805-49
```

```

; APPLICANT: Mackins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519
; CURRENT APPLICATION NUMBER: US/10/300,675
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; PRIOR FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant variant
; US-10-300-675-10

Query Match      87.1%; Score 520; DB 12; Length 118;
Best Local Similarity 85.6%; Pred. No. 4.2e-44;
Matches 101; Conservative 6; Mismatches 7; Indels 4; Gaps 1;

QY      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTGNY 60
DB      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSVAISWVROAPGQGLEWMGDIIPILGTANY 60
QY      61 AQRFGGRVTTTADSESTSTAYMELSTLTSEDTAVYYCELD---WFYIWGGCTMTVYSS 114
DB      61 AQRFGGRVTTTADSESTSTAYMELSLRSEDTAVYYCARBDNSGMYHWGGCTLVTVSS 118

RESULT 3
US-10-300-675-12
; Sequence 12, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
; APPLICANT: Mackins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519
; CURRENT APPLICATION NUMBER: US/10/300,675
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; PRIOR FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant variant
; US-10-300-675-12

Query Match      87.1%; Score 520; DB 12; Length 118;
Best Local Similarity 85.6%; Pred. No. 4.2e-44;
Matches 101; Conservative 6; Mismatches 7; Indels 4; Gaps 1;

QY      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTGNY 60
DB      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSVAISWVROAPGQGLEWMGDIIPILGTANY 60
QY      61 AQRFGGRVTTTADSESTSTAYMELSTLTSEDTAVYYCELD---WFYIWGGCTMTVYSS 114
DB      61 AQRFGGRVTTTADSESTSTAYMELSLRSEDTAVYYCARBDNSGMYHWGGCTLVTVSS 118

RESULT 4
US-10-300-675-14
; Sequence 14, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
; APPLICANT: Mackins, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519
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; CURRENT APPLICATION NUMBER: US/10/300,675
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; PRIOR FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant variant
; US-10-300-675-14

Query Match      87.1%; Score 520; DB 12; Length 118;
Best Local Similarity 85.6%; Pred. No. 4.2e-44;
Matches 101; Conservative 6; Mismatches 7; Indels 4; Gaps 1;

QY      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTGNY 60
DB      1 QVQLVSGAEVKKPKSSVKVSCKASGCTSSVAISWVROAPGQGLEWMGDIIPILGTANY 60
QY      61 AQRFGGRVTTTADSESTSTAYMELSTLTSEDTAVYYCELD---WFYIWGGCTMTVYSS 114
DB      61 AQRFGGRVTTTADSESTSTAYMELSLRSEDTAVYYCARBDNSGMYHWGGCTLVTVSS 118

RESULT 5
US-10-269-805-25
; Sequence 25, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-269-805-25

Query Match      87.1%; Score 520; DB 15; Length 124;
Best Local Similarity 84.7%; Pred. No. 4.4e-44;
Matches 105; Conservative 2; Mismatches 7; Indels 10; Gaps 1;

QY      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTGNY 60
DB      1 QVQLVSGAEVKKPKSSVKVSCKASGCTFSSVAISWVROAPGQGLEWMGDIIPILGTANY 60
QY      61 AQRFGGRVTTTADSESTSTAYMELSTLTSEDTAVYYC-----ELDWFYIWGGCTMTV 110
DB      61 AQRFGGRVTTTADSESTSTAYMELSLRSEDTAVYYCARGYDFWGSGLDAFDIWMGGCTMV 120
QY      111 TVSS 114
DB      121 TVSS 124

RESULT 6
US-10-269-805-9
; Sequence 9, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 11:01:15 ; Search time 24.484 Seconds

(without alignments)  
927.994 Million cell updates/sec

Title: US-09-674-752-51

Perfect score: 597  
Sequence: 1 QVQLVQSGAEVKKPKSSVAVK.....YCELDFWFIWGQMTVTSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubppa/PCR\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubppa/PCRUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubppa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubppa/US10\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubppa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 520   | 87.1        | 118    | 12    | US-10-300-675-6    |
| 2          | 520   | 87.1        | 118    | 12    | US-10-300-675-10   |
| 3          | 520   | 87.1        | 118    | 12    | US-10-300-675-12   |
| 4          | 520   | 87.1        | 118    | 12    | US-10-300-675-14   |
| 5          | 520   | 87.1        | 124    | 15    | US-10-269-805-25   |
| 6          | 517.5 | 86.7        | 121    | 15    | US-10-269-805-9    |
| 7          | 516.5 | 86.5        | 125    | 15    | US-10-269-805-35   |
| 8          | 516   | 86.4        | 270    | 9     | US-09-976-118-2    |
| 9          | 514.5 | 86.2        | 123    | 15    | US-10-269-805-3    |
| 10         | 514   | 86.1        | 120    | 15    | US-10-269-805-49   |
| 11         | 513.5 | 86.0        | 119    | 12    | US-10-308-817-191  |
| 12         | 511.5 | 85.7        | 121    | 15    | US-10-269-805-19   |
| 13         | 508   | 85.1        | 120    | 15    | US-10-025-687-1    |
| 14         | 508   | 85.1        | 120    | 14    | US-10-125-687-1    |
| 15         | 507   | 84.9        | 253    | 11    | US-09-880-748-1509 |

|    |       |      |     |    |                    |                   |
|----|-------|------|-----|----|--------------------|-------------------|
| 16 | 506.5 | 84.8 | 248 | 11 | US-09-880-748-1733 | Sequence 1733, Ap |
| 17 | 506.5 | 84.8 | 248 | 11 | US-09-880-748-1734 | Sequence 1734, Ap |
| 18 | 506   | 84.7 | 120 | 15 | US-10-269-805-37   | Sequence 37, Appl |
| 19 | 505.5 | 84.7 | 244 | 11 | US-09-880-748-1881 | Sequence 1881, Ap |
| 20 | 505.5 | 84.7 | 248 | 11 | US-09-880-748-1881 | Sequence 1881, Ap |
| 21 | 505.5 | 84.7 | 248 | 11 | US-09-880-748-1879 | Sequence 1879, Ap |
| 22 | 504.5 | 84.5 | 627 | 14 | US-10-047-542-47   | Sequence 47, Appl |
| 23 | 504   | 84.4 | 244 | 11 | US-09-880-748-1866 | Sequence 1866, Ap |
| 24 | 502.5 | 84.2 | 248 | 11 | US-09-880-748-1719 | Sequence 1719, Ap |
| 25 | 502.5 | 84.2 | 248 | 11 | US-09-880-748-1732 | Sequence 1732, Ap |
| 26 | 502.5 | 84.2 | 248 | 11 | US-09-880-748-1737 | Sequence 1737, Ap |
| 27 | 502   | 84.1 | 120 | 15 | US-10-269-805-15   | Sequence 15, Appl |
| 28 | 501.5 | 84.0 | 248 | 11 | US-09-880-748-1741 | Sequence 1741, Ap |
| 29 | 500.5 | 83.8 | 253 | 11 | US-09-880-748-1880 | Sequence 1880, Ap |
| 30 | 499.5 | 83.7 | 248 | 11 | US-09-880-748-1727 | Sequence 1727, Ap |
| 31 | 499.5 | 83.7 | 248 | 11 | US-09-880-748-1728 | Sequence 1728, Ap |
| 32 | 499.5 | 83.6 | 257 | 11 | US-09-880-748-1553 | Sequence 1553, Ap |
| 33 | 498.5 | 83.5 | 219 | 15 | US-10-184-508A-7   | Sequence 7, Appl1 |
| 34 | 498.5 | 83.5 | 219 | 15 | US-10-184-508A-7   | Sequence 7, Appl1 |
| 35 | 498.5 | 83.5 | 222 | 15 | US-10-184-508A-6   | Sequence 6, Appl1 |
| 36 | 498.5 | 83.5 | 222 | 15 | US-10-184-508A-6   | Sequence 6, Appl1 |
| 37 | 498.5 | 83.5 | 245 | 15 | US-10-151-882-15   | Sequence 15, Appl |
| 38 | 497.5 | 83.3 | 218 | 15 | US-10-184-508A-8   | Sequence 8, Appl1 |
| 39 | 497.5 | 83.3 | 218 | 15 | US-10-184-508A-8   | Sequence 8, Appl1 |
| 40 | 496   | 83.1 | 120 | 15 | US-10-269-805-5    | Sequence 5, Appl1 |
| 41 | 496   | 83.1 | 256 | 11 | US-09-880-748-1600 | Sequence 1600, Ap |
| 42 | 495.5 | 83.0 | 246 | 11 | US-09-880-748-2062 | Sequence 2062, Ap |
| 43 | 495.5 | 83.0 | 246 | 11 | US-09-880-748-1717 | Sequence 1717, Ap |
| 44 | 495   | 82.9 | 252 | 11 | US-09-880-748-1666 | Sequence 1666, Ap |
| 45 | 494.5 | 82.8 | 123 | 15 | US-10-269-805-17   | Sequence 17, Appl |

## ALIGNMENTS

```
RESULT 1
US-10-300-675-6
; Sequence 6, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
; APPLICANT: Watkine, Jeffrey D.
; TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies
; FILE REFERENCE: P-IX 5519
; CURRENT APPLICATION NUMBER: US/10/300,675
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 09/989,901
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-300-675-6

Query Match      87.1%; Score 520; DB 12; Length 118;
Best Local Similarity 85.6%; Pred. No. 4.2e-44;
Matches 101; Conservative 6; Mismatches 7; Indels 4; Gaps 1;

QY      1 QVQLVQSGAEVKKPKSSVAVKSCASGCTFSSHAISWRQAPQGLEMMDIPIILCTGVY 60
      |||
Db      1 QVQLVQSGAEVKKPKSSVAVKSCASGCTFSSVAISWRQAPQGLEMMDIPIILCTGVY 60
      |||

QY      61 AAKFQGRVITADDESTSTAYMBLSTSTSDTAVYCELD---WFYIWGQMTVTSS 114
      |||
Db      61 AAKFQGRVITADDESTSTAYMBLSTSTSDTAVYCARBDSGMYHWGQGLTIVTSS 118
      |||

RESULT 2
US-10-300-675-10
; Sequence 10, Application US/10300675
; Publication No. US20030198638A1
; GENERAL INFORMATION:
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DB 61 AOKFOGRVITITADESTSTAYMELSLRSDTAIVYCARWGCGDFYAMDYWGQGLTVTVSS 120

RESULT 14  
ABJ18672  
ID ABJ18672 standard; Protein; 120 AA.

AC ABJ18672;

DT 06-MAR-2003 (first entry)

DE Antibody library related heavy variable chain protein region SEQ ID No 1.

KW Library; recombinant antibody; clustering variable region; in silico;  
immunogenecity; antibody therapeutic.

OS Unidentified.

PN WO200284277-A1.

PD 24-OCT-2002.

PF 17-APR-2002; 2002WO-US12202.

PR 17-APR-2001; 2001US-284407P.

PA (ABMA-) ABMAXIS INC.

PI Luo P;

DR WPI; 2003-093043/08.

PT Constructing a library of recombinant antibodies useful as source of  
antibody candidates for screening antigens comprises clustering  
PT variable regions of antibodies having known 3-dimensional structures  
into structural ensembles -

PS Disclosure; Page 98-99; 119pp; English.

XX The invention relates to a novel method for the construction of a library  
XX of recombinant antibodies. The novel method comprises clustering variable  
XX regions of a collection of antibodies having known 3D structures into at  
XX least two families of structural ensembles, each comprising at least two  
XX different antibody sequences but with substantially identical main chain  
XX conformations. The method is useful for constructing a library of  
XX artificial antibodies in silico which provides a structurally diverse and  
XX yet functionally more relevant source of antibody candidates which can  
XX then be screened for binding a wide variety of target molecules,  
XX including small molecules, and biomacromolecules such as proteins,  
XX peptides and nucleic acids. The libraries constructed are useful as a  
XX source of antibody candidates for further screening for novel antibodies  
XX with high affinity against a wide range of antigens and having no or  
XX minimum immunogenecity to human subjects treated with antibody  
XX therapeutics. This sequence represents a protein region of an antibody  
XX relating to the novel antibody library construction method of the  
XX invention.

SQ Sequence 120 AA;

Query Match 85.1%; Score 508; DB 24; Length 120;  
Best Local Similarity 85.8%; Pred. No. 3.9e-37;  
Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2;

QY 1 QVQLVSGAIVKPKGSSVYKSCAKSGTSSSHAIISWVROAPGQGLEWMGDIIPILGTGNY 60  
DB 1 QVQLVSGAIVKPKGSSVYKSCAKSGTSSSHAIISWVROAPGQGLEWMGDIIPILGTGNY 60

QY 61 AOKFOGRVITITADESTSTAYMELSLRSDTAIVYCARWGCGDFYAMDYWGQGLTVTVSS 114  
DB 61 AOKFOGRVITITADESTSTAYMELSLRSDTAIVYCARWGCGDFYAMDYWGQGLTVTVSS 120

RESULT 15.  
ABJ18718  
ID ABJ18718 standard; Protein; 120 AA.

AC ABJ18718;

DT 06-MAR-2003 (first entry)

DE Antibody library related VH protein region 10HA.

KW Library; recombinant antibody; clustering variable region; in silico;  
immunogenecity; antibody therapeutic.

OS Unidentified.

PN WO200284277-A1.

PD 24-OCT-2002.

PF 17-APR-2002; 2002WO-US12202.

PR 17-APR-2001; 2001US-284407P.

PA (ABMA-) ABMAXIS INC.

PI Luo P;

DR WPI; 2003-093043/08.

PT Constructing a library of recombinant antibodies useful as source of  
antibody candidates for screening antigens comprises clustering  
PT variable regions of antibodies having known 3-dimensional structures  
into structural ensembles -

PS Disclosure; Fig 13B; 119pp; English.

XX The invention relates to a novel method for the construction of a library  
XX of recombinant antibodies. The novel method comprises clustering variable  
XX regions of a collection of antibodies having known 3D structures into at  
XX least two families of structural ensembles, each comprising at least two  
XX different antibody sequences but with substantially identical main chain  
XX conformations. The method is useful for constructing a library of  
XX artificial antibodies in silico which provides a structurally diverse and  
XX yet functionally more relevant source of antibody candidates which can  
XX then be screened for binding a wide variety of target molecules,  
XX including small molecules, and biomacromolecules such as proteins,  
XX peptides and nucleic acids. The libraries constructed are useful as a  
XX source of antibody candidates for further screening for novel antibodies  
XX with high affinity against a wide range of antigens and having no or  
XX minimum immunogenecity to human subjects treated with antibody  
XX therapeutics. This sequence represents a protein region of an antibody  
XX relating to the novel antibody library construction method of the  
XX invention.

SQ Sequence 120 AA;

Query Match 85.1%; Score 508; DB 24; Length 120;  
Best Local Similarity 85.8%; Pred. No. 3.9e-37;  
Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2;

QY 1 QVQLVSGAIVKPKGSSVYKSCAKSGTSSSHAIISWVROAPGQGLEWMGDIIPILGTGNY 60  
DB 1 QVQLVSGAIVKPKGSSVYKSCAKSGTSSSHAIISWVROAPGQGLEWMGDIIPILGTGNY 60

QY 61 AOKFOGRVITITADESTSTAYMELSLRSDTAIVYCARWGCGDFYAMDYWGQGLTVTVSS 114  
DB 61 AOKFOGRVITITADESTSTAYMELSLRSDTAIVYCARWGCGDFYAMDYWGQGLTVTVSS 120

Search completed: December 30, 2003, 10:54:37  
Job time : 37.756 secs

CC TMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and  
 CC a variable light chain (VLC)DR3 region. An antibody preparation of the  
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiant  
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting  
 CC activity of a TIMP-1. It is especially useful for ameliorating the  
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver  
 CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary  
 CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic  
 CC pulmonary fibrosis, benign prostatic hypertrophy, lung cancer or colon  
 CC cancer. The antibody is also useful for detecting a TIMP-1 in a test  
 CC preparation, or in diagnosing a disorder in which a TIMP-1 level is  
 CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy  
 CC chain regions of a human anti-TIMP-1 antibody of the invention.

SO Sequence 225 AA;

Query Match 85.2%; Score 508.5; DB 24; Length 225;  
 Best Local Similarity 85.1%; Pred. No. 6.5e-37;  
 Matches 103; Conservative 3; Mismatches 8; Indels 7; Gaps 2;

QY 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSHAISWVRQAPGGGLEMMGDIIPILGTGY 60  
 DB 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSVAISWVRQAPGGGLEMMGDIIPILGTANY 60

QY 61 AQRFGRRVITTADESTSTAYMELSTLTSEDTAVYYCE--LDW-----FYIMGGTMYTVSS 113  
 DB 61 AQRFGRRVITTADESTSTAYMELSLRSEDTAVYYCARGLYMAVYPIFDPMGGTLTVTSS 120

QY 114 S 114  
 DB 121 S 121

RESULT 12

AAB67618  
 ID AAB67618 standard; Protein; 245 AA.

XX AAB67618;

DT 29-MAY-2001 (first entry)

XX Human leukocyte antigen-Cw6 specific scfv fragment from clone Cw6\_2.

XX Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;

KM miscarriage; abortion; preclasis; antibody; HLA phenotyping; ss.

XX Homo sapiens.

XX MO200114558-A1.

XX 01-MAR-2001.

XX 28-AUG-2000; 2000MO-EP08388.

XX 26-AUG-1999; 99EP-0116691.

XX (MORP-) MORPHOSYS AG.

XX Kretzschmar T, Tesar M, Margot M, Kiroenke M;

XX WPI; 2001-218451/22.

XX Novel isolated human immunoglobulin or functional immunoglobulin

PT fragment specific for human leukocyte antigen Cw6, useful for treatment

PS Claim 3; Fig 1; 23pp; English.

XX AAB67617-23 represent single chain antibody (scfv) fragments which  
 CC are specific for human leukocyte antigen (HLA)-Cw6. The fragments are  
 CC derived from a synthetic human combinatorial antibody library based on  
 CC molecular consensus frameworks and CDRs randomised with trinucleotides.  
 CC The specification describes a human immunoglobulin fragments specific

CC for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in  
 CC studies of natural killer cell silencing as well as miscarriages.  
 CC HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.  
 CC Preclasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin  
 CC fragments are useful for the preparation of a pharmaceutical for the  
 CC treatment of humans. They are also useful for HLA phenotyping.

SO Sequence 245 AA;

Query Match 85.2%; Score 508.5; DB 22; Length 245;  
 Best Local Similarity 87.2%; Pred. No. 7.1e-37;  
 Matches 102; Conservative 4; Mismatches 8; Indels 3; Gaps 2;

QY 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSHAISWVRQAPGGGLEMMGDIIPILGTGY 60  
 DB 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSVAISWVRQAPGGGLEMMGDIIPILGTANY 60

QY 61 AQRFGRRVITTADESTSTAYMELSTLTSEDTAVYYCE--LDWYF--IWGGTMYTVSS 114  
 DB 61 AQRFGRRVITTADESTSTAYMELSLRSEDTAVYYCARGFDFPMDFGCGTLTVTSS 117

RESULT 13

AAW27550  
 ID AAW27550 standard; Protein; 120 AA.

XX AAW27550;

DT 23-JAN-1998 (first entry)

XX Human Ab heavy chain variable region VH1A consensus.

XX Human; antibody; preparation; library; VH1A; variable region;

KM heavy chain; consensus.

XX Homo sapiens.

XX WO9708320-A1.

XX 06-MAR-1997.

XX 19-AUG-1996; 96MO-EP03647.

XX 18-AUG-1995; 95EP-0113021.

XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.

XX Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckhuhn A;

XX WPI; 1997-179277/16.

XX N-PSDB; AAT87948.

XX Preparation of human derived antibody gene library - using synthetic

PT consensus sequences, and signal consensus antibody gene as universal

PS Example 1; Fig 5A; 436pp; English.

XX The present sequence is the human antibody heavy chain

CC variable region synthetic sequence VH1A, used in the preparation of

CC a human derived antibody gene library.

SO Sequence 120 AA;

Query Match 85.1%; Score 508; DB 18; Length 120;  
 Best Local Similarity 85.8%; Pred. No. 3.9e-37;  
 Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2;

QY 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSHAISWVRQAPGGGLEMMGDIIPILGTGY 60  
 DB 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSVAISWVRQAPGGGLEMMGDIIPILGTANY 60  
 QY 61 AQRFGRRVITTADESTSTAYMELSTLTSEDTAVYYCEL---DMFY---IWGGTMYTVSS 114

QY 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPITGNGY 60  
 DB 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPITGNGY 60  
 QY 61 AOKFGKRVTTTADSTSTAYMELSTLTSEBDTAVYYC-ELDPFY--WGQGTMTVSS 114  
 DB 61 AOKFGKRVTTTADSTSTAYMELSLRSEBDTAVYYCARPSFYLDYWGQGTIVTVSS 117

RESULT 10  
 ABB57559 standard; Peptide: 115 AA.  
 ABB57559;  
 18-MAR-2002 (first entry)

HLA-DR-specific protein MS-GPCS VH sequence.

Immunomodulatory human MHC class II antigen-binding protein; HLA;  
 human leukocyte antigen; immune system; immunosuppression; antibody;  
 major histocompatibility complex; antineumatic; antiarthritic;  
 neuroprotective; antiinflammatory; antidiabetic; antipsoriatic;  
 immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis;  
 thyromimetic; hepatocytic; immune response suppressor; narcolepsy;  
 rheumatoid arthritis; juvenile arthritis; multiple sclerosis; insulinitis;  
 Grave's disease; insulin-dependent diabetes; Hashimoto's disease;  
 systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis;  
 transplant rejection; graft versus host disease; pemphigus vulgaris;  
 glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis;  
 irritable bowel disease; Sjogren's syndrome.

Homo sapiens.  
 Synthetic.  
 WO200187338-A1.  
 22-NOV-2001.  
 14-MAY-2001; 2001WO-US15626.  
 12-MAY-2000; 2000EP-0110063.  
 06-OCT-2000; 2000US-238762P.  
 (GPCB-1) GPC BIOTECH AG.  
 (MORP-) MORPHOSYS AG.  
 Nagy Z, Tesar M, Thomassen-Wolf E;  
 WPI; 2002-075289/10.

Composition for suppressing immune response, treating diseases of  
 immune system, has polypeptide comprising antibody-based  
 antigen-binding domain of human composition, which binds antigen  
 expressed on a cell surface

Example; Fig 15; 139pp; English.

The present invention describes a composition (I), comprising a  
 polypeptide comprising an antibody-based antigen-binding domain of human  
 composition with binding specificity for an antigen expressed on the  
 surface of a cell, where treating cells expressing the antigen with the  
 polypeptides leads to suppression of an immune response, and the IC50 for  
 the suppression of immune response is 1 microm or less. (I) has  
 antirheumatic, antiarthritic, neuroprotective, antiinflammatory,  
 antidiabetic, antipsoriatic, immunosuppressive, dermatological,  
 antithyroid, nephrotropic, thyromimetic and hepatocytic activities, and  
 can be used as a suppressor of immune response. (I) is useful for  
 suppressing activation or proliferation of a cell of the immune system,  
 suppressing IL-2 secretion by a cell, the interaction of a cell of the  
 immune system with another cell, immunosuppressing a patient and for  
 killing a cell expressing an antigen, human leukocyte antigen (HLA)-DR

on the surface of the cell, where neither cytotoxic entities nor  
 immunological mechanisms are needed to cause or lead to the killing.  
 (I) (optionally linked to cytotoxic or immunogenic agent) is useful for  
 preparing a pharmaceutical preparation for the treatment of rheumatoid  
 arthritis, juvenile arthritis, multiple sclerosis, Grave's disease,  
 insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus  
 erythematosus, ankylosing spondylitis, transplant rejection, graft versus  
 host disease, Hashimoto's disease, myasthenia gravis, pemphigus vulgaris,  
 glomerulonephritis, thyroiditis, pancreatitis, insulinitis, primary biliary  
 cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.  
 ABA92469 to ABA92474 and ABB57457 to ABB57590 represent sequence used in  
 the exemplification of the present invention.

Sequence 115 AA;  
 Query Match 85.2%; Score 508.5; DB 23; Length 115;  
 Best Local Similarity 87.8%; Pred. No. 3,4e-37;  
 Matches 101; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

QY 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPITGNGY 60  
 DB 1 QVQLVSGAEVKKPGSSVKVSCKASGCTFSSHAISWVROAPGQGLEWMGDIIPITGNGY 60  
 QY 61 AOKFGKRVTTTADSTSTAYMELSTLTSEBDTAVYYC-ELDPFY--WGQGTMTVSS 114  
 DB 61 AOKFGKRVTTTADSTSTAYMELSLRSEBDTAVYYCARPSFYLDYWGQGTIVTVSS 115

RESULT 11  
 ABR01510 standard; Protein: 225 AA.  
 ABR01510;  
 16-APR-2003 (first entry)

Human anti-TIMP-1 antibody heavy chain #8.

Human; antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VCDB3;  
 matrix metalloproteinase; MMP; variable heavy chain; VHCD3; hepatocytic;  
 variable light chain; cytosolic; nephrotropic; cardiac; liver fibrosis;  
 alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;  
 lupus nephritis; glomerulosclerotic renal disease; lung cancer;  
 idiopathic pulmonary fibrosis; benign prostatic hypertrophy; colon cancer.

Homo sapiens.  
 WO200286085-A2.  
 31-OCT-2002.  
 24-APR-2002; 2002WO-US12801.  
 24-APR-2001; 2001US-285683P.  
 (PARB) BAYER CORP.  
 (MORP-) MORPHOSYS AG.  
 Pan C, Knorr AM, Schauer M, Hirsch-dietrich C, Kraft S, Krebs B;  
 WPI; 2003-129114/12.  
 N-PSDB; ABZ74781.

New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1)  
 antibodies, for diagnosing or ameliorating the symptoms of a disorder  
 in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate  
 hypertrophy or lung cancer

Claim 20; Page 153; 228pp; English.

The invention relates to a novel purified preparation of a human  
 antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)  
 and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of



CC cancer. The antibody is also useful for detecting a TIMP-1 in a test  
CC preparation, or in diagnosing a disorder in which a TIMP-1 level is  
CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy  
CC chain regions of a human anti-TIMP-1 antibody of the invention.

XX Sequence 220 AA;

Query Match 86.3%; Score 515; DB 24; Length 220;

Best Local Similarity 87.1%; Pred. No. 1.7e-37;

Matches 101; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

Qy 1 QVQLVSGAEVKKRQSSVKVSCKASGCTFSSHAISWVRQAPGQLEWNGDIIPILGTANY 60  
Db 1 QVQLVSGAEVKKRQSSVKVSCKASGCTFSSHAISWVRQAPGQLEWNGDIIPILGTANY 60

Qy 61 AOKFGKRVITTADESTSTAYMEISTLTSEDPAVYVCEDMFIYI--WGQGTMTVSS 114  
Db 61 AOKFGKRVITTADESTSTAYMEISTLTSEDPAVYVCARQEWMDYWGQGLTVTVSS 116

#### RESULT 8

ABR01538  
ID ABR01538 standard; Protein; 220 AA.

XX ABR01538;

DT 16-APR-2003 (first entry)

DE Human anti-TIMP-1 antibody heavy chain #36.

XX Human; antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VCDDR3;  
KM matrix metalloproteinase; MMP; variable heavy chain; VHCD3; hepatocarcinoma;  
KM variable light chain; cytoskeletal; nephrotropic; cardiac; liver fibrosis;  
KM alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;  
KM lupus nephritis; glomerulosclerotic renal disease; lung cancer;  
KM idiopathic pulmonary fibrosis; benign prostatic hypertrophy; colon cancer.

XX Homo sapiens.

XX WO200286085-A2.

XX 31-OCT-2002.

XX 24-APR-2002; 2002WO-US12801.

XX 24-APR-2001; 2001US-285683P.

XX (FARB ) BAYER CORP.  
XX (MORP-) MORPHOSYS AG.

PI Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;

DR WPI; 2003-129114/12.

DR N-PSDB; AB274809.

PT New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1)

PT antibodies, for diagnosing or ameliorating the symptoms of a disorder

PT in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate

PT hypertrophy or lung cancer

PS Claim 20; Page 173; 228pp; English.

XX The invention relates to a novel purified preparation of a human  
CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)  
CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of  
CC TIMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and  
CC a variable light chain (VLC)DR3 region. An antibody preparation of the  
CC invention has hepatocarcinoma, cytoskeletal, nephrotropic and cardiac  
CC activity. The human antibody is useful for decreasing an MMP-inhibiting  
CC activity of a TIMP-1. It is especially useful for ameliorating the  
CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver  
CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary  
CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic

CC pulmonary fibrosis, benign prostatic hypertrophy, lung cancer or colon  
CC cancer. The antibody is also useful for detecting a TIMP-1 in a test  
CC preparation, or in diagnosing a disorder in which a TIMP-1 level is  
CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy  
CC chain regions of a human anti-TIMP-1 antibody of the invention.

XX Sequence 220 AA;

Query Match 85.4%; Score 510; DB 24; Length 220;

Best Local Similarity 87.1%; Pred. No. 4.7e-37;

Matches 101; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

Qy 1 QVQLVSGAEVKKRQSSVKVSCKASGCTFSSHAISWVRQAPGQLEWNGDIIPILGTANY 60  
Db 1 QVQLVSGAEVKKRQSSVKVSCKASGCTFSSHAISWVRQAPGQLEWNGDIIPILGTANY 60

Qy 61 AOKFGKRVITTADESTSTAYMEISTLTSEDPAVYVCEDMFIYI--WGQGTMTVSS 114  
Db 61 AOKFGKRVITTADESTSTAYMEISTLTSEDPAVYVCARQEWMDYWGQGLTVTVSS 116

#### RESULT 9

ABR67617  
ID ABR67617 standard; Protein; 245 AA.

XX ABR67617;

DT 29-MAY-2001 (first entry)

DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6\_1.

XX Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;

KM miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.

XX Homo sapiens.

XX WO200114558-A1.

XX 01-MAR-2001.

XX 28-AUG-2000; 2000WO-EP08388.

XX 26-AUG-1999; 99EP-0116691.

XX (MORP-) MORPHOSYS AG.

PI Kretzschmar T, Tesser M, Marget M, Kroenke M;

DR WPI; 2001-218451/22.

PT Novel isolated human immunoglobulin or functional immunoglobulin

PT fragment specific for human leukocyte antigen Cw6, useful for treatment

PT of humans and for human leukocyte antigen phenotyping

PS Claim 3; Fig 1; 23pp; English.

XX AAB67617-23 represent single chain antibody (scFv) fragments which  
CC are specific for human leukocyte antigen (HLA)-Cw6. The fragments are  
CC derived from a synthetic human combinatorial antibody library based on  
CC molecular consensus frameworks and CDRA randomised with trinucleotides.  
CC The specification describes a human immunoglobulin fragments specific  
CC for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in  
CC studies of natural killer cell silencing as well as miscarriages.  
CC HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.  
CC Prolapsis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin  
CC fragments are useful for the preparation of a pharmaceutical for the  
CC treatment of humans. They are also useful for HLA phenotyping.

XX Sequence 245 AA;

Query Match 85.3%; Score 509.5; DB 22; Length 245;

Best Local Similarity 87.2%; Pred. No. 5.8e-37;

Matches 102; Conservative 5; Mismatches 7; Indels 3; Gaps 2;

| ID | AA | AA24442                                                                | standard; Protein: 481 AA. |
|----|----|------------------------------------------------------------------------|----------------------------|
| AC | XX | AA24442;                                                               |                            |
| DT | XX | 25-MAR-2003 (updated)                                                  |                            |
| DT | XX | 02-JAN-1992 (first entry)                                              |                            |
| DE | XX | Sequence of antibody molecule IgG1.                                    |                            |
| KM | XX | Antibody: immunoglobulin G1.                                           |                            |
| OS | XX | Homo sapiens.                                                          |                            |
| FT | XX | Key                                                                    | Location/Qualifiers        |
| FT | XX | Misc-difference 308                                                    | /label= N                  |
| FT | XX | /note= "Substn. to create glycan addition site"                        |                            |
| FT | XX | Misc-difference 310                                                    | /label= S                  |
| FT | XX | /note= "see above"                                                     |                            |
| FT | XX | Misc-difference 321                                                    | /label= N                  |
| FT | XX | /note= "see above"                                                     |                            |
| FT | XX | Misc-difference 329                                                    | /label= N                  |
| FT | XX | /note= "see above"                                                     |                            |
| FT | XX | Misc-difference 331                                                    | /label= S                  |
| FT | XX | /note= "see above"                                                     |                            |
| FT | XX | Misc-difference 356                                                    | /label= N                  |
| FT | XX | /note= "see above"                                                     |                            |
| FT | XX | Misc-difference 369                                                    | /label= N                  |
| FT | XX | /note= "see above"                                                     |                            |
| XX | XX | MO9209293-A1.                                                          |                            |
| XX | XX | 11-JUN-1992.                                                           |                            |
| XX | XX | 18-NOV-1991; 91WO-US08605.                                             |                            |
| XX | XX | 23-NOV-1990; 90US-0618314.                                             |                            |
| XX | XX | (GEHO ) GEN HOSPITAL CORP.                                             |                            |
| XX | XX | Seed B, Walz G;                                                        |                            |
| XX | XX | WP1; 1992-216789/26.                                                   |                            |
| XX | XX | N-PSDB; AAQ25443.                                                      |                            |
| XX | XX | Inhibition of cell adhesion mediated through ERM-1 mol. binding        |                            |
| XX | XX | - used in treating chronic inflammation, rheumatoid arthritis,         |                            |
| XX | XX | psoriasis, etc.                                                        |                            |
| XX | XX | Disclosure; Fig 1; 46pp; English.                                      |                            |
| XX | XX | The IgG1, in its nascent form, bears no stably-linked side chains. The |                            |
| XX | XX | inventors designed a molecule including several such sites for         |                            |
| XX | XX | attachment of stably-linked side chains (see AA24442, FT). The         |                            |
| XX | XX | additional N-linked glycosylation sites are introduced at locations    |                            |
| XX | XX | which impair complement fixing and Fc receptor binding ability. They   |                            |
| XX | XX | are preferably located in the CH2 region of the Ig molecule.           |                            |
| XX | XX | Antibodies bearing multiple stably-linked determinants are useful for  |                            |
| XX | XX | disrupting undesirable interactions between cells or proteins.         |                            |
| XX | XX | Disrupting this interaction has therapeutic applications, for          |                            |
| XX | XX | example, in minimizing inflammation following tissue injury.           |                            |
| XX | XX | (Updated on 25-MAR-2003 to correct PN field.)                          |                            |

| Seq                       | Sequence                                                                    | 481 AA; |
|---------------------------|-----------------------------------------------------------------------------|---------|
| Query Match               | 86.3%; Score 515.5; DB 13; Length 481;                                      |         |
| Best Local Similarity     | 81.1%; Pred. No. 3.4e-37;                                                   |         |
| Matches 103; Conservative | 3; Mismatches 8; Indels 13; Gaps 1                                          |         |
| QY                        | 1 QVQLVDSGAEVKRKGSSGVSKVSKCSKASGGTFFSSHAISWVQAPQGGLEMMGDIIPILGTGNY 60       |         |
| DB                        | 25 QVQLVDSGAEVKRKGSSGVSKVSKCSKASGGTFFSSHAISWVQAPQGGLEMMGDIIPILGTGNY 84      |         |
| QY                        | 61 AOKFQGRVTITADESTSTAYWELSLTISEDTAYVYICBLD-----WPIYWGQ 107                 |         |
| DB                        | 85 AOKFQGRVTITADESTSTAYWELSLTISEDTAYVYICARDNGAYCGSGCYSGWFPDMGQ 144          |         |
| QY                        | 108 TMTVTVSS 114                                                            |         |
| DB                        | 145 TLVTVTVSS 151                                                           |         |
| RESULT 7                  |                                                                             |         |
| ABR01512                  | ABR01512 standard; Protein; 220 AA.                                         |         |
| XX                        | ABR01512;                                                                   |         |
| AC                        | ABR01512;                                                                   |         |
| XX                        | 16-APR-2003 (first entry)                                                   |         |
| XX                        | Human anti-TIMP-1 antibody heavy chain #10.                                 |         |
| DE                        | Human anti-TIMP-1 antibody heavy chain #10.                                 |         |
| XX                        | Human antibody; tissue inhibitor of metalloproteinase-1; TIMP-1; VLCDR3;    |         |
| KW                        | matrix metalloproteinase; MMP; variable heavy chain; VHCDR3; hepatocrotic;  |         |
| KM                        | variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis;   |         |
| KV                        | alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;         |         |
| KW                        | lupus nephritis; glomerulosclerotic renal disease; lung cancer;             |         |
| XX                        | idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.   |         |
| OS                        | Homo sapiens.                                                               |         |
| XX                        | WO200286085-A2.                                                             |         |
| XX                        | 31-OCT-2002.                                                                |         |
| XX                        | 24-APR-2002; 2002WO-US12801.                                                |         |
| XX                        | 24-APR-2001; 2001US-285683P.                                                |         |
| XX                        | (FARB ) BAYER CORP.                                                         |         |
| XX                        | (MORP-) MORPHOSYS AG.                                                       |         |
| XX                        | Pan C, Knorr AM, Schauer M, Hirtz-dietrich C, Kraft S, Krebs B;             |         |
| XX                        | WPI; 2003-129114/12.                                                        |         |
| XX                        | N-PSDB; AB274783.                                                           |         |
| XX                        | New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1)             |         |
| PT                        | antibodies, for diagnosing or ameliorating the symptoms of a disorder       |         |
| PT                        | in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate           |         |
| PT                        | hypertrophy or lung cancer                                                  |         |
| XX                        | Claim 20; Page 154; 228pp; English.                                         |         |
| XX                        | The invention relates to a novel purified preparation of a human            |         |
| XX                        | antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1) |         |
| XX                        | and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of     |         |
| XX                        | TIMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and   |         |
| XX                        | a variable light chain (VLC)DR3 region. An antibody preparation of the      |         |
| XX                        | invention has hepatocrotic, cytostatic, nephrotropic and cardiant           |         |
| XX                        | activity. The human antibody is useful for decreasing an MMP-inhibiting     |         |
| XX                        | activity of a TIMP-1. It is especially useful for ameliorating the          |         |
| XX                        | symptoms of a disorder in which TIMP-1 is elevated, e.g. liver              |         |
| XX                        | fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary         |         |
| XX                        | syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic     |         |
| XX                        | pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon       |         |

```
CC      fragment.
XX      Sequence       271 AA;
SQ
Query Match          87.2%; Score 520.5; DB 23; Length 271;
Best Local Similarity 87.2%; Pred. No. 76-38;
Matches 102; Conservative 4; Mismatches 8; Indels 3; Gaps 1
Oy      1 OVOLVQSGAEYVKPGSSIVKVCSCAKGCTFFSHAIISWYNQAPCGLEMMGDIIPIIGTGN Y 60
         :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      5 EVQLVQSGAEYVKPSSSVKVCSCAKGCTFSSVAISMVRQAPOGLERMGGIIPITGYAN Y 64
         |||||||
Oy      61 AOKPCGRVTITADESTSTRAYMELSLTUSBDTAVFYCE---LDMFINKGMNTWTYS 114
         |||||||
Db      65 AKCFQGRVTTITADESTISTRAYMELSLSRSDTAIVYICANSYYDMFPYWGQTILVTYS 121
         |||||||

RESULT 4
ID      AAY99558 standard; Protein; 118 AA.
AC      AAY99558;
AA      AAY99558;
DT      20-SEP-2000 (first entry)
DE      Human LH13 monoclonal antibody heavy chain variable region.
EX      Human; LH13 monoclonal antibody; hybridoma; tumour-specific; cancer;
KW      cytostatic; cytotoxic; heavy chain variable region.
XX      Homo sapiens.
OS      Homo sapiens.
PN      WO200032635-A2.
PD      08-JUN-2000.
PF      01-DEC-1999; 99WO-US28485.
PR      02-DEC-1998; 98US-0203768.
PA      (IXSY-) IXSYS INC.
PI      Wackins JD, Huse WD;
PT      MPI; 2000-412293/35.
DR      N-PSTD; AAA48411.
XX      New tumor-specific human monoclonal antibody, useful for the treatment
PT      and diagnosis of cancer, comprises at least one complementarily
        determining region -
XX      Claim 10; Page 82-83; 84pp; English.
CC      The present sequence is the heavy chain variable region of a human
CC      tumour-specific monoclonal antibody. Neoplastic cells selectively express
CC      antigens which are not present on normal cells. Thus monoclonal
CC      antibodies can be produced that are specifically directed against
CC      tumour-specific antigens. The antibodies can be conjugated to cytotoxic
CC      or cytostatic agents and used to selectively target cancer cells for the
CC      elimination of tumours. They can also be linked to diagnostic moieties
CC      that allow the imaging of neoplastic cells. Nucleic acids encoding human
CC      tumour-specific monoclonal antibodies can be used to express the
CC      antibodies and can be recombinantly engineered to produce modified
CC      antibodies with higher affinity or higher selectivity for tumour cells.
CC      Tumour-specific antibodies were produced by hybridomas that were
CC      generated by in vitro immunisation of human spleen cell cultures with
CC      breast carcinoma cells. The nucleic acid encoding the monoclonal antibody
CC      was then isolated from the hybridoma by RT-PCR. The present sequence
CC      was produced by LH13 hybridoma cell line.
SQ      Sequence       118 AA;

```

|                                                                    |                                               |                                                                          |                                                            |                    |
|--------------------------------------------------------------------|-----------------------------------------------|--------------------------------------------------------------------------|------------------------------------------------------------|--------------------|
| Oy                                                                 |                                               | 1                                                                        | QVQLVSGAEYKPKGSSVKVSCKASGGTFFSSHAISWVRQAQGGLRWMDIIPILGTGNY | 60                 |
| Dd                                                                 |                                               | 1                                                                        | QVQLVSGAEYKPKGSSVKVSCKASGGTFFSSHAISWVRQAQGGLRWMDIIPILGTGNY | 60                 |
| Oy                                                                 |                                               | 61                                                                       | AQRKGARVTITADSTSTAYWEELTLTSBDTAIVYYCELD----                | WPYIWGGCTMTVSS 114 |
| Dd                                                                 |                                               | 61                                                                       | AQRKGARVTITADSTSTAYWEELSLSESDTAIVYYCAEDSSGMHWGGCTLVTVSS    | 118                |
| <br>RESULT 5<br>AAU97198<br>ID AAU97198 standard; protein; 270 AA. |                                               |                                                                          |                                                            |                    |
| XX                                                                 |                                               | AAU97198;                                                                |                                                            |                    |
| XX                                                                 |                                               | 27-AUG-2002 (first entry)                                                |                                                            |                    |
| XX                                                                 |                                               |                                                                          |                                                            |                    |
| DE                                                                 |                                               | Human anti-BGFR single-chain antibody isolated from clone pSEX81-63.     |                                                            |                    |
| XX                                                                 |                                               |                                                                          |                                                            |                    |
| KW                                                                 |                                               | Human; anti-epidermal growth factor receptor single-chain antibody;      |                                                            |                    |
| KM                                                                 |                                               | anti-BGFR-scFv; Igm; cancer; tumour growth; clone pSEX81-63; cytostatic. |                                                            |                    |
| XX                                                                 |                                               |                                                                          |                                                            |                    |
| OS                                                                 |                                               | Homo sapiens.                                                            |                                                            |                    |
| PN                                                                 |                                               | WO200230984-A1.                                                          |                                                            |                    |
| XX                                                                 |                                               | 18-APR-2002.                                                             |                                                            |                    |
| XX                                                                 |                                               |                                                                          |                                                            |                    |
| PF                                                                 |                                               | 12-OCT-2001; 2001WO-US31857.                                             |                                                            |                    |
| XX                                                                 |                                               |                                                                          |                                                            |                    |
| PR                                                                 |                                               | 13-OCT-2000; 2000US-240353P.                                             |                                                            |                    |
| XX                                                                 |                                               |                                                                          |                                                            |                    |
| PA                                                                 |                                               | (UABR-) UAB RES FOUND.                                                   |                                                            |                    |
| PI                                                                 |                                               | Rajesh KP, Curjel DT, Bonner JA;                                         |                                                            |                    |
| DR                                                                 |                                               | WPI; 2002-463261/49.                                                     |                                                            |                    |
| PT                                                                 |                                               | Novel human anti-epidermal growth factor receptor single-chain antibody  |                                                            |                    |
| PT                                                                 |                                               | treatng for diagnostic location and assessment of tumour growth, and in  |                                                            |                    |
| PS                                                                 |                                               | treating cancer -                                                        |                                                            |                    |
| PS                                                                 |                                               | Claim 3; Fig 2; 51pp; English.                                           |                                                            |                    |
| CC                                                                 |                                               | The present invention relates to human anti-epidermal growth factor      |                                                            |                    |
| CC                                                                 |                                               | receptor single-chain antibodies (anti-BGFR-scFvs) isolated from a       |                                                            |                    |
| CC                                                                 |                                               | human Igm phage display library using BGFR as antigen. Two isolates      |                                                            |                    |
| CC                                                                 |                                               | with different amino acid sequences were identified. The                 |                                                            |                    |
| CC                                                                 |                                               | anti-BGFR-scFvs are useful for treating cancer, and for the              |                                                            |                    |
| CC                                                                 |                                               | diagnostic location and assessment of tumour growth, where the           |                                                            |                    |
| CC                                                                 |                                               | anti-BGFR-scFv is radiolabelled. The present sequence represents         |                                                            |                    |
| CC                                                                 |                                               | human anti-BGFR single-chain antibody isolated from clone pSEX81-63.     |                                                            |                    |
| SQ                                                                 |                                               | Sequence 270 AA;                                                         |                                                            |                    |
| Query Match                                                        | 86.4%; Score 516; DB 23; Length 270;          |                                                                          |                                                            |                    |
| Matches 103;                                                       | Conservative 3; Mismatches 8; Indels 12; Gaps |                                                                          |                                                            |                    |
| Oy                                                                 |                                               | 1 QVQLVSGAEYKPKGSSVKVSCKASGGTFFSSHAISWVRQAQGGLRWMDIIPILGTGNY             | 60                                                         |                    |
| Dd                                                                 |                                               | 1 QVQLVSGAEYKPKGSSVKVSCKASGGTFFSSHAISWVRQAQGGLRWMDIIPILGTGNY             | 60                                                         |                    |
| Oy                                                                 |                                               | 61 AQRKGARVTITADSTSTAYWEELTLTSBDTAIVYYCELD-----WPYIWGGCT                 | 108                                                        |                    |
| Dd                                                                 |                                               | 61 AQRKGARVTITADSTSTAYWEELSLSESDTAIVYYCAEDDPYVGSGSYPMWPDWGCGT            | 120                                                        |                    |
| Oy                                                                 |                                               | 109 MVTWSS 114                                                           |                                                            |                    |
| Dd                                                                 |                                               | 121 LVTWSS 126                                                           |                                                            |                    |

PT treatment of hemophilia A patients with these antibodies -  
XX  
XX Example 9, Fig 11B, 61pp; English.  
XX  
CC This invention describes a novel polynucleotide (1) (and complements and  
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence  
CC coding for a human antibody with factor VIII specificity which has  
CC hemostatic activity. (1) is useful a primer or probe for detecting the  
CC presence of inhibitory antibodies directed against factor VIII. The  
CC polypeptides of the invention and the antibodies generated from them  
CC are useful in compositions for neutralizing factor VIII inhibiting  
CC antibodies in hemophilia A patients. This sequence represents a fragment  
CC of the human factor VIII antibody heavy chain variable region protein  
CC DP-10 which is used in the method of the invention.  
XX  
XX Sequence 114 AA;  
SQ  
Query Match 100.0%; Score 597; DB 21; Length 114;  
Best Local Similarity 100.0%; Pred. No. 6,1e-45;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QVQLVSGAEVKKPKSSVKVSCKASGTFSSHAISWVROAPGQGLEWMGDIIPILGQNY 60  
Db 1 QVQLVSGAEVKKPKSSVKVSCKASGTFSSHAISWVROAPGQGLEWMGDIIPILGQNY 60  
Qy 61 AQKFGKRVITTADESTSTAYMELSTLTSEDYAVYCCLEDFYINQGMVTYSS 114  
Db 61 AQKFGKRVITTADESTSTAYMELSTLTSEDYAVYCCLEDFYINQGMVTYSS 114  
RESULT 2  
AAV50971  
ID AAV50971 standard; Protein; 116 AA.  
XX  
XX AAV50971;  
AC  
XX 23-MAR-2000 (first entry)  
DT  
XX Human FVIII antibody A2 scFv heavy chain protein DP-10 #2.  
DE  
XX Human; heavy chain; antibody; factor VIII; hemostatic;  
KM hemophilia A; scFv; A2.  
XX  
XX Homo sapiens.  
OS  
XX MO9958680-A2.  
PN  
XX 18-NOV-1999.  
PD  
XX 07-MAY-1999; 99WO-NL00285.  
PF  
XX 08-MAY-1998; 98EP-0201543.  
PR  
XX (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.  
PA  
XX Voorberg JJ, Van Den Brink EN, Turenhout EM;  
PI WPI; 2000-053102/04.  
DR  
XX New polynucleotide, polypeptide and antibody useful for diagnosing the  
PT presence of neutralizing antibodies against factor VIII and for  
PT treatment of hemophilia A patients with these antibodies -  
XX  
XX Example 9, Fig 11A, 61pp; English.  
XX  
CC This invention describes a novel polynucleotide (1) (and complements and  
CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence  
CC coding for a human antibody with factor VIII specificity which has  
CC hemostatic activity. (1) is useful a primer or probe for detecting the  
CC presence of inhibitory antibodies directed against factor VIII. The  
CC polypeptides of the invention and the antibodies generated from them  
CC are useful in compositions for neutralizing factor VIII inhibiting  
CC antibodies in hemophilia A patients. This sequence represents a human

CC factor VIII antibody A2 specific scFv protein DP-10 which is used  
CC in the method of the invention.  
XX  
XX Sequence 116 AA;  
SQ  
Query Match 98.2%; Score 586; DB 21; Length 116;  
Best Local Similarity 98.3%; Pred. No. 5,7e-44;  
Matches 114; Conservative 0; Mismatches 0; Indels 2; Gaps 1;  
Qy 1 QVQLVSGAEVKKPKSSVKVSCKASGTFSSHAISWVROAPGQGLEWMGDIIPILGQNY 60  
Db 1 QVQLVSGAEVKKPKSSVKVSCKASGTFSSHAISWVROAPGQGLEWMGDIIPILGQNY 60  
Qy 61 AQKFGKRVITTADESTSTAYMELSTLTSEDYAVYCCLEDFYINQGMVTYSS 114  
Db 61 AQKFGKRVITTADESTSTAYMELSTLTSEDYAVYCCLEDFYINQGMVTYSS 116  
RESULT 3  
AAG66039  
ID AAG66039 standard; Protein; 271 AA.  
XX  
XX AAG66039;  
AC  
XX 27-FEB-2002 (first entry)  
DT  
XX scFv 1b4 antibody fragment.  
DE  
XX  
XX Ryk protein; angiogenesis; variant; receptor tyrosine kinase; cytosolic;  
KM anti-diabetic; ophthalmological; cardiac; vulnery; antiangiogenic;  
KW gene therapy; fusion protein.  
XX  
XX Synthetic.  
OS  
XX WO200185789-A2.  
PN  
XX 15-NOV-2001.  
PD  
XX 09-MAY-2001; 2001WO-US15043.  
PF  
XX 10-MAY-2000; 2000US-0568783.  
PR  
XX (FARB ) BAYER CORP.  
PA  
XX Rocznik S, Dubois-Stringfellow NA, Zolotarev A;  
PI WPI; 2002-049443/06.  
DR  
XX N-PSDB; AAI67770.  
DD  
XX Modulating angiogenesis at a site, for treating or preventing cancer,  
PT metastasis, diabetic retinopathy, cardiovascular disease, wound by  
PT supplying composition comprising variant Ryk protein to the site -  
XX  
XX Examples; Page 79-80; 81pp; English.  
XX  
XX The invention relates to modulating angiogenesis at a site by supplying  
CC a composition comprising a variant Ryk protein (1) (a member of the  
CC receptor tyrosine kinase family), or modulating formation of cells into  
CC capillary-like structures by contacting the cells with a composition  
CC comprising (1). The method is useful modulating angiogenesis at a site  
CC (preferably, within a human) or modulating the formation of cells  
CC (endothelial cells of human origin) into capillary-like structure. The  
CC (1) is useful for preventing, treating or ameliorating a medical  
CC condition e.g., cancer, metastasis, diabetic retinopathy, macular  
CC degeneration, cardiovascular disease, wound, pregnancy, or a clinical  
CC condition involving angiogenesis in the reproductive system, including  
CC regulation of placental vascularization in an individual. The variant  
CC protein is supplied to the individual as a source of polynucleotide  
CC encoding the protein and expressing the protein in vivo. (1) is used  
CC as an immunogen to produce an antibody against it. The antibodies are  
CC useful for modulating angiogenesis at a site. Polynucleotides encoding  
CC (1) is useful in gene therapy technique for treating above mentioned  
CC medical conditions. The present sequence represents the scFv 1b4 antibody

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 36.6726 Seconds

(without alignments)  
493.415 Million cell updates/sec

Title: US-09-674-752-51

Perfect score: 597  
Sequence: 1 OVQLVSGAEVKKKRGSSVKV.....XCELDWFYIWGGTMTVSS 114

Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
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8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
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10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
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17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                 |
|------------|-------|-------------|--------|-------|-----------------------------|
| 1          | 597   | 100.0       | 114    | 21    | AAV50974 Human FVIII heavy  |
| 2          | 586   | 98.2        | 116    | 21    | AAV50971 Human FVIII antibo |
| 3          | 520.5 | 87.2        | 271    | 23    | AA666039 scFv 1b4 antibody  |
| 4          | 520   | 87.1        | 118    | 21    | AAV99558 Human Lh13 monoclo |
| 5          | 516   | 86.4        | 270    | 23    | AAU97198 Human anti-RGR 81  |
| 6          | 515.5 | 86.3        | 481    | 13    | AAK24442 Sequence of antibo |
| 7          | 515   | 86.3        | 220    | 24    | ABR01512 Human anti-TIMP-1  |
| 8          | 510   | 85.4        | 220    | 24    | ABR01538 Human anti-TIMP-1  |
| 9          | 509.5 | 85.3        | 245    | 22    | AA67617 Human leukocyte an  |

|    |       |      |     |    |                             |
|----|-------|------|-----|----|-----------------------------|
| 10 | 508.5 | 85.2 | 115 | 23 | ABBS7559 HLA-DR-specific pr |
| 11 | 508.5 | 85.2 | 225 | 24 | ABR01510 Human anti-TIMP-1  |
| 12 | 508.5 | 85.2 | 245 | 22 | AA67618 Human leukocyte an  |
| 13 | 508   | 85.1 | 120 | 18 | AA672550 Human Ab heavy cha |
| 14 | 508   | 85.1 | 120 | 24 | ABJ18672 Antibody library r |
| 15 | 508   | 85.1 | 120 | 24 | ABJ18718 Antibody library r |
| 16 | 507   | 84.9 | 253 | 23 | ABP45498 Human Blys binding |
| 17 | 506.5 | 84.8 | 229 | 24 | ABR01518 Human anti-TIMP-1  |
| 18 | 506.5 | 84.8 | 248 | 23 | ABP45722 Human Blys binding |
| 19 | 506.5 | 84.8 | 248 | 23 | ABP45723 Human Blys binding |
| 20 | 505.5 | 84.7 | 125 | 22 | AAU02555 Anti-adipocyte mon |
| 21 | 505.5 | 84.7 | 219 | 24 | ABR01523 Human anti-TIMP-1  |
| 22 | 505.5 | 84.7 | 223 | 24 | ABR01535 Human anti-TIMP-1  |
| 23 | 505.5 | 84.7 | 244 | 23 | ABP45870 Human Blys binding |
| 24 | 505.5 | 84.7 | 248 | 23 | ABP45707 Human Blys binding |
| 25 | 505.5 | 84.7 | 248 | 23 | ABP45868 Human Blys binding |
| 26 | 504   | 84.4 | 222 | 24 | ABR01531 Human anti-TIMP-1  |
| 27 | 504   | 84.4 | 254 | 23 | ABP45855 Human Blys binding |
| 28 | 503.5 | 84.3 | 249 | 21 | AA636083 Recombinant human  |
| 29 | 502.5 | 84.2 | 248 | 23 | ABP45708 Human Blys binding |
| 30 | 502.5 | 84.2 | 248 | 23 | ABP45721 Human Blys binding |
| 31 | 502.5 | 84.2 | 248 | 23 | ABP45726 Human Blys binding |
| 32 | 501.5 | 84.0 | 231 | 24 | ABR01524 Human anti-TIMP-1  |
| 33 | 501.5 | 84.0 | 228 | 23 | ABP45730 Human Blys binding |
| 34 | 500.5 | 83.8 | 253 | 23 | ABP45869 Human Blys binding |
| 35 | 499.5 | 83.7 | 248 | 23 | ABP45716 Human Blys binding |
| 36 | 499.5 | 83.6 | 257 | 23 | ABP45717 Human Blys binding |
| 37 | 499   | 83.6 | 257 | 23 | ABP45542 Synthetic antibody |
| 38 | 498.5 | 83.5 | 222 | 22 | AAU04972 Synthetic antibody |
| 39 | 498.5 | 83.5 | 223 | 22 | AAU04973 APRIL binding scFv |
| 40 | 498.5 | 83.5 | 245 | 24 | ABP60521 Synthetic antibody |
| 41 | 497.5 | 83.3 | 222 | 22 | AAU04974 Synthetic antibody |
| 42 | 497.5 | 83.3 | 222 | 22 | AAU04976 Human Blys binding |
| 43 | 496   | 83.1 | 256 | 23 | ABP45589 Human Blys binding |
| 44 | 495.5 | 83.0 | 246 | 23 | ABP46051 Human Blys binding |
| 45 | 495.5 | 83.0 | 248 | 23 | ABP45706 Human Blys binding |

#### ALIGNMENTS

RESULT 1  
ID AAV50974 standard; Protein: 114 AA.  
AAV50974  
XX  
AC AAV50974;  
XX  
XX 23-MAR-2000 (first entry)  
DT  
XX Human FVIII heavy chain variable region protein fragment.  
DE  
XX Human, heavy chain; antibody; factor VIII; hemostatic; variable region;  
KW hemophilia A.  
XX  
OS Homo sapiens.  
PN WO955680-A2.  
XX  
XX 18-NOV-1999.  
PD  
XX 07-MAY-1999; 99WO-NL00285.  
PF  
XX 08-MAY-1998; 98EP-0201543.  
PR  
XX (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.  
PA Voorberg JJ, Van Den Brink EN, Turehout EM;  
PI WPI; 2000-053102/04.  
XX N-PSDB; AA243867.  
DR  
XX New polynucleotide, polypeptide and antibody useful for diagnosing the  
PT presence of neutralizing antibodies against factor VIII and for

GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: December 30, 2003, 10:47:45 ; Search time 11.576 Seconds  
(without alignment)  
416.677 Million cell updates/sec

Title: US-09-674-752-51

Perfect score: 1 QVQLVSGAEVKKPGSSVKV.....YCELDFWFIWGCGTMTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database:

Issued\_Patents\_AA:\*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 508   | 85.1        | 120    | 4     | US-09-025-769B-35 |
| 2          | 508   | 85.1        | 120    | 4     | US-09-025-769B-57 |
| 3          | 503.5 | 84.3        | 119    | 4     | US-09-025-769B-21 |
| 4          | 492.5 | 82.5        | 123    | 2     | US-08-652-816A-1  |
| 5          | 492.5 | 82.5        | 123    | 2     | US-08-652-816A-6  |
| 6          | 492.5 | 82.5        | 123    | 2     | US-08-652-816A-8  |
| 7          | 492.5 | 82.5        | 123    | 2     | US-08-652-816A-9  |
| 8          | 476.5 | 79.8        | 121    | 2     | US-08-232-081B-41 |
| 9          | 474.5 | 79.5        | 119    | 3     | US-08-983-607-50  |
| 10         | 474.5 | 79.5        | 120    | 2     | US-08-428-197-12  |
| 11         | 474.5 | 79.5        | 120    | 5     | PCT-US93-10555-12 |
| 12         | 474.5 | 79.5        | 120    | 5     | PCT-US93-10555-13 |
| 13         | 474.5 | 79.5        | 120    | 5     | PCT-US93-10555-13 |
| 14         | 471.5 | 78.0        | 476    | 2     | US-08-378-939-10  |
| 15         | 470.5 | 78.8        | 123    | 2     | US-08-652-816A-7  |
| 16         | 461   | 77.2        | 147    | 1     | US-08-217-918-4   |
| 17         | 455   | 76.2        | 102    | 1     | US-07-834-539A-55 |
| 18         | 455   | 76.2        | 102    | 1     | US-08-053-131-63  |
| 19         | 455   | 76.2        | 102    | 1     | US-08-645-641-63  |
| 20         | 455   | 76.2        | 102    | 1     | US-07-853-408B-63 |
| 21         | 455   | 76.2        | 102    | 2     | US-08-096-762-63  |
| 22         | 455   | 76.2        | 102    | 2     | US-08-800-353-55  |
| 23         | 455   | 76.2        | 102    | 2     | US-08-308-865-63  |
| 24         | 455   | 76.2        | 102    | 5     | PCT-US92-06185-55 |
| 25         | 455   | 76.2        | 102    | 5     | PCT-US92-10983-63 |
| 26         | 455   | 76.2        | 117    | 3     | US-09-042-353-232 |
| 27         | 455   | 76.2        | 117    | 4     | US-08-758-417A-80 |

|    |       |      |     |   |                   |                   |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 452   | 75.7 | 128 | 1 | US-08-202-047-22  | Sequence 22, App1 |
| 29 | 452   | 75.7 | 128 | 3 | US-08-364-690-22  | Sequence 22, App1 |
| 30 | 452   | 75.7 | 128 | 4 | US-08-635-109-3   | Sequence 3, App1  |
| 31 | 449.5 | 75.3 | 125 | 3 | US-09-199-149-3   | Sequence 3, App1  |
| 32 | 441.5 | 74.0 | 129 | 2 | US-08-561-521-45  | Sequence 45, App1 |
| 33 | 441.5 | 74.0 | 129 | 4 | US-08-525-539A-77 | Sequence 77, App1 |
| 34 | 441.5 | 74.0 | 129 | 5 | PCT-US95-01219-45 | Sequence 45, App1 |
| 35 | 435.5 | 72.9 | 122 | 5 | PCT-US95-00067-2  | Sequence 2, App1  |
| 36 | 432.5 | 72.4 | 119 | 1 | US-08-458-516-10  | Sequence 10, App1 |
| 37 | 432.5 | 72.4 | 232 | 1 | US-08-458-516-22  | Sequence 22, App1 |
| 38 | 432.5 | 72.4 | 235 | 1 | US-08-458-516-23  | Sequence 23, App1 |
| 39 | 432.5 | 72.4 | 449 | 1 | US-08-458-516-13  | Sequence 13, App1 |
| 40 | 432   | 72.4 | 118 | 2 | US-08-428-257A-78 | Sequence 78, App1 |
| 41 | 432   | 72.4 | 118 | 3 | US-07-587-264-60  | Sequence 60, App1 |
| 42 | 431.5 | 72.3 | 117 | 1 | US-07-634-278-105 | Sequence 105, App |
| 43 | 431.5 | 72.3 | 117 | 1 | US-08-477-728-105 | Sequence 105, App |
| 44 | 431.5 | 72.3 | 117 | 1 | US-08-474-040-105 | Sequence 105, App |
| 45 | 431.5 | 72.3 | 117 | 1 | US-08-487-200-105 | Sequence 105, App |

## ALIGNMENTS

RESULT 1  
US-09-025-769B-35  
Sequence 35, Application US/09025769B  
Patent No. 6300064  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Illeg, Vlc  
APPLICANT: Ge, Liming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
FAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULAR TYPE: protein  
US-09-025-769B-35

Query Match 85.1%; Score 508; DB 4; Length 120;  
Best Local Similarity 85.8%; Pred. No. 2,8e-45;  
Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2;

QY 1 QVQLVSGAEVYKPKGSSVYKVSCKASGCTPSSHAISWVRQAPQGLIEMWGDIIPILGTGY 60  
DB 1 QVQLVSGAEVYKPKGSSVYKVSCKASGCTPSSHAISWVRQAPQGLIEMWGDIIPILGTGY 60  
QY 61 AOKFGRTITADESTSTAYMELSTLTSEDTAVYTCR---DMFY---IMGGTAVTVSS 114  
DB 61 AOKFGRTITADESTSTAYMELSLRSEDVAVYICARWGDDGFYANDYWGGLTVTVSS 120

## RESULT 2

US-09-025-769B-57  
Sequence 57, Application US/09025769B

Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

APPLICANT: Plueckthun, Andreas

TITLE OF INVENTION: Protein/(poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-769B-57

Query Match 85.1%; Score 508; DB 4; Length 120;

Best Local Similarity 85.8%; Pred. No. 2,8e-45;

Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2;

QY 1 QVQLVSGAEVYKPKGSSVYKVSCKASGCTPSSHAISWVRQAPQGLIEMWGDIIPILGTGY 60  
DB 1 QVQLVSGAEVYKPKGSSVYKVSCKASGCTPSSHAISWVRQAPQGLIEMWGDIIPILGTGY 60  
QY 61 AOKFGRTITADESTSTAYMELSTLTSEDTAVYTCR---DMFY---IMGGTAVTVSS 114  
DB 61 AOKFGRTITADESTSTAYMELSLRSEDVAVYICARWGDDGFYANDYWGGLTVTVSS 120

## RESULT 3

US-09-025-769B-21

Sequence 21, Application US/09025769B

Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

APPLICANT: Plueckthun, Andreas

TITLE OF INVENTION: Protein/(poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-769B-21

Query Match 84.3%; Score 503.5; DB 4; Length 119;

Best Local Similarity 84.9%; Pred. No. 8.1e-45;

Matches 101; Conservative 3; Mismatches 10; Indels 5; Gaps 1;

QY 1 QVQLVSGAEVYKPKGSSVYKVSCKASGCTPSSHAISWVRQAPQGLIEMWGDIIPILGTGY 60  
DB 1 QVQLVSGAEVYKPKGSSVYKVSCKASGCTPSSHAISWVRQAPQGLIEMWGDIIPILGTGY 60  
QY 61 AOKFGRTITADESTSTAYMELSTLTSEDTAVYTCR---DMFYIMGGTAVTVSS 114  
DB 61 AOKFGRTITADESTSTAYMELSLRSEDVAVYICARWDDGFYANDYWGGLTVTVSS 119

## RESULT 4

US-08-652-816A-1

Sequence 1, Application US/08652816A

Patent No. 5872215

GENERAL INFORMATION:

APPLICANT: Oebourn, JK

APPLICANT: Allen, DJ

APPLICANT: McCafferty, JG

TITLE OF INVENTION: Specific binding members, materials and

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 36.6726 Seconds  
(without alignment)  
493.415 Million cell updates/sec

Title: US-09-674-752-51

Perfect score: 597  
Sequence: 1 QVQLVQSGAEVKKPKSSSKV.....YCELDWFYIMCGTMTVSS 114

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: A.GeneSeq.19Jun03.\*  
2: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1980.DAT.\*  
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10: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1988.DAT.\*  
11: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1989.DAT.\*  
12: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1990.DAT.\*  
13: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1991.DAT.\*  
14: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1992.DAT.\*  
15: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1993.DAT.\*  
16: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1994.DAT.\*  
17: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1995.DAT.\*  
18: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1996.DAT.\*  
19: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1997.DAT.\*  
20: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1998.DAT.\*  
21: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1999.DAT.\*  
22: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT.\*  
23: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT.\*  
24: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT.\*  
25: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 597   | 100.0       | 114    | 21    | AAV50974    |
| 2          | 586   | 98.2        | 116    | 21    | AAV50971    |
| 3          | 520.5 | 87.2        | 271    | 23    | AA66039     |
| 4          | 520   | 87.1        | 118    | 21    | AAV99558    |
| 5          | 516   | 86.4        | 270    | 21    | AAU97198    |
| 6          | 515.5 | 86.3        | 481    | 13    | AA24442     |
| 7          | 515   | 86.3        | 220    | 24    | ABR01512    |
| 8          | 510   | 85.4        | 220    | 24    | ABR01538    |
| 9          | 509.5 | 85.3        | 245    | 22    | AA67617     |

|    |       |      |     |    |          |                    |
|----|-------|------|-----|----|----------|--------------------|
| 10 | 508.5 | 85.2 | 115 | 23 | AB65759  | HLA-DR-specific pr |
| 11 | 508.5 | 85.2 | 225 | 24 | ABR01510 | Human anti-TIMP-1  |
| 12 | 508.5 | 85.2 | 245 | 22 | AA67618  | Human leukocyte an |
| 13 | 508   | 85.1 | 120 | 18 | AA27550  | Human Ab heavy cha |
| 14 | 508   | 85.1 | 120 | 24 | ABJ18672 | Antibody library r |
| 15 | 508   | 85.1 | 120 | 24 | ABJ18718 | Antibody library r |
| 16 | 507   | 84.9 | 253 | 23 | ABP45498 | Human Blys binding |
| 17 | 506.5 | 84.8 | 229 | 24 | ABR01518 | Human anti-TIMP-1  |
| 18 | 506.5 | 84.8 | 248 | 23 | ABP45722 | Human Blys binding |
| 19 | 506.5 | 84.8 | 248 | 23 | ABP45723 | Human Blys binding |
| 20 | 505.5 | 84.7 | 125 | 22 | AAU02555 | Anti adipocyte mon |
| 21 | 505.5 | 84.7 | 219 | 24 | ABR01523 | Human anti-TIMP-1  |
| 22 | 505.5 | 84.7 | 223 | 24 | ABR01535 | Human anti-TIMP-1  |
| 23 | 505.5 | 84.7 | 244 | 23 | ABP45870 | Human Blys binding |
| 24 | 505.5 | 84.7 | 248 | 23 | ABP45707 | Human Blys binding |
| 25 | 505.5 | 84.7 | 248 | 23 | ABP45868 | Human Blys binding |
| 26 | 504   | 84.4 | 222 | 24 | ABR01551 | Human anti-TIMP-1  |
| 27 | 504   | 84.4 | 254 | 23 | ABP45855 | Human Blys binding |
| 28 | 503.5 | 84.3 | 249 | 21 | AA636083 | Recombinant human  |
| 29 | 502.5 | 84.2 | 248 | 23 | ABP45708 | Human Blys binding |
| 30 | 502.5 | 84.2 | 248 | 23 | ABP45721 | Human Blys binding |
| 31 | 502.5 | 84.2 | 248 | 23 | ABP45726 | Human Blys binding |
| 32 | 501.5 | 84.0 | 231 | 24 | ABR01524 | Human anti-TIMP-1  |
| 33 | 501.5 | 84.0 | 248 | 23 | ABP45730 | Human Blys binding |
| 34 | 500.5 | 83.8 | 253 | 23 | ABP45869 | Human Blys binding |
| 35 | 499.5 | 83.7 | 248 | 23 | ABP45716 | Human Blys binding |
| 36 | 499.5 | 83.7 | 248 | 23 | ABP45717 | Human Blys binding |
| 37 | 499   | 83.6 | 257 | 23 | ABP45542 | Human Blys binding |
| 38 | 498.5 | 83.5 | 222 | 22 | AAU04972 | Synthetic antibody |
| 39 | 498.5 | 83.5 | 223 | 22 | AAU04973 | Synthetic antibody |
| 40 | 498.5 | 83.5 | 245 | 24 | ABP60521 | APRIL binding scfv |
| 41 | 497.5 | 83.3 | 222 | 22 | AAU04974 | Synthetic antibody |
| 42 | 497.5 | 83.3 | 222 | 22 | ABP45976 | Synthetic antibody |
| 43 | 496   | 83.1 | 256 | 23 | ABP45589 | Human Blys binding |
| 44 | 495.5 | 83.0 | 246 | 23 | ABP46051 | Human Blys binding |
| 45 | 495.5 | 83.0 | 248 | 23 | ABP45706 | Human Blys binding |

## ALIGNMENTS

RESULT 1  
ID AAV50974 standard; Protein: 114 AA.  
AAV50974  
XX AAV50974;  
AC  
XX  
XX  
DT 23-MAR-2000 (first entry)  
XX  
DE Human FVIII heavy chain variable region protein fragment.  
XX  
XX Human; heavy chain; antibody; factor VIII; hemostatic; variable region;  
KW hemophilic A.  
XX  
OS Homo sapiens.  
XX  
XX  
XX W09956680-A2.  
XX  
PD 18-NOV-1999.  
XX  
PP 07-MAY-1999; 99WO-NL00285.  
XX  
PR 08-MAY-1998; 98BP-0201543.  
XX  
PA (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.  
XX Voorberg JJ, Van Den Brink EN, Turehout EAM;  
PI WPI: 2000-053102/04.  
XX N-PSDB; AA243867.  
DR  
XX  
PT New polynucleotide, polypeptide and antibody useful for diagnosing the  
presence of neutralizing antibodies against factor VIII and for



CC fragment.  
XX  
SQ Sequence 271 AA;

Query Match 87.2%; Score 520.5; DB 23; Length 271;  
Best Local Similarity 87.2%; Pred. No. 7e-38;  
Matches 102; Conservative 4; Mismatches 8; Indels 3; Gaps 1;

QY 1 QVQLVQSGAEVKKPSSSVKVCCKASGTFSSHAISWVRQAPQGLMMGDIIPILGTGNY 60  
DB 5 EVQLVQSGAEVKKPSSSVKVCCKASGTFSSHAISWVRQAPQGLMMGDIIPILGTGNY 64

QY 61 AOKFGGRVTITADESTSTAYMELSTLTSEDYAVYYCE---LDWFIYWGQGTMTVSS 114  
DB 65 AOKFGGRVTITADESTSTAYMELSLRSEDTAVYYCARSYDWFYWGQGTMTVSS 121

RESULT 4  
ID AAY99558 standard; protein; 118 AA.  
XX  
AC AAY99558;

DT 20-SEP-2000 (first entry)

DE Human LH13 monoclonal antibody heavy chain variable region.

XX Human; LH13 monoclonal antibody; hybridoma; tumour-specific; cancer;  
KM cytostatic; cytotoxic; heavy chain variable region.

XX Homo sapiens.

PN WO200032635-A2.

PD 08-JUN-2000.

PF 01-DEC-1999; 99WO-US28485.

XX 02-DEC-1998; 98US-0203768.

XX (IXSY-) IXSYS INC.

PI Wackine JD, Huse WD;

XX WPI: 2000-412293/35.

DR N-PSDB; AAA48411.

XX New tumour-specific human monoclonal antibody, useful for the treatment  
PT and diagnosis of cancer, comprises at least one complementarity  
PT determining region -

XX Claim 10; Page 82-83; 84pp; English.

XX The present sequence is the heavy chain variable region of a human  
CC tumour-specific monoclonal antibody. Neoplastic cells selectively express  
CC antigens which are not present on normal cells. Thus monoclonal  
CC antibodies can be produced that are specifically directed against  
CC tumour-specific antigens. The antibodies can be conjugated to cytotoxic  
CC or cytostatic agents and used to selectively target cancer cells for the  
CC elimination of tumours. They can also be linked to diagnostic moieties  
CC that allow the imaging of neoplastic cells. Nucleic acids encoding human  
CC tumour-specific monoclonal antibodies can be used to express the  
CC antibodies and can be recombinantly engineered to produce modified  
CC antibodies with higher affinity or higher selectivity for tumour cells.  
CC Tumour-specific antibodies were produced by hybridomas that were  
CC generated by in vitro immunisation of human spleen cell cultures with  
CC breast carcinoma cells. The nucleic acid encoding the monoclonal antibody  
CC was then isolated from the hybridoma by RT-PCR. The present sequence  
XX was produced by LH13 hybridoma cell line.

XX Sequence 118 AA;

Query Match 87.1%; Score 520; DB 21; Length 118;

Best Local Similarity 85.6%; Pred. No. 3.4e-38;  
Matches 101; Conservative 6; Mismatches 7; Indels 4; Gaps 1;

QY 1 QVQLVQSGAEVKKPSSSVKVCCKASGTFSSHAISWVRQAPQGLMMGDIIPILGTGNY 60  
DB 1 QVQLVQSGAEVKKPSSSVKVCCKASGTFSSHAISWVRQAPQGLMMGDIIPILGTGNY 60

QY 61 AOKFGGRVTITADESTSTAYMELSTLTSEDYAVYYCELD---WFIYWGQGTMTVSS 114  
DB 61 AOKFGGRVTITADESTSTAYMELSLRSEDTAVYYCARDESSGMHYWGQGTMTVSS 118

RESULT 5  
ID AAU97198 standard; protein; 270 AA.  
XX  
AC AAU97198;

DT 27-AUG-2002 (first entry)

DE Human anti-EGFR single-chain antibody isolated from clone pSEX81-63.

XX Human; anti-epidermal growth factor receptor single-chain antibody;  
KM anti-EGFR-scFv; IGM; cancer; tumour growth; clone pSEX81-63; cytostatic.

XX Homo sapiens.

PN WO200230984-A1.

PD 18-APR-2002.

PF 12-OCT-2001; 2001WO-US31857.

XX 13-OCT-2000; 2000US-240353P.

XX (UABR-) UAB RES FOUND.

PI Raleach KP, Curriel DT, Bonner JA;

XX WPI: 2002-463261/49.

XX Novel human anti-epidermal growth factor receptor single-chain antibody  
PT useful for diagnostic location and assessment of tumour growth, and in  
PT treating cancer -  
PT  
XX  
XX Claim 3; Fig 2; 51pp; English.

XX The present invention relates to human anti-epidermal growth factor  
CC receptor single-chain antibodies (anti-EGFR-scFvs) isolated from a  
CC human IGM phage display library using EGFR as antigen. Two isolates  
CC with different amino acid sequences were identified. The  
CC anti-EGFR-scFvs are useful for treating cancer, and for the  
CC diagnostic location and assessment of tumour growth, where the  
CC anti-EGFR-scFv is radiolabelled. The present sequence represents  
CC human anti-EGFR single-chain antibody isolated from clone pSEX81-63.

XX Sequence 270 AA;

Query Match 86.4%; Score 516; DB 23; Length 270;  
Best Local Similarity 81.7%; Pred. No. 1.7e-37;  
Matches 103; Conservative 3; Mismatches 8; Indels 12; Gaps 1;

QY 1 QVQLVQSGAEVKKPSSSVKVCCKASGTFSSHAISWVRQAPQGLMMGDIIPILGTGNY 60  
DB 1 QVQLVQSGAEVKKPSSSVKVCCKASGTFSSHAISWVRQAPQGLMMGDIIPILGTGNY 60

QY 61 AOKFGGRVTITADESTSTAYMELSTLTSEDYAVYYCELD---WFIYWGQGT 108  
DB 61 AOKFGGRVTITADESTSTAYMELSLRSEDTAVYYCARDPYVYSGSYRPNWFPWGQGT 120

QY 109 MVTYSS 114

DB 121 LTVSS 126

CC cancer. The antibody is also useful for detecting a TIMP-1 in a test  
CC preparation, or in diagnosing a disorder in which a TIMP-1 level is  
CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy  
CC chain regions of a human anti-TIMP-1 antibody of the invention.

XX  
SQ Sequence 220 AA;

Query Match 86.3%; Score 515; DB 24; Length 220;  
Best Local Similarity 87.1%; Pred. No. 1, 7e-37;  
Matches 101; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

QY 1 QVQLVSGAEVKKPGSSSVKVCSCASGCTFSSHAISWVRQAPGGLEMMGDIIPILCTGNY 60  
DB 1 QVQLVSGAEVKKPGSSSVKVCSCASGCTFSSVAISWVRQAPGGLEMMGDIIPILCTGNY 60  
QY 61 AOKFGQRTVITADESTSTAYMELSTLTSEDTAVYYCELDWFI--WGQTMVTSS 114  
DB 61 AOKFGQRTVITADESTSTAYMELSLRSEDTAVYYCARQWYMDWVGQTLVTSS 116

# RESULT 8

ABR01538  
ID ABR01538 standard; Protein; 220 AA.

XX  
AC ABR01538;

XX  
DT 16-APR-2003 (first entry)

XX  
DE Human anti-TIMP-1 antibody heavy chain #36.

XX  
KM Human; antibody: tissue inhibitor of metalloproteinase-1; TIMP-1; VLCDR3;  
KM matrix metalloproteinase; MMP; variable heavy chain; VHCDR3; hepatotropic;  
KM variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis;  
KM alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;  
KM lupus nephritis; glomerulosclerotic renal disease; lung cancer;  
KM idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.

XX  
OS Homo sapiens.

XX  
PN WO200286085-A2.

XX  
PD 31-OCT-2002.

XX  
PF 24-APR-2002; 2002WO-US12801.

XX  
PR 24-APR-2001; 2001US-285683P.

XX  
PA (FARB ) BAYER CORP.  
(MORP-) MORPHOSYS AG.

XX  
PI Pan C, Knorr AM, Schauer M, Hirth-dietrich C, Kraft S, Krebs B;

XX  
DR WPI; 2003-129114/12.

XX  
DR N-PDB; AB274809.

XX  
PT New human anti-TIMP-1 (tissue inhibitor of metalloproteinase-1)

XX  
PT antibodies, for diagnosing or ameliorating the symptoms of a disorder

XX  
PT in which TIMP-1 is elevated, e.g. liver fibrosis, benign prostate

XX  
PT hypertrophy or lung cancer.

XX  
PS Claim 20; Page 173; 228pp; English.

XX  
CC The invention relates to a novel purified preparation of a human  
CC antibody, which binds to a tissue inhibitor of metalloproteinase-1 (TIMP-1)  
CC and neutralises a matrix metalloproteinase (MMP)-inhibiting activity of  
CC TIMP-1. The antibody comprises a variable heavy chain (VH)CDR3 region and  
CC a variable light chain (VL)CDR3 region. An antibody preparation of the  
CC invention has hepatotropic, cytostatic, nephrotropic and cardiant  
CC activity. The human antibody is useful for decreasing an MMP-inhibiting  
CC activity of a TIMP-1. It is especially useful for ameliorating the  
CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver  
CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary  
CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic

CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon  
CC cancer. The antibody is also useful for detecting a TIMP-1 in a test  
CC preparation, or in diagnosing a disorder in which a TIMP-1 level is  
CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy  
CC chain regions of a human anti-TIMP-1 antibody of the invention.

XX  
SQ Sequence 220 AA;

Query Match 85.4%; Score 510; DB 24; Length 220;  
Best Local Similarity 87.1%; Pred. No. 4, 7e-37;  
Matches 101; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

QY 1 QVQLVSGAEVKKPGSSSVKVCSCASGCTFSSHAISWVRQAPGGLEMMGDIIPILCTGNY 60  
DB 1 QVQLVSGAEVKKPGSSSVKVCSCASGCTFSSVAISWVRQAPGGLEMMGDIIPILCTGNY 60  
QY 61 AOKFGQRTVITADESTSTAYMELSTLTSEDTAVYYCELDWFI--WGQTMVTSS 114  
DB 61 AOKFGQRTVITADESTSTAYMELSLRSEDTAVYYCARQWYMDWVGQTLVTSS 116

# RESULT 9

AAB67617  
ID AAB67617 standard; Protein; 245 AA.

XX  
AC AAB67617;

XX  
DT 29-MAY-2001 (first entry)

XX  
DE Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6\_1.

XX  
KM Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;

XX  
KM miscarriage; abortion; psoriasis; antibody; HLA phenotyping; 88.

XX  
OS Homo sapiens.

XX  
PN WO200114558-A1.

XX  
PD 01-MAR-2001.

XX  
PF 28-AUG-2000; 2000WO-EP08388.

XX  
PR 26-AUG-1999; 99EP-0116691.

XX  
PA (MORP-) MORPHOSYS AG.

XX  
PI Kretzschmar T, Tesar M, Margot M, Kroenke M;

XX  
DR WPI; 2001-218451/22.

XX  
PT Novel isolated human immunoglobulin or functional immunoglobulin

XX  
PT fragment specific for human leukocyte antigen Cw6, useful for treatment

XX  
PT of humans and for human leukocyte antigen phenotyping.

XX  
PS Claim 3; Fig 1; 23pp; English.

XX  
CC AAB67617-23 represent single chain antibody (scFv) fragments which  
CC are specific for human leukocyte antigen (HLA)-Cw6. The fragments are  
CC derived from a synthetic human combinatorial antibody library based on  
CC molecular consensus frameworks and CDRs randomised with trinucleotides.  
CC The specification describes a human immunoglobulin fragments specific  
CC for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in  
CC studies of natural killer cell silencing as well as miscarriages.  
CC HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.  
CC Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin  
CC fragments are useful for the preparation of a pharmaceutical for the  
CC treatment of humans. They are also useful for HLA phenotyping.

XX  
SQ Sequence 245 AA;

Query Match 85.3%; Score 509.5; DB 22; Length 245;  
Best Local Similarity 87.2%; Pred. No. 5, 8e-37;  
Matches 102; Conservative 5; Mismatches 7; Indels 3; Gaps 2;

CC TMP-1. The antibody comprises a variable heavy chain (VHC)DR3 region and  
 CC a variable light chain (VLC)DR3 region. An antibody preparation of the  
 CC invention has hepatotropic, cytostatic, nephrotropic and cardiant  
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting  
 CC activity of a TIMP-1. It is especially useful for ameliorating the  
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver  
 CC fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary  
 CC syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic  
 CC pulmonary fibrosis, benign prostate hypertrophy, lung cancer or colon  
 CC cancer. The antibody is also useful for detecting a TIMP-1 in a test  
 CC preparation, or in diagnosing a disorder in which a TIMP-1 level is  
 CC elevated. The sequences shown in ABR01502-ABR01545 represent the heavy  
 CC chain regions of a human anti-TIMP-1 antibody of the invention.

XX Sequence 225 AA;

Query Match 85.2%; Score 508.5; DB 24; Length 225;  
 Best Local Similarity 85.1%; Pred. No. 6.5e-37;  
 Matches 103; Conservative 3; Mismatches 8; Indels 7; Gaps 2;

QY 1 QVQLVDSGAEVKKPKGSSVKVSCKASGCTFSSHAISWROAPGQGLEWMGDIIPILGTGNY 60  
 DB 1 QVQLVDSGAEVKKPKGSSVKVSCKASGCTFSSHAISWROAPGQGLEWMGDIIPILGTGNY 60  
 QY 61 AQRFGSRVITTADESTSTAYMELSTLTSEDTAVYYCE--LDW----FTYMGQGTMTVTS 113  
 DB 61 AQRFGSRVITTADESTSTAYMELSTLTSEDTAVYYCARGLYMAVYPPFDWGQGTTLTVTS 120  
 QY 114 S 114  
 DB 121 S 121

RESULT 12

ID AAB67618 standard; Protein; 245 AA.

AC AAB67618;

DT 29-MAY-2001 (first entry)

XX Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6\_2.

KM Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;

XX misexpression; abortion; psoriasis; antibody; HLA phenotyping; ss.

OS Homo sapiens.

PN WO200114558-A1.

PD 01-MAR-2001.

PF 28-AUG-2000; 2000WO-EP08388.

PR 26-AUG-1999; 99EP-0116691.

XX (MORP-) MORPHOSYS AG.

PI Kretzschmar T, Teear M, Marget M, Kroenke M;

DR WPI; 2001-218451/22.

XX Novel isolated human immunoglobulin or functional immunoglobulin

PT fragment specific for human leukocyte antigen Cw6, useful for treatment

PS Claim 3; Fig 1; 23pp; English.

CC AAB67617-23 represent single chain antibody (scFv) fragments which  
 CC are specific for human leukocyte antigen (HLA)-Cw6. The fragments are  
 CC derived from a synthetic human combinatorial antibody library based on  
 CC molecular consensus frameworks and CDRs randomised with trinucleotides.  
 CC The specification describes a human immunoglobulin fragments specific

CC for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in  
 CC studies of natural killer cell silencing as well as miscarriages.  
 CC HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.  
 CC Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin  
 CC fragments are useful for the preparation of a pharmaceutical for the  
 CC treatment of humans. They are also useful for HLA phenotyping.

XX Sequence 245 AA;

Query Match 85.2%; Score 508.5; DB 22; Length 245;  
 Best Local Similarity 87.2%; Pred. No. 7.1e-37;  
 Matches 102; Conservative 4; Mismatches 8; Indels 3; Gaps 2;

QY 1 QVQLVDSGAEVKKPKGSSVKVSCKASGCTFSSHAISWROAPGQGLEWMGDIIPILGTGNY 60  
 DB 1 QVQLVDSGAEVKKPKGSSVKVSCKASGCTFSSHAISWROAPGQGLEWMGDIIPILGTGNY 60  
 QY 61 AQRFGSRVITTADESTSTAYMELSTLTSEDTAVYYCE--LDWRY--IMGQGTMTVTS 114  
 DB 61 AQRFGSRVITTADESTSTAYMELSTLTSEDTAVYYCARGPDYFMDWQGTTLTVTS 117

RESULT 13

ID AAM27550 standard; Protein; 120 AA.

AC AAM27550;

DT 23-JAN-1998 (first entry)

XX Human Ab heavy chain variable region VH1A consensus.

XX Human; antibody; preparation; library; VH1A; variable region;

KM heavy chain; consensus.

OS Homo sapiens.

PN WO9708320-A1.

PD 06-MAR-1997.

PF 19-AUG-1996; 96WO-EP03647.

PR 18-AUG-1995; 95EP-0113021.

XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.

PI Ge L, Ilaag V, Knappik A, Moroney S, Pack P, Plueckthun A;

DR N-PSDB; AAT67948.

PF 1997-179277/16.

XX Preparation of human derived antibody gene library - using synthetic

XX consensus sequences, and signal consensus antibody gene as universal

XX framework for highly diverse antibody libraries

XX Example 1; Fig 5A; 436pp; English.

XX The present sequence is the human antibody heavy chain

XX variable region synthetic sequence VH1A, used in the preparation of

XX a human derived antibody gene library.

XX Sequence 120 AA;

Query Match 85.1%; Score 508; DB 18; Length 120;  
 Best Local Similarity 85.8%; Pred. No. 3.9e-37;  
 Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2;  
 QY 1 QVQLVDSGAEVKKPKGSSVKVSCKASGCTFSSHAISWROAPGQGLEWMGDIIPILGTGNY 60  
 DB 1 QVQLVDSGAEVKKPKGSSVKVSCKASGCTFSSHAISWROAPGQGLEWMGDIIPILGTGNY 60  
 QY 61 AQRFGSRVITTADESTSTAYMELSTLTSEDTAVYYCEL--DWFY--IMGQGTMTVTS 114



; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 60/328,604  
; PRIOR FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-269-805-9

Query Match 86.7%; Score 517.5; DB 15; Length 121;  
Best Local Similarity 86.0%; Pred. No. 7.7e-44;  
Matches 104; Conservative 3; Mismatches 7; Indels 7; Gaps 1;

OY 1 OVOLVQSGAEVKKPKSSSVKSCASGCTFSSHAISMVROAPQGLMMGDIIPILGTNY 60  
DB 1 OVOLVQSGAEVKKPKSSSVKSCASGCTFSSHAISMVROAPQGLMMGDIIPILGTNY 60  
OY 61 AOKFGRTITADESTSTAYMELSTLTSEDTAVYYC-----ELDMFYMGQGTMTV 113  
DB 61 AOKFGRTITADESTSTAYMELSLRSBEDTAVYYCAFPPTETDADIMGQGTMTV 120  
OY 114 S 114  
DB 121 S 121

RESULT 7  
US-10-269-805-35  
; Sequence 35, Application US/10269805  
; Publication No. US20030124129A1  
; GENERAL INFORMATION:  
; APPLICANT: OLINER, JONATHAN D.  
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS  
; FILE REFERENCE: A-722  
; CURRENT APPLICATION NUMBER: US/10/269,805  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 60/328,604  
; PRIOR FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 35  
; LENGTH: 125  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-269-805-35

Query Match 86.5%; Score 516.5; DB 15; Length 125;  
Best Local Similarity 83.2%; Pred. No. 1e-43;  
Matches 104; Conservative 3; Mismatches 7; Indels 11; Gaps 1;

OY 1 OVOLVQSGAEVKKPKSSSVKSCASGCTFSSHAISMVROAPQGLMMGDIIPILGTNY 60  
DB 1 OVOLVQSGAEVKKPKSSSVKSCASGCTFSSHAISMVROAPQGLMMGDIIPILGTNY 60  
OY 61 AOKFGRTITADESTSTAYMELSTLTSEDTAVYYC-----LDMFYMGQGTMTV 109  
DB 61 AOKFGRTITADESTSTAYMELSLRSBEDTAVYYCARSPYIDILTGIDAFDIMGQGTMTV 120  
OY 110 TVVSS 114  
DB 121 TVVSS 125

RESULT 8  
US-09-976-118-2  
; Sequence 2, Application US/09976118  
; Patent No. US20020058033A1  
; GENERAL INFORMATION:  
; APPLICANT: Raiech, Kevin Paul  
; APPLICANT: Curiel, David T.  
; APPLICANT: Bonner, James Allen

; TITLE OF INVENTION: Human Anti-Epidermal Growth Factor Receptor  
; TITLE OF INVENTION: Single-Chain Antibodies  
; FILE REFERENCE: D6355  
; CURRENT APPLICATION NUMBER: US/09/976,118  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 60/240,353  
; PRIOR FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 2  
; LENGTH: 270  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: amino acid sequence of anti-EGFR scFv  
; OTHER INFORMATION: clone pSEX81-63  
US-09-976-118-2

Query Match 86.4%; Score 516; DB 9; Length 270;  
Best Local Similarity 81.7%; Pred. No. 2.6e-43;  
Matches 103; Conservative 3; Mismatches 8; Indels 12; Gaps 1;

OY 1 OVOLVQSGAEVKKPKSSSVKSCASGCTFSSHAISMVROAPQGLMMGDIIPILGTNY 60  
DB 1 OVOLVQSGAEVKKPKSSSVKSCASGCTFSSHAISMVROAPQGLMMGDIIPILGTNY 60  
OY 61 AOKFGRTITADESTSTAYMELSTLTSEDTAVYYCELD-----WFIYMGQGT 108  
DB 61 AOKFGRTITADESTSTAYMELSLRSBEDTAVYYCARDPDPYGGSGTYPMFDPWGCT 120  
OY 109 MVTVSS 114  
DB 121 LVTVSS 126

RESULT 9  
US-10-269-805-3  
; Sequence 3, Application US/10269805  
; Publication No. US20030124129A1  
; GENERAL INFORMATION:  
; APPLICANT: OLINER, JONATHAN D.  
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS  
; FILE REFERENCE: A-722  
; CURRENT APPLICATION NUMBER: US/10/269,805  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: US 60/328,604  
; PRIOR FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-269-805-3

Query Match 86.2%; Score 514.5; DB 15; Length 123;  
Best Local Similarity 83.7%; Pred. No. 1.5e-43;  
Matches 103; Conservative 4; Mismatches 7; Indels 9; Gaps 2;

OY 1 OVOLVQSGAEVKKPKSSSVKSCASGCTFSSHAISMVROAPQGLMMGDIIPILGTNY 60  
DB 1 OVOLVQSGAEVKKPKSSSVKSCASGCTFSSHAISMVROAPQGLMMGDIIPILGTNY 60  
OY 61 AOKFGRTITADESTSTAYMELSTLTSEDTAVYYC-----ELDM--FYMGQGTMTV 111  
DB 61 AOKFGRTITADESTSTAYMELSLRSBEDTAVYYCARGVGDVDPDMLSPDYMGQGTMTV 120  
OY 112 VSS 114  
DB 121 VSS 123

RESULT 10  
US-10-269-805-49

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; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-125-687-1
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Query Match      85.1%; Score 508; DB 15; Length 120;
Best Local Similarity 85.8%; Pred. No. 6,6e-43;
Matches 103; Conservative 3; Mismatches 8; Indels 6; Gaps 2;
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   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVSGAEVKKPGSSSVVSCASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTNY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Q: 61 AOKFQGRVTITADESTIAYMELSTLTSEDYAVYCEL---DMFY---IMGGTMYTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AOKFQGRVTITADESTIAYMELSLRSEDYAVYCARWGSDGFYAMDYWGQTLVTVSS 120
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## RESULT 15

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US-09-880-748-1509
; Sequence 1509, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1509
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1509
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Query Match      84.9%; Score 507; DB 11; Length 253;
Best Local Similarity 79.7%; Pred. No. 1.9e-42;
Matches 102; Conservative 4; Mismatches 8; Indels 14; Gaps 1;
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   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVSGAEVKKPGSSSVVSCASGCTFSSHAISWVROAPGQGLEWMGDIIPILGTNY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Q: 61 AOKFQGRVTITADESTIAYMELSTLTSEDYAVYCYC-----ELDMFYIYWGQ 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AOKFQGRVTITADKSTIAYMELSLRSEDYAVYCARQGYDILTGYPPEGGMFDPWGK 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Q: 107 GTMTVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GTMTVTVSS 128
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Search completed: December 30, 2003, 11:45:25  
Job time : 24.4484 secs

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| 4  | 492.5 | 121 | 3 | US-08-428-1055-13  |
| 5  | 492.5 | 119 | 2 | US-08-428-1055-13  |
| 6  | 492.5 | 120 | 2 | PCT-US93-1055-10   |
| 7  | 476.5 | 120 | 5 | PCT-US93-939-7     |
| 8  | 474.5 | 120 | 5 | US-08-378-816A-7   |
| 9  | 474.5 | 120 | 5 | US-08-652-816A-4   |
| 10 | 474.5 | 120 | 2 | US-08-217-918-63   |
| 11 | 474.5 | 123 | 2 | US-07-824-538-63   |
| 12 | 471.5 | 147 | 1 | US-08-645-408B-63  |
| 13 | 471.5 | 102 | 1 | US-08-851-762-55   |
| 14 | 461   | 102 | 1 | US-01-096-353-63   |
| 15 | 455   | 102 | 1 | US-08-800-865-63   |
| 16 | 455   | 102 | 2 | US-08-308-06185-63 |
| 17 | 455   | 102 | 2 | US-08-308-06185-63 |
| 18 | 455   | 102 | 2 | PCT-US92-10983-232 |
| 19 | 455   | 102 | 5 | PCT-US92-353-80    |
| 20 | 455   | 102 | 5 | US-09-042-417A-80  |
| 21 | 455   | 102 | 3 | US-08-758-417A-80  |
| 22 | 455   | 117 | 4 |                    |
| 23 | 455   |     |   |                    |
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| 26 | 455   |     |   |                    |
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Sequence 4, Appl  
 Sequence 55, Appl  
 Sequence 63, Appl  
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 Sequence 232, Appl  
 Sequence 80, Appl

MUR-5-10-  
 US-09-022-5-10-  
 Query Match Similarity  
 Best Loc 1001  
 Matched

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 30, 2003, 10:47:45 ; Search time 12.3883 Seconds  
(without alignments)  
416.677 Million cell updates/sec

Title: US-09-674-752-53

Perfect score: 642  
Sequence: 1 EVQLVESGGDLVPGSGSLRL.....GKYYGMDVMGCGITTVVSS 122

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/ECTUS.COMB.pep: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                             |
|------------|-------|-------------|--------|----|-----------------------------------------|
| 1          | 525   | 81.8        | 120    | 4  | US-09-025-769B-38<br>Sequence 38, Appl  |
| 2          | 525   | 81.8        | 120    | 4  | US-09-025-769B-63<br>Sequence 63, Appl  |
| 3          | 525   | 81.8        | 281    | 4  | US-09-025-769B-178<br>Sequence 178, App |
| 4          | 524.5 | 81.7        | 249    | 4  | US-10-039-785-53<br>Sequence 53, Appl   |
| 5          | 518   | 80.7        | 122    | 2  | US-07-934-373C-21<br>Sequence 21, Appl  |
| 6          | 518   | 80.7        | 122    | 3  | US-08-437-642B-21<br>Sequence 21, Appl  |
| 7          | 518   | 80.7        | 122    | 4  | US-08-146-206C-21<br>Sequence 21, Appl  |
| 8          | 518   | 80.7        | 122    | 5  | PCR-US93-07832-21<br>Sequence 21, Appl  |
| 9          | 513   | 79.9        | 140    | 3  | US-08-983-607-32<br>Sequence 32, Appl   |
| 10         | 510   | 79.4        | 263    | 4  | US-09-069-821-3<br>Sequence 3, Appl     |
| 11         | 510   | 79.4        | 283    | 4  | US-09-420-592A-6<br>Sequence 6, Appl    |
| 12         | 506.5 | 78.9        | 125    | 2  | US-08-428-197-1<br>Sequence 1, Appl     |
| 13         | 506.5 | 78.9        | 125    | 3  | PCR-US93-10555-1<br>Sequence 1, Appl    |
| 14         | 501.5 | 78.1        | 113    | 3  | US-08-974-899-6<br>Sequence 9, Appl     |
| 15         | 499.5 | 77.8        | 125    | 1  | US-08-476-039-99<br>Sequence 99, Appl   |
| 16         | 499.5 | 77.8        | 125    | 1  | US-08-476-349A-99<br>Sequence 99, Appl  |
| 17         | 498   | 77.6        | 120    | 2  | US-07-934-373C-4<br>Sequence 4, Appl    |
| 18         | 498   | 77.6        | 120    | 3  | US-08-437-642B-4<br>Sequence 4, Appl    |
| 19         | 498   | 77.6        | 120    | 4  | US-08-146-206C-4<br>Sequence 4, Appl    |
| 20         | 497   | 77.4        | 120    | 5  | PCR-US93-07832-4<br>Sequence 47, Appl   |
| 21         | 497   | 77.4        | 124    | 3  | US-08-983-607-47<br>Sequence 28, Appl   |
| 22         | 497   | 77.4        | 131    | 3  | US-08-983-607-28<br>Sequence 51, Appl   |
| 23         | 495   | 77.1        | 124    | 3  | US-08-983-607-51<br>Sequence 46, Appl   |
| 24         | 491.5 | 76.6        | 117    | 3  | US-08-983-607-46<br>Sequence 12, Appl   |
| 25         | 489   | 76.2        | 112    | 5  | PCR-US93-08435-12<br>Sequence 24, Appl  |
| 26         | 488.5 | 76.1        | 117    | 4  | US-09-025-769B-14<br>Sequence 30, Appl  |
| 27         | 488.5 | 76.1        | 123    | 2  | US-08-665-202-30<br>Sequence 30, Appl   |

|    |       |      |     |   |                                        |
|----|-------|------|-----|---|----------------------------------------|
| 28 | 488.5 | 76.1 | 123 | 4 | US-09-315-574-30<br>Sequence 30, Appl  |
| 29 | 487   | 75.9 | 116 | 2 | US-08-428-197-2<br>Sequence 2, Appl    |
| 30 | 487   | 75.9 | 116 | 5 | PCT-US93-10555-2<br>Sequence 2, Appl   |
| 31 | 487   | 75.9 | 122 | 5 | PCT-US93-08435-43<br>Sequence 43, Appl |
| 32 | 486   | 75.7 | 115 | 3 | US-08-983-607-36<br>Sequence 36, Appl  |
| 33 | 485.5 | 75.6 | 117 | 3 | US-09-157-370-1<br>Sequence 1, Appl    |
| 34 | 485   | 75.5 | 126 | 3 | US-08-983-607-48<br>Sequence 48, Appl  |
| 35 | 484.5 | 75.5 | 119 | 2 | US-07-968-925-11<br>Sequence 11, Appl  |
| 36 | 484.5 | 75.5 | 119 | 2 | US-08-362-780-11<br>Sequence 11, Appl  |
| 37 | 484   | 75.4 | 122 | 5 | PCT-US93-08435-14<br>Sequence 14, Appl |
| 38 | 481.5 | 75.0 | 120 | 2 | US-08-428-197-20<br>Sequence 20, Appl  |
| 39 | 481.5 | 75.0 | 120 | 2 | PCT-US93-10555-20<br>Sequence 20, Appl |
| 40 | 481   | 74.9 | 118 | 2 | US-08-958-201-2<br>Sequence 2, Appl    |
| 41 | 481   | 74.9 | 118 | 2 | US-08-958-201-4<br>Sequence 4, Appl    |
| 42 | 481   | 74.9 | 144 | 1 | US-08-026-320A-2<br>Sequence 2, Appl   |
| 43 | 480.5 | 74.8 | 115 | 2 | US-08-428-197-42<br>Sequence 42, Appl  |
| 44 | 480.5 | 74.8 | 115 | 5 | PCT-US93-10555-42<br>Sequence 42, Appl |
| 45 | 480.5 | 74.8 | 120 | 2 | US-08-428-197-22<br>Sequence 22, Appl  |

## ALIGNMENTS

RESULT 1  
US-09-025-769B-38  
; Sequence 38, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULAR TYPE: protein  
; US-09-025-769B-38  
Query Match 81.8%; Score 525; DB 4; Length 120;  
Best Local Similarity 82.0%; Pred. No. 1.9e-43;  
Matches 100; Conservative 10; Mismatches 10; Indels 2; Gaps 1;



QY 1 EVOLVESGDLVOPGSLRLSCAAGFTFSNFMASWVRQAPGKGLFWVAIIGRSSTTFY 60  
DB 1 EVOLVESGGGLVOPGSLRLSCAAGFTFSYAMSWVRQAPGKGLFWVAISGSGSTTY 60  
QY 61 ADVSKRFTISRDNKNTLYLENNSLRAEDTAIYYCAKRGYKYGYGMDVMGQGTITVY 120  
DB 61 ADVSKRFTISRDNKNTLYLQNNSLRAEDTAIYYCARWGDDG--FYAMDYMGQGTILVTV 118  
QY 121 SS 122  
DB 119 SS 120

RESULT 2  
US-09-025-769B-63  
; Sequence 63, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckhuhn, Andreas  
; TITLE OF INVENTION: Protein/(Poly) peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-63

Query Match 81.8%; Score 525; DB 4; Length 120;  
Best Local Similarity 82.0%; Pred. No. 1.9e-43;  
Matches 100; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

QY 1 EVOLVESGDLVOPGSLRLSCAAGFTFSNFMASWVRQAPGKGLFWVAIIGRSSTTFY 60  
DB 1 EVOLVESGGGLVOPGSLRLSCAAGFTFSYAMSWVRQAPGKGLFWVAISGSGSTTY 60  
QY 61 ADVSKRFTISRDNKNTLYLENNSLRAEDTAIYYCAKRGYKYGYGMDVMGQGTITVY 120  
DB 61 ADVSKRFTISRDNKNTLYLQNNSLRAEDTAIYYCARWGDDG--FYAMDYMGQGTILVTV 118  
QY 121 SS 122

DB 119 SS 120

RESULT 3  
US-09-025-769B-178  
; Sequence 178, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckhuhn, Andreas  
; TITLE OF INVENTION: Protein/(Poly) peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 178:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-178

Query Match 81.8%; Score 525; DB 4; Length 281;  
Best Local Similarity 82.0%; Pred. No. 4.9e-43;  
Matches 100; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

QY 1 EVOLVESGDLVOPGSLRLSCAAGFTFSNFMASWVRQAPGKGLFWVAIIGRSSTTFY 60  
DB 26 EVOLVESGGGLVOPGSLRLSCAAGFTFSYAMSWVRQAPGKGLFWVAISGSGSTTY 85  
QY 61 ADVSKRFTISRDNKNTLYLENNSLRAEDTAIYYCAKRGYKYGYGMDVMGQGTITVY 120  
DB 86 ADVSKRFTISRDNKNTLYLQNNSLRAEDTAIYYCARWGDDG--FYAMDYMGQGTILVTV 143  
QY 121 SS 122  
DB 144 SS 145

RESULT 4  
US-10-039-785-53  
; Sequence 53, Application US/10039785  
; Patent No. 6538938  
; GENERAL INFORMATION:  
; APPLICANT: Salcedo et al.

```
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
/ TITLE OF INVENTION: Receptors
/ FILE REFERENCE: PF550
/ CURRENT APPLICATION NUMBER: US/10/039,785
/ CURRENT FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: 60/369,860
/ PRIOR FILING DATE: 2002-04-05
/ PRIOR APPLICATION NUMBER: 60/341,237
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: 60/331,310
/ PRIOR FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: 60/331,044
/ PRIOR FILING DATE: 2001-11-07
/ PRIOR APPLICATION NUMBER: 60/327,364
/ PRIOR FILING DATE: 2001-10-09
/ PRIOR APPLICATION NUMBER: 60/323,807
/ PRIOR FILING DATE: 2001-09-21
/ PRIOR APPLICATION NUMBER: 60/309,176
/ PRIOR FILING DATE: 2001-08-02
/ PRIOR APPLICATION NUMBER: 60/294,981
/ PRIOR FILING DATE: 2001-06-04
/ PRIOR APPLICATION NUMBER: 60/293,473
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 53
/ LENGTH: 249
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: T1006F07 scfV
US-10-039-785-53

Query Match      81.7%; Score 524.5; DB 4; Length 249;
Best Local Similarity 80.0%; Pred. No. 4,8e-43;
Matches 100; Conservative 12; Mismatches 10; Indels 3; Gaps 1;

QY      1 EVOLVESGGDVLVPGGSLRLSQAASGFTFSNFMASWVRQAPGKLEWVAALGSGSTTFY 60
DB      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSTYAMSWVRQAPGKLEWVAISGSGSTYY 60
QY      61 ADSVKGRTISRDSKNTVYLEMNSLRAPDAIYYCAKRGGRGYKYGMVDWGQGT 117
DB      61 ADSVKGRTISRDSKNTLYIQMNSLRAPDAIYYCAKRGGRGYKYGMVDWGQGT 120
QY      118 VTWSS 122
DB      121 VTWSS 125

RESULT 5
US-07-934-373C-21
/ Sequence 21, Application US/07934373C
/ Patent No. 5821337
/ GENERAL INFORMATION:
/ APPLICANT: Paul J. Carter
/ APPLICANT: Leonard G. Presta
/ TITLE OF INVENTION: Immunoglobulin Variants
/ NUMBER OF SEQUENCES: 48
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Winpatin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/934,373C
```

```
/ FILING DATE: 21-Aug-1992
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/05126
/ FILING DATE: 15-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/715272
/ FILING DATE: 14-JUN-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 40,378
/ REFERENCE/DOCKET NUMBER: P0709P2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-1994
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 21:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 122 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
US-07-934-373C-21

Query Match      80.7%; Score 518; DB 2; Length 122;
Best Local Similarity 82.1%; Pred. No. 9,1e-43;
Matches 101; Conservative 9; Mismatches 11; Indels 2; Gaps 2;

QY      1 EVOLVESGGDVLVPGGSLRLSQAASGFTFSNFMASWVRQAPGKLEWVAALGSGSTTFY 60
DB      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISGSGSTYY 60
QY      61 ADSVKGRTISRDSKNTVYLEMNSLRAPDAIYYCAKRGGRGYKYGMVDWGQGT 119
DB      61 ADSVKGRTISRDSKNTLYIQMNSLRAPDAIYYCAKRGGRGYKYGMVDWGQGT 119
QY      120 VSS 122
DB      120 VSS 122

RESULT 6
US-08-437-642B-21
/ Sequence 21, Application US/08437642B
/ Patent No. 6054297
/ GENERAL INFORMATION:
/ APPLICANT: Paul J. Carter
/ APPLICANT: Leonard G. Presta
/ TITLE OF INVENTION: Immunoglobulin Variants
/ NUMBER OF SEQUENCES: 47
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Winpatin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/437,642B
/ FILING DATE: 09-May-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/934373
/ FILING DATE: 21-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/146206
/ FILING DATE: 17-NOV-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/05126
/ FILING DATE: 15-JUN-1992
```

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Prior Application Data:
Application Number: 07/715272
Filing Date: 14-JUN-1991
Attorney/Agent Information:
Name: Lee, Wendy M.
Registration Number: 40,378
Reference/Docket Number: P0709P2C1
Telecommunication Information:
Telephone: 650/225-1994
Telefax: 650/952-9881
Information for SEQ ID NO: 21:
Sequence Characteristics:
Length: 122 amino acids
Type: Amino Acid
Topology: Linear
US-08-437-642B-21

Query Match      80.7% Score 518; DB 3; Length 122;
Best Local Similarity 82.1%; Pred. No. 9,1e-43;
Matches 101; Conservative 9; Mismatches 11; Indels 2; Gaps 2

QY      1 EVOLVESGDDLVPQGSRLRLSCAASGFTFSNFMASWVRQAPKGLBMYAALIGRSGTTFY 60
        |||||
Db       1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSVAASWVRQAPKGLBMYSVISGGSGTTFY 60
        |||||

QY      61 ADVYKGRFTISRDNSKNTVYLEMNSLRADDTAIIYCAKGRGSGYKTYGM-DWGCGTTFY 119
        |||||
Db       61 ADVYKGRFTISRDNSKNTVLYIQMSLRADDTAVYYCA-RGRGVSLSLGYDYWGCGTTFY 119
        |||||

QY      120 VSS 122
        |||
Db       120 VSS 122

RESULT 7
US-08-146-206C-21
Sequence 21, Application US/08146206C
Patent No. 6407213
General Information:
Applicant: Carter, Paul J.
Applicant: Presta, Leonard G.
Title of Invention: Method for Making Humanized Antibodies
Number of Sequences: 26
Correspondence Address:
Address: Genentech, Inc.
Street: 1 DNA Way
City: South San Francisco
State: California
Country: USA
ZIP: 94080

Computer Readable Form:
Medium Type: 3.5 inch, 1.44 Mb floppy disk
Computer: IBM PC compatible
Operating System: PC-DOS/MS-DOS
Software: WinPatIn (Genentech)
Current Application Data:
Application Number: US/08/146,206C
Filing Date: 17-NOV-6407213-1993
Classification: 530
Prior Application Data:
Application Number: 07/715272
Filing Date: 14-JUN-1991
Attorney/Agent Information:
Name: Lee, Wendy M.
Registration Number: 40,378
Reference/Docket Number: P0709P1
Telecommunication Information:
Telephone: 650/225-1994
Telefax: 650/952-9881
Information for SEQ ID NO: 21:
Sequence Characteristics:
Length: 122 amino acids
Type: Amino Acid

```

```

? TOPOLOGY: Linear
US-08-146-206C-21

Query Match      80.7%; Score 518; DB 4; Length 122;
Best Local Similarity 82.1%; Pred. No. 9,le-43;
Matches 101; Conservative 9; Mismatches 11; Indels 2; Gaps 2

QY      1 EVOLVESGDLVDPGGSLRLSCAASGFTFSNFAMSWROARPGKLEWVAALIGRSCTTFY 60
        |||
Db       1 EVOLVESGGGLVQGGSLRLSCAASGFTFSYASMSWRQAPRKGLEWVISGGCGSTFY 60
QY      61 ADSVKGRFTISRDSKRTVYLNNLSLPAEDTAIYYCAKRGRGYKYGM-DVMCGITVT 119
        |||
Db       61 ADSVKGRFTISRDSKRTVYLQNNLSLABDPAIYYCA-RGRVGISLSGLYDWGGTLVT 119
QY      120 VSS 122
        |||
Db       120 VSS 122

RESULT 8
PCT-US93-07832-21
? Sequence 21, Application PC/RUS9307832
? GENERAL INFORMATION:
? APPLICANT: Genentech, Inc.
? TITLE OF INVENTION: Immunoglobulin Variants
? NUMBER OF SEQUENCES: 40
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Genentech, Inc.
? STREET: 460 Point San Bruno Blvd
? CITY: South San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94080
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: patin (Genentech)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: PCT/US93/07832
? FILING DATE: 19930820
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/715272
? FILING DATE: 14-JUN-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/US92/05126
? FILING DATE: 15-JUN-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/934373
? FILING DATE: 21-AUG-1992
? ATTORNEY/AGENT INFORMATION:
? NAME:
? REGISTRATION NUMBER:
? REFERENCE/DOCKET NUMBER: 709P2PCT
? TELECOMMUNICATION INFORMATION:
? TELEPHONE:
? TELEFAX: 415/952-9881
? TELERX: 910/371-7168
? INFORMATION FOR SEQ ID NO: 21:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 122 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
PCT-US93-07832-21

80.7%; Score 518; DB 5; Length 122;
Best Local Similarity 82.1%; Pred. No. 9,le-43;
Matches 101; Conservative 9; Mismatches 11; Indels 2; Gaps 2

1 EVOLVESGDVLVDPGGSLRLSCAASGFTFSNFAMSWROARPGKLEWVAALIGRSCTTFY 60
|||||||

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Db 1 EVOLVESGGGLVQPGSGRLSCAASGFTFSYAMSWVRQAPGKGLEWTVISGGSGSTYY 60  
QY 61 ADVSKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCAKRGGRGYYTG-DMVGQGTYYT 119  
Db 61 ADVSKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCA-KRGVYSLSGLYDYGQGTLYT 119  
QY 120 VSS 122  
119  
Db 120 VSS 122

## RESULT 9

US-08-983-607-32

; Sequence 32, Application US/08983607

; Patent No. 6140470

; GENERAL INFORMATION:

; APPLICANT: Alan Garen

; APPLICANT: Xiaohong Cai

; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-

; TITLE OF INVENTION: bodies

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Department of Molecular Biophysics

; ADDRESSEE: and Biochemistry, Yale University

; STREET: 266 Whitney Avenue

; CITY: New Haven

; STATE: Connecticut

; COUNTRY: United States of America

; ZIP: 06520-8114

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" 1.44 Mb diskette

; COMPUTER: IBM PC

; OPERATING SYSTEM: MS DOS

; SOFTWARE: Word Processing

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/983,607

; FILING DATE: April 27, 1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/IB96/01032

; FILING DATE: June 28, 1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Mary M. Kineky

; REGISTRATION NUMBER: 32423

; REFERENCE/DOCKET NUMBER: OCR-679

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 203-773-9544

; TELEFAX: 203-773-1183

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 140 residues

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE:

; DESCRIPTION: polypeptide

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens (melanoma patient immu-

; ORGANISM: nized with autologous tumor cells)

; INDIVIDUAL ISOLATE: peripheral blood lymphocytes

; IMMEDIATE SOURCE:

; LIBRARY: DM414 scFv antibodies obtained from

; LIBRARY: fuses fusion phage construct

; CLONE: V86

; FEATURE:

; NAME/KEY: heavy chain and linker

; US-08-983-607-32

Query Match 79.9%; Score 513; DB 3; Length 140;  
Best Local Similarity 80.2%; Pred. No. 3,2e-42;  
Matches 101; Conservative 11; Mismatches 8; Indels 6; Gaps 3;

QY 1 EVOLVESGGGLVQPGSGRLSCAASGFTFSNPAWSVRQAPGKGLEWVAIIGRSGTTFY 60  
Db 1 QVQLVQSGGGLVQPGSGRLSCAASGFTFSYAMSWVRQAPGKGLEWVAIISGSGSTYY 60  
QY 61 ADVSKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCAK- - -RGGRGYYGMDVGQGT 116  
Db 61 ADVSKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCAKGRGGRGYYGMDVGQGT 118  
QY 117 TTVTSS 122  
119  
Db 119 MVTWSS 124

## RESULT 10

US-09-069-821-3

; Sequence 3, Application US/09069821

; Patent No. 6323322

; GENERAL INFORMATION:

; APPLICANT: FILIPILA, DAVID

; APPLICANT: MANG, MAOLIANG

; APPLICANT: SHORR, ROBERT

; APPLICANT: WHITLOW, MARC

; APPLICANT: LEE, LHSYNG S.

; TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS

; TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN &amp; FOX P.L.L.C.

; STREET: 1100 NEW YORK AVE., NW, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/069,821

; FILING DATE: 30-APR-1998

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/067,341

; FILING DATE: 02-DEC-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/063,074

; FILING DATE: 27-OCT-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/050,472

; FILING DATE: 23-JUN-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/044,449

; FILING DATE: 30-APR-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: KIM, JUDITH U.

; REGISTRATION NUMBER: 40,679

; REFERENCE/DOCKET NUMBER: 0977, 2280003

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)371-2500

; TELEFAX: (202)371-2540

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 263 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

; US-09-069-821-3

Query Match 79.4%; Score 510; DB 4; Length 263;  
Best Local Similarity 77.1%; Pred. No. 1,3e-41;  
Matches 101; Conservative 11; Mismatches 9; Indels 10; Gaps 3;

```

OY      1  VVOLVESSGDLVQPGGSLRLSCAASGFTFSNFMAMSVRQAPGKLEWVAIIGGRS--GTT 58
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      130  EVOLVESGGGLVQPGGSLRLSCAASGFTFSNFMAMSVRQAPGKLEWVAISGKTGGST 189

OY      59  FVADSVKGRFTISRDNSKNTVYLENSLRRAEDTAIYYCAKRGGRG-----YKYYGMDV 111
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      190  YVADSVKGRFTISRDNSKNTVYLENSLRRAEDTAIYYCA-RGRXGXSLSGYHHYHFDY 248

OY      112  WGGGTTVTYVSS 122
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      249  WGGGTLVTYVSS 259

RESULT 11
US-09-420-592A-6
; Sequence 6, Application US/09420592A
; Patent No. 6333396
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6333396el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300001
; CURRENT FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/104,949
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Kabat
; OTHER INFORMATION: Consensus
; NAME/KEY: UNSURE
; LOCATION: (232)
; OTHER INFORMATION: May be any amino acid.
; NAME/KEY: UNSURE
; LOCATION: (234)
; OTHER INFORMATION: May be any amino acid.
; NAME/KEY: UNSURE
; LOCATION: (239)
; OTHER INFORMATION: May be any amino acid.
US-09-420-592A-6

Query Match      79.4%; Score 510; DB 4; Length 283;
Best Local Similarity 77.1%; Pred. No. 1,4e-41;
Matches 101; Conservative 11; Mismatches 9; Indels 10; Gaps 3;

OY      1  EVOLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSVRQAPGKLEWVAIIGGRS--GTT 58
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      130  EVOLVESGGGLVQPGGSLRLSCAASGFTFSNFMAMSVRQAPGKLEWVAISGKTGGST 189

OY      59  FVADSVKGRFTISRDNSKNTVYLENSLRRAEDTAIYYCAKRGGRG-----YKYYGMDV 111
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      190  YVADSVKGRFTISRDNSKNTVYLENSLRRAEDTAIYYCA-RGRXGXSLSGYHHYHFDY 248

OY      112  WGGGTTVTYVSS 122
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      249  WGGGTLVTYVSS 259

RESULT 12
US-08-428-197-1
; Sequence 1, Application US/08428197
; Patent No. 5891438
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH

```

```

TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERNATIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSER: Speneley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howell, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: PD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 18/2
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..125
US-08-428-197-1

Query Match      78.9%; Score 506.5; DB 2; Length 125;
Best Local Similarity 77.3%; Pred. No. 1,2e+41;
Matches 99; Conservative 9; Mismatches 11; Indels 9; Gaps 2;

QY      1 EVQLVESGGD.LVQPFGSLRLSCAASGFTSNFAMSWVRQAPGKGLEWVAIAIGRSGTTPY 60
        |||||
DB       1 EVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMSVMVRQAPGKGLEWVAISGGSGSYTY 60
        |||||

QY      61 ADSVKGRTIISHDNSKNTLYLEMNSLRADDTALFYCAKGRGGYKYTG-----MDVWGQ 114
        |||||
DB       61 ADSVKGRTIISHDNSKNTLYLQWNSLRADDTAVYYCTK---GQVLAYYGSGSYHWFDPWQG 117
        |||||

QY      115 GTTVTVSS 122
        |||||
DB       118 GTLVTVSS 125
        |||||

RESULT 13
PCT-US93-10555-1
Sequence 1, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERNATIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSER: Speneley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500

```

CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10555  
FILING DATE: 29-OCT-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Howell, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: PD-2630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: 18/2  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..125  
PCT-US93-10555-1

Query Match 78.9%; Score 506.5; DB 5; Length 125;  
Best Local Similarity 77.3%; Pred. No. 1.2e-41;  
Matches 99; Conservative 9; Mismatches 11; Indels 9; Gaps 2;

QY 1 EVQLVESGGDLVPGGSLRLSCAASGFTFSNFMASWVRQAPGKGLEWYAAIGRSGTTFY 60  
DB 1 EVQLVESGGDLVPGGSLRLSCAASGFTFSNFMASWVRQAPGKGLEWYAAIGRSGTTFY 60  
QY 61 ADVSKGRFTISRDNKNTLYVLENNSLRAEDTAIYYCARGRGGYKYYG-----MDWVGQ 114  
DB 61 ADVSKGRFTISRDNKNTLYVLENNSLRAEDTAIYYCTK---GQVLYSGSTYMFDPWQ 117  
QY 115 GTTVVSS 122  
DB 118 GTLVTVSS 125

RESULT 14  
US-08-974-899-6  
Sequence 6, Application US/08974899  
Patent No. 6037454  
GENERAL INFORMATION:  
APPLICANT: Presta, Leonard G.  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: Humanized Anti-CD1a Antibodies  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Minipatin (Genentech)  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,899  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/031971  
FILING DATE: 11/27/96  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P1014R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 113 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-974-899-6

Query Match 78.1%; Score 501.5; DB 3; Length 113;  
Best Local Similarity 78.7%; Pred. No. 3.2e-41;  
Matches 96; Conservative 9; Mismatches 8; Indels 9; Gaps 1;

QY 1 EVQLVESGGDLVPGGSLRLSCAASGFTFSNFMASWVRQAPGKGLEWYAAIGRSGTTFY 60  
DB 1 EVQLVESGGDLVPGGSLRLSCAASGFTFSNFMASWVRQAPGKGLEWYVSISSGSGSTTFY 60  
QY 61 ADVSKGRFTISRDNKNTLYVLENNSLRAEDTAIYYCARGRGGYKYYGMDVWGQSTTVV 120  
DB 61 ADVSKGRFTISRDNKNTLYVLENNSLRAEDTAIYYCAR-----GFDVWGQSTTVV 111  
QY 121 SS 122  
DB 112 SS 113

RESULT 15  
US-08-478-039-99  
Sequence 99, Application US/08478039  
Patent No. 5681722  
GENERAL INFORMATION:  
APPLICANT: Newman, Roland A.  
APPLICANT: Raab, Ronald W.  
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince St.  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,039  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/379,072  
FILING DATE: 25-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/912,292  
FILING DATE: 10-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/856,281  
FILING DATE: 23-MAR-1992  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/735,064  
FILING DATE: 25-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Teekin Eaq., Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-160  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 18/2  
US-08-478-039-99

Query Match 77.8%; Score 499.5; DB 1; Length 125;  
Best Local Similarity 77.3%; Pred. No. 5.6e-41;  
Matches 99; Conservative 8; Mismatches 12; Indels 9; Gaps 2;

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| QY | 1   | EVQLVESGGDLVQPGSGLRISCAASGFTFSNFMASWVRQAPGKGLEWVAIAIGRSQTTPY | 60  |
|    |     |                                                              |     |
| DB | 1   | EVQLVESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVAIAISGSGSTYY   | 60  |
|    |     |                                                              |     |
| QY | 61  | ADSVKGRFTISRDNKNTVYLEMNSLRAPDAIYYCAKRGSGYKYYG-----MDVMGQ     | 114 |
|    |     |                                                              |     |
| DB | 61  | ADSVKGRFTISRDNKNTVYLEMNSLRAPDAIYYCAK---GQVLYYGSGSYHMFDPMGQ   | 117 |
|    |     |                                                              |     |
| QY | 115 | GTTVTVSS                                                     | 122 |
|    |     |                                                              |     |
| DB | 118 | GTLVTVSS                                                     | 125 |

Search completed: December 30, 2003, 11:05:37  
Job time: 13.4716 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.  
OM protein - protein search, using sw model  
Run on: December 30, 2003, 10:47:45 ; Search time 11.576 Seconds  
(without alignments)  
416.677 Million cell updates/sec  
Title: US-09-674-752-51  
Perfect score: 597  
Sequence: 1 QVQLVQSGAEVKKPGSSVKV.....YCELDWFIWGQGTMTVSS 114  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 328717 seqs, 42310858 residues  
Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/prodata/1/iaa/6C COMB.pcp.\*  
6: /cgn2\_6/prodata/1/iaa/6D COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 508   | 85.1        | 120    | 4     | US-09-025-769B-35 |
| 2          | 508   | 85.1        | 120    | 4     | US-09-025-769B-57 |
| 3          | 503.5 | 84.3        | 119    | 4     | US-09-025-769B-21 |
| 4          | 492.5 | 82.5        | 123    | 2     | US-08-652-816A-1  |
| 5          | 492.5 | 82.5        | 123    | 2     | US-08-652-816A-6  |
| 6          | 492.5 | 82.5        | 123    | 2     | US-08-652-816A-8  |
| 7          | 492.5 | 82.5        | 123    | 2     | US-08-652-816A-9  |
| 8          | 476.5 | 79.8        | 121    | 2     | US-08-232-081B-41 |
| 9          | 474.5 | 79.5        | 119    | 3     | US-08-383-607-50  |
| 10         | 474.5 | 79.5        | 120    | 2     | US-08-428-197-12  |
| 11         | 474.5 | 79.5        | 120    | 2     | US-08-428-197-13  |
| 12         | 474.5 | 79.5        | 120    | 5     | PCT-US93-10555-12 |
| 13         | 474.5 | 79.5        | 120    | 5     | PCT-US93-10555-13 |
| 14         | 471.5 | 79.0        | 476    | 2     | US-08-378-939-10  |
| 15         | 470.5 | 78.8        | 123    | 2     | US-08-652-816A-7  |
| 16         | 461   | 77.2        | 147    | 1     | US-08-217-918-4   |
| 17         | 455   | 76.2        | 102    | 1     | US-07-834-539A-55 |
| 18         | 455   | 76.2        | 102    | 1     | US-08-653-131-63  |
| 19         | 455   | 76.2        | 102    | 1     | US-08-645-641-63  |
| 20         | 455   | 76.2        | 102    | 1     | US-07-853-408B-63 |
| 21         | 455   | 76.2        | 102    | 2     | US-08-096-762-63  |
| 22         | 455   | 76.2        | 102    | 2     | US-08-308-353-55  |
| 23         | 455   | 76.2        | 102    | 2     | US-08-308-865-63  |
| 24         | 455   | 76.2        | 102    | 5     | PCT-US92-06185-55 |
| 25         | 455   | 76.2        | 102    | 5     | PCT-US92-10983-63 |
| 26         | 455   | 76.2        | 117    | 3     | US-09-042-353-232 |
| 27         | 455   | 76.2        | 117    | 4     | US-08-758-417A-80 |

28 452 75.7 128 1 US-08-202-047-22 Sequence 22, Appl  
29 452 75.7 128 3 US-08-964-690-22 Sequence 22, Appl  
30 452 75.7 128 4 US-08-635-109-3 Sequence 3, Appl  
31 449.5 75.3 125 3 US-09-199-149-3 Sequence 3, Appl  
32 441.5 74.0 129 2 US-08-561-521-45 Sequence 45, Appl  
33 441.5 74.0 129 4 US-08-525-539A-77 Sequence 77, Appl  
34 441.5 74.0 129 5 PCT-US95-01219-45 Sequence 45, Appl  
35 435.5 72.9 122 5 PCT-US95-00067-2 Sequence 10, Appl  
36 432.5 72.4 119 1 US-08-458-516-10 Sequence 22, Appl  
37 432.5 72.4 222 1 US-08-458-516-22 Sequence 22, Appl  
38 432.5 72.4 235 1 US-08-458-516-23 Sequence 13, Appl  
39 432.5 72.4 449 1 US-08-458-516-13 Sequence 78, Appl  
40 432 72.4 118 2 US-08-428-257A-78 Sequence 60, Appl  
41 432 72.4 118 3 US-07-987-264-60 Sequence 105, App  
42 431.5 72.3 117 1 US-07-634-278-105 Sequence 105, App  
43 431.5 72.3 117 1 US-08-477-728-105 Sequence 105, App  
44 431.5 72.3 117 1 US-08-474-040-105 Sequence 105, App  
45 431.5 72.3 117 1 US-08-487-200-105 Sequence 105, App

## ALIGNMENTS

RESULT 1  
US-09-025-769B-35  
; Sequence 35, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 120 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-025-769B-35

Query Match 85.1%; Score 508; DB 4; Length 120;  
Best Local Similarity 85.8%; Pred. No. 2.8e-45;  
Matches 103; Conservative 8; Mismatches 6; Gaps 2;



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QY 1 QVQLVQSGAEVKKPGSSVKVSKASGGTFFSSHAISWVRQAPQGQLEWMGDIIPILGTGNY 60
DB 1 QVQLVQSGAEVKKPGSSVKVSKASGGTFFSSVAISWVRQAPQGQLEWMGGIIPFGTANY 60
QY 61 AOKFQGRVTITADESTSTAYMELSLTSEDVAVYCYCEL---DWFY---IWGGTMTVTVSS 114
DB 61 AOKFQGRVTITADESTSTAYMELSLRSEDVAVYCARWGGDGFYAMDYWGQGLTLTVTVSS 120

```

## RESULT 2

```

US-09-025-769B-57
; Sequence 57, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9090
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-57

```

```

Query Match 85.1%; Score 508; DB 4; Length 120;
Best Local Similarity 85.8%; Pred. No. 2.8e-45;
Matches 103; Conservative 3; Mismatches 8; Indels 8; Gaps 2;

QY 1 QVQLVQSGAEVKKPGSSVKVSKASGGTFFSSHAISWVRQAPQGQLEWMGDIIPILGTGNY 60
DB 1 QVQLVQSGAEVKKPGSSVKVSKASGGTFFSSVAISWVRQAPQGQLEWMGGIIPFGTANY 60
QY 61 AOKFQGRVTITADESTSTAYMELSLTSEDVAVYCYCEL---DWFY---IWGGTMTVTVSS 114
DB 61 AOKFQGRVTITADESTSTAYMELSLRSEDVAVYCARWGGDGFYAMDYWGQGLTLTVTVSS 120

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## RESULT 3

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US-09-025-769B-21
; Sequence 21, Application US/09025769B
; Patent No. 6300064

```

```

; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9090
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-21

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```

Query Match 84.3%; Score 503.5; DB 4; Length 119;
Best Local Similarity 84.9%; Pred. No. 8.1e-45;
Matches 101; Conservative 3; Mismatches 10; Indels 5; Gaps 1;

QY 1 QVQLVQSGAEVKKPGSSVKVSKASGGTFFSSHAISWVRQAPQGQLEWMGDIIPILGTGNY 60
DB 1 QVQLVQSGAEVKKPGSSVKVSKASGGTFFSSVAISWVRQAPQGQLEWMGGIIPFGTANY 60
QY 61 AOKFQGRVTITADESTSTAYMELSLTSEDVAVYCYE-----LDMFYIWGGTMTVTVSS 114
DB 61 AOKFQGRVTITADESTSTAYMELSLRSEDVAVYCARAPGVCSGFDYWGQGLTLTVTVSS 119

```

## RESULT 4

```

US-08-652-816A-1
; Sequence 1, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America

```



```
Db      121 GTMTVSS 128
      || |||||
Matches 102; Conservative 7; Mismatches 10; Indels 3; Gaps 2;

RESULT 11
US-09-811-123-3
; Sequence 3, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Slikowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
; FILE REFERENCE: ANTIBODY-MAYTANSINOID CONJUGATES
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-3

Query Match      81.2%; Score 521.5; DB 9; Length 119;
Best Local Similarity 83.6%; Pred. No. 7e-41;
Matches 102; Conservative 7; Mismatches 10; Indels 3; Gaps 2;

Qy      1 EVLVESGGLVQPGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAATIGRSGTTFY 60
Db      1 EVLVESGGLVQPGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAATIGRSGTTFY 60
Qy      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYGMDVWGQGTTLTV 120
Db      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYGMDVWGQGTTLTV 120
Qy      121 SS 122
Db      118 SS 119

Query Match      81.2%; Score 521.5; DB 15; Length 119;
Best Local Similarity 83.6%; Pred. No. 7e-41;
Matches 102; Conservative 7; Mismatches 10; Indels 3; Gaps 2;

RESULT 12
US-10-268-501-6
; Sequence 6, Application US/10268501
; Publication No. US20030086924A1
; GENERAL INFORMATION:
; APPLICANT: Slikowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P1
; CURRENT APPLICATION NUMBER: US/10/268,501
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 6
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain consensus sequence
US-10-268-501-6

Query Match      81.2%; Score 521.5; DB 15; Length 119;
Best Local Similarity 83.6%; Pred. No. 7e-41;
Matches 102; Conservative 7; Mismatches 10; Indels 3; Gaps 2;

RESULT 13
US-09-880-748-1974
; Sequence 1974, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1974
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1974

Query Match      81.0%; Score 520; DB 11; Length 248;
Best Local Similarity 78.7%; Pred. No. 2.1e-40;
Matches 96; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

Qy      1 EVLVESGGLVQPGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAATIGRSGTTFY 60
Db      1 EVLVQSGGGLVQPGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVSYISSSGTTIY 60
Qy      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYGMDVWGQGTTLTV 120
Db      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYGMDVWGQGTTLTV 120
Qy      121 SS 122
Db      121 SS 122

RESULT 14
US-10-291-265-427
; Sequence 427, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: NO. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
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Db      121 VTVSS 125
|||||
RESULT 8
US-10-039-785-53
; Sequence 53, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,991
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 53
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1006F07 scFv
US-10-039-785-53

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Query Match      81.7%; Score 524.5; DB 13; Length 249;
Best Local Similarity 80.0%; Pred. No. 8e-41;
Matches 100; Conservative 12; Mismatches 10; Indels 3; Gaps 1;

Qy      1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKGLWVAIAIGRSCTTFY 60
      |||||
Db      1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVAISGGSTYY 60
      |||||
Qy      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKR-----GRGKYKYGMDVWGQTT 117
      |||||
Db      61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAREPFSQWGHYSYGMVWGQTM 120
      |||||
Qy      118 VTVSS 122
      |||||
Db      121 VTVSS 125
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RESULT 9
US-09-880-748-1605
; Sequence 1605, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816

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; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1605
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1605

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Query Match      81.7%; Score 524.5; DB 11; Length 251;
Best Local Similarity 80.0%; Pred. No. 8.1e-41;
Matches 100; Conservative 11; Mismatches 11; Indels 3; Gaps 1;

Qy      1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKGLWVAIAIGRSCTTFY 60
      |||||
Db      1 EVQLVQSGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVAISGGSTYY 60
      |||||
Qy      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKGRG---CYKYYGMDVWGQTT 117
      |||||
Db      61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARRSYDILTGYTYGMDVWGKGTW 120
      |||||
Qy      118 VTVSS 122
      |||||
Db      121 VTVSS 125
      |||||

```

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RESULT 10
US-09-880-748-1701
; Sequence 1701, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1701
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1701

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Query Match      81.3%; Score 522; DB 11; Length 254;
Best Local Similarity 78.1%; Pred. No. 1.4e-40;
Matches 100; Conservative 11; Mismatches 11; Indels 6; Gaps 1;

Qy      1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKGLWVAIAIGRSCTTFY 60
      |||||
Db      1 QVQLQESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVAISGGSTYY 60
      |||||
Qy      61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRG-----RGKYKYGMDVWGQ 114
      |||||
Db      61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKQDTYYDILTGHYYGMDVWGR 120
      |||||
Qy      115 GTTVTVSS 122

```

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; ORGANISM: Homo sapiens
US-09-840-459-76

Query Match      82.8%; Score 531.5; DB 10; Length 125;
Best Local Similarity 82.5%; Pred. No. 8.8e-42;
Matches 104; Conservative 8; Mismatches 9; Indels 5; Gaps 2;

Qy 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSVWRQAPGKGLEWVAIAIGRSSTTFY 60
Db 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSVWRQAPGKGLEWVAIAIGRSSTTFY 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAK-----RGRGGYKYYGMDVWGQGT 116
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAKDIETAMFPY-YYGMDVWGQGT 119
Qy 117 TVTVSS 122
Db 120 TVTVSS 125

RESULT 5
US-10-025-687-4
; Sequence 4, Application US/10025687
; Publication No. US20020142255A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/025,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-025-687-4

Query Match      81.8%; Score 525; DB 14; Length 120;
Best Local Similarity 82.0%; Pred. No. 3.4e-41;
Matches 100; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

Qy 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSVWRQAPGKGLEWVAIAIGRSSTTFY 60
Db 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSVWRQAPGKGLEWVAIAIGRSSTTFY 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAKRGGRGKYKYYGMDVWGQGT 120
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCARWGGDG--FYAMDYWGQGT 118
Qy 121 SS 122
Db 119 SS 120

RESULT 6
US-10-125-687-4
; Sequence 4, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-705
; CURRENT APPLICATION NUMBER: US/10/125,687
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
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```
; FEATURE:
; OTHER INFORMATION: Human consensus antibody heavy chain variable region
US-10-125-687-4

Query Match      81.8%; Score 525; DB 15; Length 120;
Best Local Similarity 82.0%; Pred. No. 3.4e-41;
Matches 100; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

Qy 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSVWRQAPGKGLEWVAIAIGRSSTTFY 60
Db 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSVWRQAPGKGLEWVAIAIGRSSTTFY 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAKRGGRGKYKYYGMDVWGQGT 120
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCARWGGDG--FYAMDYWGQGT 118
Qy 121 SS 122
Db 119 SS 120

RESULT 7
US-10-139-785-53
; Sequence 53, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospesifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 53
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1006F07 scFv
US-10-139-785-53

Query Match      81.7%; Score 524.5; DB 12; Length 249;
Best Local Similarity 80.0%; Pred. No. 8e-41;
Matches 100; Conservative 12; Mismatches 10; Indels 3; Gaps 1;

Qy 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSVWRQAPGKGLEWVAIAIGRSSTTFY 60
Db 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSVWRQAPGKGLEWVAIAIGRSSTTFY 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAKRGGRGKYKYYGMDVWGQGT 117
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAREPSFOQMGHYSYGMVWGQGT 120
Qy 118 VTVSS 122
```

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Matches 105; Conservative 9; Mismatches 8; Indels 6; Gaps 1;
QY 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSGLTFF 60
    |||||
Db 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSGLTFF 60
    |||||
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAKRG-----GGYKYYGMDVWGQ 114
    |||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAKRRNYDFWSGXYYYYGMDVWGQ 120
    |||||
QY 115 GTTVTVSS 122
    |||||
Db 121 GTTVTVSS 128
    |||||

RESULT 2
US-09-840-459-79
; Sequence 79, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2000-02-03
; PRIOR FILING DATE: 1999-07-22
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(128)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-79

Query Match 85.5%; Score 549; DB 10; Length 128;
Best Local Similarity 82.0%; Pred. No. 2.2e-43;
Matches 105; Conservative 9; Mismatches 8; Indels 6; Gaps 1;
QY 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSGLTFF 60
    |||||
Db 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSGLTFF 60
    |||||
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAKRG-----GGYKYYGMDVWGQ 114
    |||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAKRRNYDFWSGXYYYYGMDVWGQ 120
    |||||
QY 115 GTTVTVSS 122
    |||||
Db 121 GTTVTVSS 128
    |||||

RESULT 3
US-09-840-459-84
; Sequence 84, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2000-02-03
; PRIOR FILING DATE: 1999-07-22
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(128)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-79

Query Match 85.5%; Score 549; DB 10; Length 128;
Best Local Similarity 82.0%; Pred. No. 2.2e-43;
Matches 105; Conservative 9; Mismatches 8; Indels 6; Gaps 1;
QY 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSGLTFF 60
    |||||
Db 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSGLTFF 60
    |||||
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAKRG-----GGYKYYGMDVWGQ 114
    |||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAKRRNYDFWSGXYYYYGMDVWGQ 120
    |||||
QY 115 GTTVTVSS 122
    |||||
Db 121 GTTVTVSS 128
    |||||

RESULT 4
US-09-840-459-76
; Sequence 76, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR FILING DATE: 1999-07-22
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-84

Query Match 85.3%; Score 547.5; DB 10; Length 125;
Best Local Similarity 84.0%; Pred. No. 3e-43;
Matches 105; Conservative 8; Mismatches 9; Indels 3; Gaps 1;
QY 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSGLTFF 60
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Db 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKGLEWVAIAIGRSGLTFF 60
    |||||
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAK-----RGRGGYKYYGMDVWGQ 117
    |||||
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAKAVRVGVISYYYYGMDVWGQ 120
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QY 118 VTVSS 122
    |||||
Db 121 VTVSS 125
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OM protein - protein search, using sw model

Run on: December 30, 2003, 11:01:15 ; Search time 26.1641 Seconds  
(without alignments)  
927.994 Million cell updates/sec

Title: US-09-674-752-53

Perfect score: 642

Sequence: 1 EVQLVDSGDLVQPGGSLRL.....GKYIGMDVWGQGTIVTVSS 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 549   | 85.5        | 128    | 10 | US-09-840-459-77   |
| 2          | 549   | 85.5        | 128    | 10 | US-09-840-459-77   |
| 3          | 547.5 | 85.3        | 125    | 10 | US-09-840-459-84   |
| 4          | 531.5 | 82.8        | 125    | 10 | US-09-840-459-76   |
| 5          | 525   | 81.8        | 120    | 14 | US-10-025-687-4    |
| 6          | 525   | 81.8        | 120    | 15 | US-10-125-687-4    |
| 7          | 524.5 | 81.7        | 249    | 12 | US-10-139-785-53   |
| 8          | 524.5 | 81.7        | 249    | 13 | US-10-039-785-53   |
| 9          | 524.5 | 81.7        | 251    | 11 | US-09-880-748-1605 |
| 10         | 522   | 81.3        | 254    | 11 | US-09-880-748-1701 |
| 11         | 521.5 | 81.2        | 119    | 9  | US-09-811-123-3    |
| 12         | 521.5 | 81.2        | 119    | 15 | US-10-268-501-6    |
| 13         | 520   | 81.0        | 248    | 11 | US-09-880-748-1974 |
| 14         | 519.5 | 80.9        | 313    | 12 | US-10-291-265-427  |
| 15         | 519   | 80.8        | 118    | 15 | US-10-001-934-39   |

|    |       |      |     |    |                    |
|----|-------|------|-----|----|--------------------|
| 16 | 518   | 80.7 | 253 | 12 | US-10-120-414-76   |
| 17 | 517   | 80.5 | 124 | 10 | US-09-840-459-81   |
| 18 | 516   | 80.4 | 124 | 15 | US-10-040-244-16   |
| 19 | 515.5 | 80.3 | 224 | 11 | US-09-972-656-68   |
| 20 | 515.5 | 80.3 | 253 | 11 | US-09-880-748-989  |
| 21 | 515   | 80.2 | 248 | 11 | US-09-880-748-1965 |
| 22 | 515   | 80.2 | 251 | 11 | US-09-880-748-908  |
| 23 | 514   | 80.1 | 136 | 12 | US-10-045-674-487  |
| 24 | 514   | 80.1 | 367 | 12 | US-10-045-674-453  |
| 25 | 513.5 | 80.0 | 119 | 12 | US-10-044-896-6    |
| 26 | 511   | 79.6 | 128 | 10 | US-09-840-459-78   |
| 27 | 511   | 79.6 | 252 | 11 | US-09-880-748-1431 |
| 28 | 510.5 | 79.5 | 248 | 11 | US-09-880-748-913  |
| 29 | 510   | 79.4 | 248 | 11 | US-09-880-748-921  |
| 30 | 510   | 79.4 | 251 | 11 | US-09-880-748-1456 |
| 31 | 510   | 79.4 | 251 | 11 | US-09-880-748-1740 |
| 32 | 510   | 79.4 | 252 | 11 | US-09-880-748-1637 |
| 33 | 510   | 79.4 | 254 | 11 | US-09-880-748-1739 |
| 34 | 510   | 79.4 | 263 | 10 | US-09-956-086-3    |
| 35 | 510   | 79.4 | 263 | 10 | US-09-956-087-3    |
| 36 | 510   | 79.4 | 283 | 10 | US-09-983-580-6    |
| 37 | 510   | 79.4 | 283 | 10 | US-09-985-442-6    |
| 38 | 509.5 | 79.4 | 244 | 12 | US-10-322-673-45   |
| 39 | 509.5 | 79.4 | 251 | 11 | US-09-880-748-1171 |
| 40 | 508.5 | 79.2 | 123 | 10 | US-09-840-459-92   |
| 41 | 508.5 | 79.2 | 123 | 10 | US-09-840-459-82   |
| 42 | 508   | 79.1 | 124 | 10 | US-09-840-459-89   |
| 43 | 508   | 79.1 | 124 | 12 | US-10-308-817-190  |
| 44 | 508   | 79.1 | 245 | 12 | US-10-322-673-43   |
| 45 | 507.5 | 79.0 | 431 | 12 | US-10-045-674-588  |

#### ALIGNMENTS

#### RESULT 1

US-09-840-459-77  
; Sequence 77, Application US/09840459  
; Patent No. US20020150576A1  
; GENERAL INFORMATION:  
; APPLICANT: LaRosa, Gregory J.  
; APPLICANT: Horvath, Christopher  
; APPLICANT: Newman, Walter  
; APPLICANT: Jones, S. Tarran  
; APPLICANT: O'Brien, Siobhan H.  
; APPLICANT: O'Keefe, Theresa  
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
; TITLE OF INVENTION: METHODS OF USE THEREFOR  
; FILE REFERENCE: 1855.1052-012  
; CURRENT APPLICATION NUMBER: US/09/840.459  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: PCT/US01/03537  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/497,625  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/359,193  
; PRIOR FILING DATE: 1999-07-22  
; PRIOR APPLICATION NUMBER: 09/121,781  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 77  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(128)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-840-459-77

Query Match 85.5%; Score 549; DB 10; Length 128;  
Best Local Similarity 82.0%; Pred. No. 2.2e-43;

XX CC This invention relates to a novel humanised, chimeric or human  
 CC monoclonal antibody or its antigen binding portion that specifically  
 CC binds to insulin-like growth factor I receptor (IGF-IR). The antibodies  
 CC of the invention can act as an inhibitor of binding of IGF-I or IGF-II  
 CC with IGF-IR and can inhibit *in vivo* tumour growth and IGF-IR tyrosine  
 CC phosphorylation. The antibodies of the invention are useful for  
 CC diagnosing the presence or location of an IGF-IR-expressing tumour in a  
 CC subject. The antibody or its antigen-binding portion is also useful for  
 CC treating cancer in a human. The method for this further involves an anti  
 CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent.  
 CC The antibodies may also be useful for increasing IGF-IR activity and  
 CC thus restoring IGF-IR activity in a condition characterised by low  
 CC IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the  
 CC invention is also useful for inducing apoptosis of specific cells in a  
 CC patient, and to treat non-cancerous states or disease, e.g. acromegaly,  
 CC gigantism, priortias and atherosclerosis. Fully human anti-IGF-IR  
 CC antibodies minimise the immunogenic and allergic responses intrinsic to  
 CC mouse or mouse-derived monoclonal antibodies and thus increase the  
 CC efficacy and safety of the administered antibodies. The present sequence  
 CC represents an anti-insulin-like growth factor I receptor antibody of the  
 CC invention.

XX SQ Sequence 124 AA;

Query Match 81.5%; Score 523.5; DB 23; Length 124;  
 Best Local Similarity 80.6%; Pred. No. 1.7e-41;  
 Matches 100; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

Qy 2 VOLVESGGDLVQPGSLRLSCAASGFTFSNFMVSRQAPGKLEWVAALGGRSGTTFYA 61  
 Db 1 VOLVESGGGLVQPGSLRLSCTASGFTFSYAMNVRQAPGKLEWVAISGSGGTTFYA 60  
 Qy 62 DSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKR---GRGGYKYGYMDVWGQGTTV 118  
 Db 61 DSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKLGHSDSYIYYGYMDVWGQGTTV 120  
 Qy 119 TVSS 122  
 Db 121 TVSS 124

RESULT 15  
 ABP56504  
 ID ABP56504 standard; Protein; 121 AA.

XX AC ABP56504;

XX DT 20-MAR-2003 (first entry)

XX DE Human anti-Fc-epsilon-R1 alpha autoantibody heavy chain LTM-alpha-15.

XX KW Autoantibody; Fc-epsilon-R1 receptor alpha-chain; immunosuppressive;  
 KW allergic disease; urticaria; late phase allergic reaction; malignancy;  
 KW intrinsic asthma; drug intolerance; food intolerance; immunoglobulin E;  
 KW conditional autoimmunity; IgE mediated disease.

XX OS Homo sapiens.  
 XX OS Synthetic.

XX PN WO200202085-A2.

XX PD 17-OCT-2002.

XX PF 03-APR-2002; 2002WO-EP03660.

XX PR 04-APR-2001; 2001US-281024P.

XX PA (ZLBB-) ZLB BIOPLASMA AG.

XX PI Miescher S;

XX DR WPI; 2003-103348/09.

XX PT Identifying and obtaining inhibitor of a pathological process for  
 PT treating e.g. autoimmunity comprises determining if a compound is  
 PT capable of modulating the binding of the Fc-epsilon-R1 receptor and an  
 PT autoantibody against its alpha-chain -

PS Claim 20; Page 22; 29pp; English.

XX CC The present invention describes a method for identifying and obtaining  
 CC an inhibitor of a pathological process. The method comprises determining  
 CC if a compound is capable of modulating the binding of the Fc-epsilon-R1  
 CC receptor alpha-chain and an autoantibody against its alpha-chain. Also  
 CC described: (1) use of the autoantibody against the Fc-epsilon-R1 receptor  
 CC alpha-chain for identifying and obtaining an inhibitor of a pathological  
 CC process; (2) use of the identified inhibitor for inhibiting activity of  
 CC the autoantibody against the Fc-epsilon-R1 receptor alpha-chain; and  
 CC (3) a compound identified by the method, which binds but does not  
 CC activate the receptor; and (4) a polypeptide capable of specific binding  
 CC to the Fc-epsilon-R1 receptor alpha-chain. The method is useful for  
 CC obtaining an inhibitor of a pathological process e.g. imbalance between  
 CC cell-bound and free IgE e.g. allergic disease (urticaria, late phase  
 CC allergic reactions, intrinsic asthma, drug intolerance and food  
 CC intolerance), IgE mediated disease or malignancy. The compound is useful  
 CC for treating a pathological process, particularly conditional  
 CC autoimmunity. The present sequence represents a human recombinant  
 CC anti-Fc-epsilon-R1 alpha autoantibody heavy chain protein sequence from  
 CC the present invention.

XX SQ Sequence 121 AA;

Query Match 81.4%; Score 522.5; DB 24; Length 121;  
 Best Local Similarity 82.8%; Pred. No. 2.1e-41;  
 Matches 101; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

Qy 1 EVQLVESGGDLVQPGSLRLSCAASGFTFSNFMVSRQAPGKLEWVAALGGRSGTTFY 60  
 Db 1 EVQLVESGGGLVQPGSLRLSCAASGFTFSYANVSRQAPGKLEWVAISGSGSTFY 60  
 Qy 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGGYKYGYMDVWGQGTTVT 120  
 Db 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKGERWLPSTY-MDVWKGKTTVT 119  
 Qy 121 SS 122  
 Db 120 SS 121

Search completed: December 30, 2003, 10:54:38  
 Job time : 40.3295 secs



XX The present sequence is the consensus single chain fragment  
 CC Vh3-V-kappa-2. Vh3-V-kappa-2, which comprises the human antibody  
 CC heavy and light chain variable region consensus sequences Vh3 and  
 CC V-kappa-2, was used in the preparation of a human derived antibody  
 CC gene library.

XX SQ Sequence 281 AA;  
 Query Match 81.8%; Score 525; DB 18; Length 281;  
 Best Local Similarity 82.0%; Pred. No. 3e-41;  
 Matches 100; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

Qy 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKLEWVAIGRSGTTFY 60  
 Db 26 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKLEWVAIGRSGTTFY 85  
 Qy 61 ADSVKGRFTISRDNKNTVYLENLSRAEDTAIYYCAKRGVYKYGMDVWGQTTV 120  
 Db 86 ADSVKGRFTISRDNKNTVYLENLSRAEDTAIYYCAKRGVYKYGMDVWGQTTV 143  
 Qy 121 SS 122  
 Db 144 SS 145

RESULT 13  
 ABP45594  
 ID ABP45594 standard; Protein; 251 AA.  
 AC ABP45594;  
 DT 19-AUG-2002 (first entry)  
 DE Human BlyS binding scFv SEQ ID 1605.  
 KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW anti-AIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.  
 OS WO200202641-A1.  
 PN 10-JAN-2002.  
 PD 15-JUN-2001; 2001WO-US19110.  
 PF 16-JUN-2000; 2000US-212210P.  
 PR 17-OCT-2000; 2000US-240816P.  
 PR 16-MAR-2001; 2001US-276248P.  
 PR 21-MAR-2001; 2001US-277379P.  
 PR 25-MAY-2001; 2001US-293499P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX WPI; 2002-114799/15.  
 DR Antibodies against B Lymphocyte Stimulating polypeptides, useful for  
 PT the diagnosis and treatment of cancers and immune disorders -  
 XX Claim 1; Page 2318-2319; 3148pp; English.  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and anti-AIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS  
 CC and so may be used to detect and quantitate the presence of BlyS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BlyS. They may also be  
 CC administered to treat diseases associated with aberrant BlyS expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method  
 CC of the invention.

XX SQ Sequence 251 AA;  
 Query Match 81.7%; Score 524.5; DB 23; Length 251;  
 Best Local Similarity 80.0%; Pred. No. 3e-41;  
 Matches 100; Conservative 11; Mismatches 11; Indels 3; Gaps 1;

Qy 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKLEWVAIGRSGTTFY 60  
 Db 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMWVRQAPGKLEWVAIGRSGTTFY 60  
 Qy 61 ADSVKGRFTISRDNKNTVYLENLSRAEDTAIYYCAKRGVYKYGMDVWGQTT 117  
 Db 61 ADSVKGRFTISRDNKNTVYLENLSRAEDTAIYYCAKRGVYKYGMDVWGQTT 120  
 Qy 118 VTVSS 122  
 Db 121 VTVSS 125

RESULT 14  
 ABG77138  
 ID ABG77138 standard; Protein; 124 AA.  
 AC ABG77138;  
 DT 24-OCT-2002 (first entry)  
 DE Anti-IGF-IR antibody (2.13.2) variable region heavy chain protein.  
 KW Inulin-like growth factor I receptor; antibody; human;  
 KW cytostatic; osteopathic; antiatherosclerotic; antipsoriatic;  
 KW IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic;  
 KW neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;  
 KW atherosclerosis.  
 XX Homo sapiens.  
 OS WO200253596-A2.  
 PN 11-JUL-2002.  
 PD 20-DEC-2001; 2001WO-US51113.  
 PF 05-JAN-2001; 2001US-259927P.  
 PR (PFIZ ) PFIZER INC.  
 PA (ABGE-) ABGENIX INC.  
 XX Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;  
 XX WPI; 2002-575410/61.  
 DR N-FSDB; ABS62700.  
 XX Novel humanized, chimeric monoclonal antibody that specifically binds  
 PT to insulin-like growth factor I (IGF-I) receptor useful for inhibiting  
 PT binding of IGF-I or IGF-II to receptor and for treating cancer in  
 XX humans -  
 PS Claim 13; Page 127; 172pp; English.

```

DR N-PSDB; AAT87951.
XX
PT Preparation of human derived antibody gene library - using synthetic
PT consensus sequences, and signal consensus antibody gene as universal
PT framework for highly diverse antibody libraries
XX
PS Example 1; Fig 5D; 436pp; English.
XX
CC The present sequence is the human antibody heavy chain
CC variable region synthetic sequence VH3, used in the preparation of
CC a human derived antibody gene library.
XX
SQ Sequence 120 AA;
    Query Match      81.8%; Score 525; DB 18; Length 120;
    Best Local Similarity 82.0%; Pred. No. 1.2e-41;
    Matches 100; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

QY 1 EVQLVESGGDLVQPQGSRLRLSCAASGFTFSNFMAMSVWRQAPQKGLWVAIAIGRSGTTFY 60
DB 1 EVQLVESGGDLVQPQGSRLRLSCAASGFTFSNFMAMSVWRQAPQKGLWVAIAIGRSGTTFY 60
QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGCGYKYGYGMDVWGQGTFTTV 120
DB 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGCGYKYGYGMDVWGQGTFTTV 118
QY 121 SS 122
DB 119 SS 120

RESULT 12
AAW27560
ID AAW27560 standard; Protein; 281 AA.
XX
AC AAW27560;
XX
DT 23-JAN-1998 (first entry)
XX
DE Consensus single chain fragment VH3-V-kappa-2.
XX
KW Human; antibody; preparation; library; VH3; variable region;
KW light chain; heavy chain; V-kappa-2; single chain; consensus.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Peptide /label= sig_peptide
FT Peptide 22..281
FT Peptide /label= mat_peptide
XX
PN WO9708320-A1.
XX
PD 06-MAR-1997.
XX
PF 19-AUG-1996; 96WO-EP03647.
XX
PR 18-AUG-1995; 95EP-0113021.
XX
PA (MORP-) MORPHOSYS GES PROTEINOPTIMERUNG MBH.
XX
PI Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;
XX
DR WPI; 1997-179277/16.
XX
DR N-PSDB; AAT87958.
XX
PT Preparation of human derived antibody gene library - using synthetic
PT consensus sequences, and signal consensus antibody gene as universal
PT framework for highly diverse antibody libraries
XX
PS Example 2; Fig 8; 436pp; English.

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DR N-PSDB; AAT87951.
XX
PT Preparation of human derived antibody gene library - using synthetic
PT consensus sequences, and signal consensus antibody gene as universal
PT framework for highly diverse antibody libraries
XX
PS Example 1; Fig 5D; 436pp; English.
XX
CC The present sequence is the human antibody heavy chain
CC variable region synthetic sequence VH3, used in the preparation of
CC a human derived antibody gene library.
XX
SQ Sequence 120 AA;
    Query Match      81.8%; Score 525; DB 18; Length 120;
    Best Local Similarity 82.0%; Pred. No. 1.2e-41;
    Matches 100; Conservative 10; Mismatches 10; Indels 2; Gaps 1;

QY 1 EVQLVESGGDLVQPQGSRLRLSCAASGFTFSNFMAMSVWRQAPQKGLWVAIAIGRSGTTFY 60
DB 1 EVQLVESGGDLVQPQGSRLRLSCAASGFTFSNFMAMSVWRQAPQKGLWVAIAIGRSGTTFY 60
QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGCGYKYGYGMDVWGQGTFTTV 120
DB 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGCGYKYGYGMDVWGQGTFTTV 118
QY 121 SS 122
DB 119 SS 120

RESULT 11
ABJ18675
ID ABJ18675 standard; Protein; 120 AA.
XX
AC ABJ18675;
XX
DT 06-MAR-2003 (first entry)
XX
DE Antibody library related heavy variable chain protein region SEQ ID No 4.
XX
KW Library; recombinant antibody; clustering variable region; in silico;
KW immunogenicity; antibody therapeutic.
XX
OS Unidentified.
XX
PN WO200284277-A1.
XX
PD 24-OCT-2002.
XX
PF 17-APR-2002; 2002WO-US12202.
XX
PR 17-APR-2001; 2001US-284407P.
XX
PA (ABMA-) ABMAXIS INC.
XX
PI Luo P;
XX
DR WPI; 2003-093043/08.
XX
PT Constructing a library of recombinant antibodies useful as source of
PT antibody candidates for screening antigens comprises clustering
PT variable regions of antibodies having known 3-dimensional structures
PT into structural ensembles -
XX
XX
PS Disclosure; Page 101; 119pp; English.
XX
CC The invention relates to a novel method for the construction of a library
CC of recombinant antibodies. The novel method comprises clustering variable
CC regions of a collection of antibodies having known 3D structures into at
CC least two families of structural ensembles, each comprising at least two
CC different antibody sequences but with substantially identical main chain
CC conformations. The method is useful for constructing a library of

```

CC a cell expressing CCR2. They are useful for inhibiting or treating  
 CC HIV infection. The proteins of the invention are useful for inhibiting  
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as  
 CC inflammatory disorder, autoimmune disorders such as rheumatoid  
 CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,  
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,  
 CC and in the manufacture of a medicament for treating CCR2 mediated  
 CC disease. They are also useful for treating allergy, anaphylaxis,  
 CC malignancy, chronic and acute inflammation, histamine and IgE-  
 CC mediated allergic reaction, shock, stenosis, allograft rejection,  
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired  
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular  
 CC intervention, including angioplasty and/or stent placement in a mammal.  
 CC Humanised antibodies are also useful for inhibiting narrowing of the  
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of  
 CC a vessel in a mammal, preferably associated with vascular intervention.  
 CC The present sequence is human heavy chain variable (VH) region, 038064.  
 CC  
 XX  
 SQ Sequence 125 AA;

Query Match 82.8%; Score 531.5; DB 22; Length 125;  
 Best Local Similarity 82.5%; Pred. No. 3.1e-42;  
 Matches 104; Conservative 8; Mismatches 9; Indels 5; Gaps 2;  
 QY 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMNSWVRQAPGKLEWVAIGRSCTTFY 60  
 DB 1 EVLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISGGSTYY 60  
 QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAK---RGRGGYKYYGMDVWGQGT 116  
 DB 61 ADSVKGRFTISRDNKNTLYLQMNLSLRADTAIYYCAKDIEDTAMFFY-YIGMDVWGQGT 119

QY 117 TVTVSS 122  
 DB 120 TVTVSS 125

RESULT 9  
 ABG77157  
 ID ABG77157 standard; Protein; 470 AA.  
 AC ABG77157;  
 XX  
 XX 24-OCT-2002 (first entry)  
 XX  
 XX Amino acid sequence of anti-IGF-IR antibody 2.13.2 Vh domain.  
 XX  
 XX Insulin-like growth factor I receptor; antibody; human;  
 KW cytosolic; osteopathic; antiatherosclerotic; antipsoriatic;  
 KW IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic;  
 KW neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;  
 KW atherosclerosis.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200253596-A2.  
 XX  
 XX 11-JUL-2002.  
 XX  
 XX 20-DEC-2001; 2001WO-US51113.  
 XX  
 XX 05-JAN-2001; 2001US-259927P.  
 XX  
 XX (PFIZ ) PFIZER INC.  
 XX (ABGE-) ABGENIX INC.  
 XX  
 XX Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;  
 XX WPI; 2002-575410/61.  
 XX  
 XX Novel humanized, chimeric monoclonal antibody that specifically binds  
 PT to insulin-like growth factor I (IGF-I) receptor useful for inhibiting  
 PT binding of IGF-I or IGF-II to receptor and for treating cancer in

PT humans  
 XX Claim 16; Figure 19B; 172pp; English.  
 XX  
 CC This invention relates to a novel humanised, chimeric or human  
 CC monoclonal antibody or its antigen binding portion that specifically  
 CC binds to insulin-like growth factor I receptor (IGF-IR). The antibodies  
 CC of the invention can act as an inhibitor of binding of IGF-I or IGF-II  
 CC with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine  
 CC phosphorylation. The antibodies of the invention are useful for  
 CC diagnosing the presence or location of an IGF-IR-expressing tumour in a  
 CC subject. The antibody or its antigen-binding portion is also useful for  
 CC treating cancer in a human. The method for this further involves an anti  
 CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent.  
 CC The antibodies may also be useful for increasing IGF-IR activity and  
 CC thus restoring IGF-IR activity in a condition characterised by low  
 CC IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the  
 CC invention is also useful for inducing apoptosis of specific cells in a  
 CC patient, and to treat non-cancerous states or disease, e.g. acromegaly,  
 CC gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-IR  
 CC antibodies minimise the immunogenic and allergic responses intrinsic to  
 CC mouse or mouse-derived monoclonal antibodies and thus increase the  
 CC efficacy and safety of the administered antibodies. The present sequence  
 CC represents an anti-insulin-like growth factor I receptor antibody of the  
 CC invention.  
 XX  
 SQ Sequence 470 AA;  
 Query Match 82.3%; Score 528.5; DB 23; Length 470;  
 Best Local Similarity 80.8%; Pred. No. 2.5e-41;  
 Matches 101; Conservative 9; Mismatches 12; Indels 3; Gaps 1;  
 QY 1 EVLVESGGDLVQPGGSLRLSCAASGFTFSNFMNSWVRQAPGKLEWVAIGRSCTTFY 60  
 DB 20 EVLVESGGGLVQPGGSLRLSCTASGFTFSYAMSWVRQAPGKLEWVAISGGSTTFY 79  
 QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAK---RGRGGYKYYGMDVWGQGT 117  
 DB 80 ADSVKGRFTISRDNKNTLYLQMNLSLRADTAIYYCAKDLGWSDSYIYYGMDVWGQGT 139  
 QY 118 TVTVSS 122  
 DB 140 TVTVSS 144  
 RESULT 10  
 AAW27553  
 ID AAW27553 standard; Protein; 120 AA.  
 XX  
 AC AAW27553;  
 XX  
 XX 23-JAN-1998 (first entry)  
 XX  
 XX Human Ab heavy chain variable region VH3 consensus.  
 XX  
 XX Human; antibody; preparation; library; VH3; variable region;  
 KW heavy chain; consensus.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO9708320-A1.  
 XX  
 XX 06-MAR-1997.  
 XX  
 XX 19-AUG-1996; 96WO-EP03647.  
 XX  
 XX 18-AUG-1995; 95EP-0113021.  
 XX  
 XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.  
 XX  
 XX Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;  
 XX WPI; 1997-179277/16.  
 DR



RESULT 5  
 ABG77158  
 ID ABG77158 standard; Protein; 470 AA.  
 AC ABG77158;  
 XX  
 DT 24-OCT-2002 (first entry)  
 XX  
 DE Germline protein sequence of anti-IGF-IR antibody DP-47(3-23)/D6-19/JH6.  
 XX  
 KW Insulin-like growth factor I receptor; antibody; human;  
 KW cytosatic; osteopathic; antiatherosclerotic; anti-psoriatic;  
 KW IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic;  
 KW neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;  
 KW atherosclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200253596-A2.  
 XX  
 PD 11-JUL-2002.  
 XX  
 PF 20-DEC-2001; 2001WO-US51113.  
 XX  
 PR 05-JAN-2001; 2001US-259927P.  
 XX  
 PA (PFIZ ) PFIZER INC.  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;  
 XX  
 DR WPI; 2002-575410/61.  
 XX  
 PT Novel humanized, chimeric monoclonal antibody that specifically binds  
 PT to insulin-like growth factor I (IGF-I) receptor useful for inhibiting  
 PT binding of IGF-I or IGF-II to receptor and for treating cancer in  
 PT humans -  
 XX  
 PS Disclosure; Figure 19B; 172pp; English.  
 XX  
 CC This invention relates to a novel humanised, chimeric or human  
 CC monoclonal antibody or its antigen binding portion that specifically  
 CC binds to insulin-like growth factor I receptor (IGF-IR). The antibodies  
 CC of the invention can act as an inhibitor of binding of IGF-I or IGF-II  
 CC with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine  
 CC phosphorylation. The antibodies of the invention are useful for  
 CC diagnosing the presence or location of an IGF-IR-expressing tumour in a  
 CC subject. The antibody or its antigen-binding portion is also useful for  
 CC treating cancer in a human. The method for this further involves an anti  
 CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent.  
 CC The antibodies may also be useful for increasing IGF-IR activity and  
 CC thus restoring IGF-IR activity in a condition characterised by low  
 CC IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the  
 CC invention is also useful for inducing apoptosis of specific cells in a  
 CC patient, and to treat non-cancerous states or disease, e.g. acromegaly,  
 CC gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-IR  
 CC antibodies minimise the immunogenic and allergic responses intrinsic to  
 CC mouse or mouse-derivatised monoclonal antibodies and thus increase the  
 CC efficacy and safety of the administered antibodies. The present sequence  
 CC represents an anti-insulin-like growth factor I receptor antibody of the  
 CC invention.  
 XX  
 CC Sequence 470 AA;  
 XX  
 Query March 84.8%; Score 544.5; DB 23; Length 470;  
 Best Local Similarity 83.2%; Pred. No. 8e-43;  
 Matches 104; Conservative 9; Mismatches 9; Indels 3; Gaps 1;  
 1 EVQLVESGGDLVPGGSLRLSCAASGTPFSNFMWSVRQAPGKGLEWVAATIGRSGLTTFY 60  
 20 EVQLLESGGGLVPGGSLRLSCAASGTPFSSTAMSWVRQAPGKGLEWVAISGGSGSIYY 79

61 ADSVKGRPTISRDNSTNTVYLEMNSLRADTAIYYCAKGRGG---YKYGMVDVWGQTT 117  
 80 ADSVKGRPTISRDNSTNTVYLEMNSLRADTAIYYCAKGYSSGYYYIYGMVDVWGQTT 139  
 118 VTVSS 122  
 140 VTVSS 144  
 RESULT 6  
 ABG77142  
 ID ABG77142 standard; Protein; 125 AA.  
 AC ABG77142;  
 XX  
 DT 24-OCT-2002 (first entry)  
 XX  
 DE Anti-IGF-IR antibody (4.9.2) variable region heavy chain protein.  
 XX  
 KW Insulin-like growth factor I receptor; antibody; human;  
 KW cytosatic; osteopathic; antiatherosclerotic; anti-psoriatic;  
 KW IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic;  
 KW neuropathy; osteoporosis; acromegaly; gigantism; psoriasis;  
 KW atherosclerosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200253596-A2.  
 XX  
 PD 11-JUL-2002.  
 XX  
 PF 20-DEC-2001; 2001WO-US51113.  
 XX  
 PR 05-JAN-2001; 2001US-259927P.  
 XX  
 PA (PFIZ ) PFIZER INC.  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;  
 XX  
 DR WPI; 2002-575410/61.  
 XX  
 PT Novel humanized, chimeric monoclonal antibody that specifically binds  
 PT to insulin-like growth factor I (IGF-I) receptor useful for inhibiting  
 PT binding of IGF-I or IGF-II to receptor and for treating cancer in  
 PT humans -  
 XX  
 PS Claim 13; Page 130; 172pp; English.  
 XX  
 CC This invention relates to a novel humanised, chimeric or human  
 CC monoclonal antibody or its antigen binding portion that specifically  
 CC binds to insulin-like growth factor I receptor (IGF-IR). The antibodies  
 CC of the invention can act as an inhibitor of binding of IGF-I or IGF-II  
 CC with IGF-IR and can inhibit in vivo tumour growth and IGF-IR tyrosine  
 CC phosphorylation. The antibodies of the invention are useful for  
 CC diagnosing the presence or location of an IGF-IR-expressing tumour in a  
 CC subject. The antibody or its antigen-binding portion is also useful for  
 CC treating cancer in a human. The method for this further involves an anti  
 CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent.  
 CC The antibodies may also be useful for increasing IGF-IR activity and  
 CC thus restoring IGF-IR activity in a condition characterised by low  
 CC IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the  
 CC invention is also useful for inducing apoptosis of specific cells in a  
 CC patient, and to treat non-cancerous states or disease, e.g. acromegaly,  
 CC gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-IR  
 CC antibodies minimise the immunogenic and allergic responses intrinsic to  
 CC mouse or mouse-derivatised monoclonal antibodies and thus increase the  
 CC efficacy and safety of the administered antibodies. The present sequence  
 CC represents an anti-insulin-like growth factor I receptor antibody of the  
 CC invention.  
 XX  
 CC Sequence 125 AA;

DR WPI; 2001-488888/53.  
XX Humanized immunoglobulin for treating a CC-chemokine receptor  
PT 2-mediated disorder in a patient, comprises a binding specificity for  
PT CCR2, and a non-human antigen binding region and human immunoglobulin  
PT -  
XX  
XX Disclosure; Page 168; 183pp; English.  
XX  
XX The patent discloses a humanised antibody or its antigen-binding  
CC fragment, having binding specificity for CC-chemokine receptor 2  
CC (CCR2), comprising an antigen binding region of non-human origin  
CC and at least a portion of an immunoglobulin of human origin. The  
CC humanised antibodies are useful for inhibiting the interaction of  
CC a cell expressing CCR2. They are useful for inhibiting or treating  
CC HIV infection. The proteins of the invention are useful for inhibiting  
CC leukocyte trafficking, for treating CCR2-mediated disorders such as  
CC inflammatory disorder, autoimmune disorders such as rheumatoid  
CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,  
CC and for inhibiting restenosis. They are useful in therapy or diagnosis,  
CC and in the manufacture of a medicament for treating CCR-2 mediated  
CC disease. They are also useful for treating allergy, anaphylaxis,  
CC malignancy, chronic and acute inflammation, histamine and IgE-  
CC mediated allergic reaction, shock, stenosis, allograft rejection,  
CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired  
CC immune deficiency syndrome (AIDS), restenosis associated with vascular  
CC intervention, including angioplasty and/or stent placement in a mammal.  
CC Humanised antibodies are also useful for inhibiting narrowing of the  
CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of  
CC a vessel in a mammal, preferably associated with vascular intervention.  
CC The present sequence is human heavy chain variable (VH) region, 038062.  
XX  
SQ Sequence 128 AA;  
Query Match 85.5%; Score 549; DB 22; Length 128;  
Best Local Similarity 82.0%; Pred. No. 7.3e-44; Indels 6; Gaps 1;  
Matches 105; Conservative 9; Mismatches 8;  
QY 1 EVQLVESGDLVQPGGSLRLSCAASGFTFSNFMAMSVWVRQAPGKLEWVAIAIGRSGTTFY 60  
Db 1 EVQLVESGDLVQPGGSLRLSCAASGFTFSNFMAMSVWVRQAPGKLEWVAISGSGSTYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAKGR-----GGYKYYGMDVWGQ 114  
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAKDRNYDFWSGXYYYGMDVWGQ 120  
QY 115 GTTVTVSS 122  
Db 121 GTTVTVSS 128  
RESULT 4  
AAE07021  
ID AAE07021 standard; Protein; 125 AA.  
XX  
AC AAE07021;  
XX  
XX 16-OCT-2001 (first entry)  
XX  
XX Human heavy chain variable (VH) region, 4G12.  
XX  
KW Human; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;  
KW neuroprotective; immunosuppressive; human immunodeficiency virus;  
KW HIV infection; cytotoxic; vasotropic; leukocyte trafficking; allergy;  
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;  
KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;  
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;  
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;  
KW AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody;  
KW neointimal hyperplasia; VH; heavy chain variable region.  
XX  
OS Homo sapiens.  
XX

PH Key Location/Qualifiers  
FT Region 31..35  
FT /label= CDR1  
FT /note= "Complementarity determining region 1"  
FT Region 50..66  
FT /label= CDR2  
FT /note= "Complementarity determining region 2"  
FT Region 99..114  
FT /label= CDR3  
FT /note= "Complementarity determining region 3"  
XX WO200157226-A1.  
XX 09-AUG-2001.  
XX 02-FEB-2001; 2001WO-US03537.  
XX 03-FEB-2000; 2000US-0497625.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;  
XX WPI; 2001-488888/53.  
XX Humanized immunoglobulin for treating a CC-chemokine receptor  
PT 2-mediated disorder in a patient, comprises a binding specificity for  
PT CCR2, and a non-human antigen binding region and human immunoglobulin  
PT -  
XX Disclosure; Page 171; 183pp; English.  
XX  
CC The patent discloses a humanised antibody or its antigen-binding  
CC fragment, having binding specificity for CC-chemokine receptor 2  
CC (CCR2), comprising an antigen binding region of non-human origin  
CC and at least a portion of an immunoglobulin of human origin. The  
CC humanised antibodies are useful for inhibiting the interaction of  
CC a cell expressing CCR2. They are useful for inhibiting or treating  
CC HIV infection. The proteins of the invention are useful for inhibiting  
CC leukocyte trafficking, for treating CCR2-mediated disorders such as  
CC inflammatory disorder, autoimmune disorders such as rheumatoid  
CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis,  
CC and for inhibiting restenosis. They are useful in therapy or diagnosis,  
CC and in the manufacture of a medicament for treating CCR-2 mediated  
CC disease. They are also useful for treating allergy, anaphylaxis,  
CC malignancy, chronic and acute inflammation, histamine and IgE-  
CC mediated allergic reaction, shock, stenosis, allograft rejection,  
CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired  
CC immune deficiency syndrome (AIDS), restenosis associated with vascular  
CC intervention, including angioplasty and/or stent placement in a mammal.  
CC Humanised antibodies are also useful for inhibiting narrowing of the  
CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of  
CC a vessel in a mammal, preferably associated with vascular intervention.  
CC The present sequence is human heavy chain variable (VH) region, 4G12.  
XX  
SQ Sequence 125 AA;  
Query Match 85.3%; Score 547.5; DB 22; Length 125;  
Best Local Similarity 84.0%; Pred. No. 9.9e-44;  
Matches 105; Conservative 8; Mismatches 9; Indels 3; Gaps 1;  
QY 1 EVQLVESGDLVQPGGSLRLSCAASGFTFSNFMAMSVWVRQAPGKLEWVAIAIGRSGTTFY 60  
Db 1 EVQLVESGDLVQPGGSLRLSCAASGFTFSNFMAMSVWVRQAPGKLEWVAISGSGSTYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAK---RGRGGYKYYGMDVWGQTT 117  
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIYYCAKAVVRGVISYYYGMDVWGQTT 120  
QY 118 VTVSS 122  
Db 121 VTVSS 125

XX PS Example 9; Fig 11A; 61pp; English.

XX CC This invention describes a novel polynucleotide (I) (and complements and

XX CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence

XX CC coding for a human antibody with factor VIII specificity which has

XX CC hemostatic activity. (I) is useful a primer or probe for detecting the

XX CC presence of inhibitory antibodies directed against factor VIII. The

XX CC polypeptides of the invention and the antibodies generated from them

XX CC are useful in compositions for neutralizing factor VIII inhibiting

XX CC antibodies in hemophilia A patients. This sequence represents a human

XX CC factor VIII antibody A2 specific scFv protein DP-47 which is used

XX CC in the method of the invention.

XX SQ Sequence 122 AA;

Query Match 100.0%; Score 642; DB 21; Length 122;

Best Local Similarity 100.0%; Pred. No. 1.4e-52;

Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKLEWVAIAIGRSSTTFY 60

DB 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKLEWVAIAIGRSSTTFY 60

QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYYGMDVMQGGTTTV 120

DB 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYYGMDVMQGGTTTV 120

QY 121 SS 122

DB 121 SS 122

RESULT 2

AAV50975

ID AAV50975 standard; Protein; 122 AA.

XX AC AAV50975;

XX DT 23-MAR-2000 (first entry)

XX DE Human FVIII heavy chain variable region DP-47 protein fragment.

XX KW Human; heavy chain; antibody; factor VIII; hemostatic; variable region;

XX KW hemophilia A.

XX OS Homo sapiens.

XX PN WO9958680-A2.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-NL00285.

XX PR 08-MAY-1998; 98EP-0201543.

XX PA (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING.

XX PI Voorberg JJ, Van Den Brink EN, Turenhout EAM;

XX PN WPI; 2000-053102/04.

XX DR N-PSDB; AAZ43868.

XX PT New polynucleotide, polypeptide and antibody useful for diagnosing the

XX PT presence of neutralizing antibodies against factor VIII and for

XX PT treatment of hemophilia A patients with these antibodies -

XX PS Example 9; Fig 11c; 61pp; English.

XX CC This invention describes a novel polynucleotide (I) (and complements and

XX CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence

XX CC coding for a human antibody with factor VIII specificity which has

XX CC hemostatic activity. (I) is useful a primer or probe for detecting the

CC presence of inhibitory antibodies directed against factor VIII. The

CC polypeptides of the invention and the antibodies generated from them

CC are useful in compositions for neutralizing factor VIII inhibiting

CC antibodies in hemophilia A patients. This sequence represents a fragment

CC of the human factor VIII antibody heavy chain variable region protein

CC DP-47 which is used in the method of the invention.

XX SQ Sequence 122 AA;

Query Match 100.0%; Score 642; DB 21; Length 122;

Best Local Similarity 100.0%; Pred. No. 1.4e-52;

Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKLEWVAIAIGRSSTTFY 60

DB 1 EVQLVESGGDLVQPGGSLRLSCAASGFTFSNFMAMSWVRQAPGKLEWVAIAIGRSSTTFY 60

QY 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYYGMDVMQGGTTTV 120

DB 61 ADSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGKYKYYGMDVMQGGTTTV 120

QY 121 SS 122

DB 121 SS 122

RESULT 3

AAE07014

ID AAE07014 standard; Protein; 128 AA.

XX AC AAE07014;

XX DT 16-OCT-2001 (first entry)

XX DE Human heavy chain variable (VH) region, 038062.

XX KW Human; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;

XX KW neuroprotective; immunosuppressive; human immunodeficiency virus;

XX KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;

XX KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;

XX KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;

XX KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;

XX KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;

XX KW AIDS; inflammatory glomerulopathy; vascular intervention; LD9 antibody;

XX KW neointimal hyperplasia; VH; heavy chain variable region.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT Region 31..35

XX FT /label= CDR1

XX FT /note= "Complementarity determining region 1"

XX FT Region 50..66

XX FT /label= CDR2

XX FT /note= "Complementarity determining region 2"

XX FT Region 99..117

XX FT /label= CDR3

XX FT /note= "Complementarity determining region 3"

XX FT Misc-difference 109

XX FT /label= Unknown

XX PN WO200157226-A1.

XX PD 09-AUG-2001.

XX PF 02-FEB-2001; 2001WO-US03537.

XX PR 03-FEB-2000; 2000US-0497625.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;

XX PN

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:42:39 ; Search time 39.2461 Seconds  
(without alignments)  
493.415 Million cell updates/sec

Title: US-09-674-752-53

Perfect score: 642

Sequence: 1 EVQLVESGGDLVQPGSSRL.....GKYKGMVDVWGQGITVTVSS 122

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq 19Jun03:\*

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                  |
|------------|-------|-------------|--------|----|------------------------------|
| 1          | 642   | 100.0       | 122    | 21 | AAV50973 Human FVIII antibo  |
| 2          | 642   | 100.0       | 122    | 21 | AAV50975 Human FVIII heavy   |
| 3          | 549   | 85.5        | 128    | 22 | AAE07014 Human heavy chain   |
| 4          | 547.5 | 85.3        | 125    | 23 | AAE07021 Human heavy chain   |
| 5          | 544.5 | 84.8        | 470    | 23 | ABG77158 Germeline protein 8 |
| 6          | 544.5 | 84.0        | 125    | 23 | ABG77142 Anti-IGF-IR antibo  |
| 7          | 537.5 | 83.7        | 384    | 22 | AAW24101 Human EST encoded   |
| 8          | 531.5 | 82.8        | 125    | 22 | AAE07013 Human heavy chain   |
| 9          | 528.5 | 82.3        | 470    | 23 | ABG77157 Amino acid sequenc  |

|    |       |      |     |    |                              |
|----|-------|------|-----|----|------------------------------|
| 10 | 525   | 81.8 | 120 | 18 | AAW27553 Human Ab heavy cha  |
| 11 | 525   | 81.8 | 120 | 24 | ABJ18675 Antibody library r  |
| 12 | 525   | 81.8 | 281 | 18 | AAW27560 Consensus single c  |
| 13 | 524.5 | 81.7 | 251 | 23 | ABP45594 Human BlyS binding  |
| 14 | 523.5 | 81.5 | 124 | 23 | ABG77138 Anti-IGF-IR antibo  |
| 15 | 522.5 | 81.4 | 121 | 24 | ABP56504 Human anti-Fc-epsi  |
| 16 | 522.5 | 81.4 | 121 | 24 | ABP56506 Human anti-Fc-epsi  |
| 17 | 522   | 81.3 | 254 | 23 | ABP45690 Human BlyS binding  |
| 18 | 521.5 | 81.2 | 117 | 22 | AAE12061 Human anti-tissue   |
| 19 | 521.5 | 81.2 | 119 | 22 | AAE2088 Human Vh consensus   |
| 20 | 521.5 | 81.2 | 119 | 22 | AAE60401 Consensus human he  |
| 21 | 521.5 | 81.2 | 119 | 22 | AAE1586 Human variable hea   |
| 22 | 521.5 | 81.2 | 119 | 23 | AAU74541 Human subgroup V H  |
| 23 | 521   | 81.0 | 222 | 24 | ABR01515 Human anti-TIMP-1   |
| 24 | 520   | 81.0 | 248 | 23 | ABP45963 Human BlyS binding  |
| 25 | 519.5 | 80.9 | 313 | 22 | AAU14320 Human novel protei  |
| 26 | 519   | 80.8 | 118 | 23 | AAU83803 MS-GPC-6 heavy cha  |
| 27 | 519   | 80.8 | 118 | 23 | ABBS7561 HLA-DR-specific pr  |
| 28 | 518   | 80.7 | 253 | 24 | ABJ19830 Human VEGF-2 relat  |
| 29 | 517   | 80.5 | 124 | 22 | AAE07018 Human heavy chain   |
| 30 | 516.5 | 80.5 | 121 | 24 | ABP56507 Human anti-Fc-epsi  |
| 31 | 516   | 80.4 | 177 | 24 | ABJ36939 Anti-CD40 monoclone |
| 32 | 515.5 | 80.3 | 221 | 24 | ABR01534 Human anti-TIMP-1   |
| 33 | 515.5 | 80.3 | 253 | 23 | ABP44978 Human BlyS binding  |
| 34 | 515   | 80.2 | 248 | 23 | ABP45954 Human BlyS binding  |
| 35 | 515   | 80.2 | 251 | 23 | ABP44897 Human BlyS binding  |
| 36 | 514   | 80.1 | 136 | 24 | ABP55473 Synthetic 3-23 VH   |
| 37 | 514   | 80.1 | 367 | 24 | ABP55467 MALI3 protein seq   |
| 38 | 513.5 | 80.0 | 119 | 23 | AAE28151 Human consensus he  |
| 39 | 513.5 | 80.0 | 245 | 22 | AAE67620 Human leukocyte an  |
| 40 | 513   | 79.9 | 128 | 18 | AAW06242 Heavy chain variab  |
| 41 | 513   | 79.9 | 140 | 18 | AAW13524 Anti-melanoma anti  |
| 42 | 511   | 79.6 | 122 | 14 | AAE30773 Consensus humanise  |
| 43 | 511   | 79.6 | 128 | 22 | AAE07015 Human heavy chain   |
| 44 | 511   | 79.6 | 252 | 23 | ABP45420 Human BlyS binding  |
| 45 | 510.5 | 79.5 | 121 | 19 | AAW47180 Variable heavy (VH  |

#### ALIGNMENTS

##### RESULT 1

AAV50973

ID AAV50973 standard; Protein; 122 AA.

XX

AC AAV50973;

XX

DT 23-MAR-2000 (first entry)

XX

DE Human FVIII antibody A2 scFv heavy chain protein DP-47 #2.

XX

KW Human; heavy chain; antibody; factor VIII; hemostatic;

KW

hemophilia A; scFv; A2.

XX

OS Homo sapiens.

XX

PN WO9958680-A2.

XX

PD 18-NOV-1999.

XX

PF 07-MAY-1999; 99WO-NL00285.

XX

PR 08-MAY-1998; 98EP-0201543.

XX

(SANQ-) STICHTING SANQUIN BLOEDVOORZIENING.

PA

Voorberg JJ, Van Den Brink EN, Turenhout EAM;

XX

WPI; 2000-053102/04.

XX

PT New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies -



```
RESULT 14
Q91WPS PRELIMINARY; PRT; 479 AA.
AC Q91WPS;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 51.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013656; AAH13656.1; -.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 51603 MW; ECB2D087748584F CRC64;

Query Match 69.9%; Score 448.5; DB 11; Length 479;
Best Local Similarity 70.5%; Pred. No. 1.6e-36;
Matches 86; Conservative 15; Mismatches 14; Indels 7; Gaps 2;

Qy 1 EVQLVESGGDLVOPGSGSLRLSCAASGFTFSNFAAMSWVRQAPGKLEWVAALIGRSGLTTFY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 20 EVQLVESGGGLVKPGGSLKLSCAASGLTFSNYAMSWVRQSPKRLIEWAAALNSNGNTYY 79
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 ADSVKGRTTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGGYKYYG---MDVWGQTT 117
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 PDNVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGGYKYYG---MDVWGQTT 138
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 118 VTUSS 122
   |||||
Db 139 ITVSS 143

Search completed: December 30, 2003, 11:01:10
Job time : 30.7319 secs
```

```
Query Match 69.9%; Score 448.5; DB 11; Length 479;
Best Local Similarity 70.5%; Pred. No. 1.6e-36;
Matches 86; Conservative 15; Mismatches 14; Indels 7; Gaps 2;

Qy 1 EVQLVESGGDLVOPGSGSLRLSCAASGFTFSNFAAMSWVRQAPGKLEWVAALIGRSGLTTFY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 20 EVQLVESGGGLVKPGGSLKLSCAASGLTFSNYAMSWVRQSPKRLIEWAAALNSNGNTYY 79
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 ADSVKGRTTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGGYKYYGMDVWGQTTT 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 SDTMKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGGRGGYKYYGMDVWGQTTT 132
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 SS 122
   ||
Db 133 SS 134
```

```
RESULT 15
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 52.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786; AAH04786.1; -.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;
```

```
Db 116 8 116
RESULT 11
Q8N5K4 PRELIMINARY; PRT; 499 AA.
AC Q8N5K4; 2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strauberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032249; AAH32249.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-Cl.
DR InterPro; IPR003596; IG_MHC.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IG; 1.
DR SMART; SM00407; IG; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 499 AA; 53376 MW; 93ASC89582054F32 CRC64;

Query Match 71.3%; Score 457.5; DB 4; Length 499;
Best Local Similarity 70.0%; Pred. No. 2.1e-37;
Matches 91; Conservative 12; Mismatches 16; Indels 11; Gaps 2;

QY 1 EVQLVESGGDLVPGGSLRLSCAASGFTFSNFMAMSVVRQAPGKLEWVAIAIGRSSTTFY 60
DB 20 EVQLVESGGGVVPRGGSRLRLSCATSGFTFDDSGASVVRQAPGKLEWVSSINWNGGSTNY 79

QY 61 ADSVKGRFTISRDNKNTVYLEWNSLRADTAIYYCAKRGGRGKY-----YGMVW 112
DB 80 ADSVKGRFTISRDNKNSLYLQWNSLRVEDTALYYCA--RDPTKYCSGSGCLGYMDVW 136

QY 113 GQGTIVTVSS 122
DB 137 GKGTIVTVSS 146

RESULT 12
Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Single chain Fv (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Teujimoto Y., Aada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme .Isolation from a
RT human synthetic phage display library and characterization."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -
DR HSSP; P01772; 2FB4.

DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 70.6%; Score 453; DB 4; Length 122;
Best Local Similarity 74.6%; Pred. No. 1e-37;
Matches 91; Conservative 5; Mismatches 26; Indels 0; Gaps 0;

QY 1 EVQLVESGGDLVPGGSLRLSCAASGFTFSNFMAMSVVRQAPGKLEWVAIAIGRSSTTFY 60
DB 1 EVQLVESGGGVVPRGGSRLRLSCAASRFTFSNYGMHVRQAPGKLEWVAIAISNDGSNKFY 60

QY 61 ADSVKGRFTISRDNKNTVYLEWNSLRADTAIYYCAKRGGRGKYKYGMDVWQGTIVTV 120
DB 61 ADSVKGRFTISRDNKNSLYLQWNSLRADTAIYYCARR-----RYALDYWGQGTIV 112

QY 121 SS 122
DB 121 SS 122
```

```

RESULT 8
ID Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Vh3 protein (Fragment).
GN Vh3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD1439.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Query Match 71.8%; Score 461; DB 4; Length 147;
Best Local Similarity 71.4%; Pred. No. 2e-38;
Matches 90; Conservative 9; Mismatches 23; Indels 4; Gaps 1;

QY 1 EVQLVESGDDLVPGGSLRLSCAASGFTFSNFMWVQAQPGKLEWVAIGRSGTTFY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVHLVESGGGVVPGGSLRLSCAASGFTFSNFMWVQAQPGKLEWVAIGRSGTTFY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ADSVKGRTISRDNKNTVYLEMNSLRADTAIYYCAKRGKGRGKYKYGMDVWGQGT 116
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AGSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGKGRGKYKYGMDVWGQGT 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 117 TVTVSS 122
   ||||
Db 121 LVTVSS 126

RESULT 9
ID Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2FB4.

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DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 71.6%; Score 459.5; DB 4; Length 113;
Best Local Similarity 73.8%; Pred. No. 2.1e-38;
Matches 90; Conservative 9; Mismatches 14; Indels 9; Gaps 1;

QY 1 EVQLVESGDDLVPGGSLRLSCAASGFTFSNFMWVQAQPGKLEWVAIGRSGTTFY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVESGGGVVPGGSLRLSCAASGFTFSNFMWVQAQPGKLEWVAIRYDGSNKTY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ADSVKGRTISRDNKNTVYLEMNSLRADTAIYYCAKRGKGRGKYKYGMDVWGQGT 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTISRDNKNTVYLEMNSLRADTAIYYCAKRGKGRGKYKYGMDVWGQGT 111
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 SS 122
   ||
Db 112 SS 113

RESULT 10
ID Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 116
SQ SEQUENCE 116 AA; 12434 MW; ODA0148154DD6061 CRC64;

Query Match 71.6%; Score 459.5; DB 4; Length 116;
Best Local Similarity 76.0%; Pred. No. 2.1e-38;
Matches 92; Conservative 8; Mismatches 16; Indels 5; Gaps 2;

QY 2 VQLVESGDDLVPGGSLRLSCAASGFTFSNFMWVQAQPGKLEWVAIGRSGTTFY 61
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 VQLVESGGGVVPGGSLRLSCAASGFTFSNFMWVQAQPGKLEWVAISYDGSNKTY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 DSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGKGRGKYKYGMDVWGQGT 121
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DSVKGRFTISRDNKNTVYLEMNSLRADTAIYYCAKRGKGRGKYKYGMDVWGQGT 115
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 S 122

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Qy 119 TVSS 122  
Db 140 TVSS 143

## RESULT 2

Q96BB9 PRELIMINARY; PRT; 597 AA.  
AC Q96BB9; 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RA Strauberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC015760; AAH15760.1; -  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig\_5.  
DR SMART; SM00406; IGV\_1.  
DR PROSITE; PSS0835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 597 AA; 65039 MW; 4FC3AD8BCE263D9 CRC64;

Query Match 76.9%; Score 493.5; DB 4; Length 597;  
Best Local Similarity 76.0%; Pred. No. 6.5e-41;  
Matches 95; Conservative 13; Mismatches 14; Indels 3; Gaps 1;

Qy 1 EVOLVESGCDLVOPGSLRLSCAAGFTFSNFAMSWVRQAPGKLEWVAALIGRSGTTFY 60  
Db 20 EVOLVESGGGVOPGSLRLSCAAGFTFSNFAMSWVRQAPGKLEWVAALIGRSGTTFY 79  
Qy 61 ADSVKGRTISRDNKNTVYLEMNSLRADTAIYCCAKRGGRG--GYKYGMADWVGSTT 117  
Db 80 ADSVKGRTISRDNKNTVYLEMNSLRADTAIYCCAKRGGRG--GYKYGMADWVGSTT 139  
Qy 118 TVSS 122  
Db 140 TVSS 144

## RESULT 3

Q9UL71 PRELIMINARY; PRT; 121 AA.  
AC Q9UL71; 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035043; AAD56279.1; -

DR HSSP; P01772; 2FB4.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV\_1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 121  
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 75.0%; Score 481.5; DB 4; Length 121;  
Best Local Similarity 76.2%; Pred. No. 1.4e-40;  
Matches 93; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

Qy 1 EVOLVESGCDLVOPGSLRLSCAAGFTFSNFAMSWVRQAPGKLEWVAALIGRSGTTFY 60  
Db 1 EVOLVESGGGVOPGSLRLSCAAGFTFSNFAMSWVRQAPGKLEWVAALIGRSGTTFY 60  
Qy 61 ADSVKGRTISRDNKNTVYLEMNSLRADTAIYCCAKRGGRGKYXYGMADWVGSTT 120  
Db 61 ADSVKGRTISRDNKNTVYLEMNSLRADTAIYCCAKRGGRGKYXYGMADWVGSTT 119  
Qy 121 SS 122  
Db 120 SS 121

## RESULT 4

Q8TC77 PRELIMINARY; PRT; 471 AA.  
AC Q8TC77; 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strauberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC024289; AAH24289.1; -  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig\_4.  
DR SMART; SM00406; IGV\_1.  
DR PROSITE; PSS0835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 471 AA; 51791 MW; 388FTF4CF588660E CRC64;

Query Match 73.2%; Score 470; DB 4; Length 471;  
Best Local Similarity 72.1%; Pred. No. 1.1e-38;  
Matches 88; Conservative 18; Mismatches 16; Indels 0; Gaps 0;

Qy 1 EVOLVESGCDLVOPGSLRLSCAAGFTFSNFAMSWVRQAPGKLEWVAALIGRSGTTFY 60  
Db 20 EVOLVESGGGVOPGSLRLSCAAGFTFSNFAMSWVRQAPGKLEWVAALIGRSGTTFY 79  
Qy 61 ADSVKGRTISRDNKNTVYLEMNSLRADTAIYCCAKRGGRGKYXYGMADWVGSTT 120  
Db 80 ADSVKGRTISRDNKNTVYLEMNSLRADTAIYCCAKRGGRGKYXYGMADWVGSTT 119  
Qy 121 SS 122  
Db 140 SS 141

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:46:19 ; Search time 29.7319 Seconds  
(without alignment)  
1058.876 Million cell updates/sec

Title: US-09-674-752-53

Perfect score: 642  
Sequence: 1 EVQLVESGGDLVQPGSRLR.....GKRYGMDVWGQTTVTVSS 122

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_23.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 515   | 80.2        | 573    | 4     | Q8WU38      |
| 2          | 493.5 | 76.9        | 597    | 4     | Q96BB9      |
| 3          | 481.5 | 75.0        | 121    | 4     | Q9UL71      |
| 4          | 470   | 73.2        | 471    | 4     | Q8TC77      |
| 5          | 464   | 72.3        | 613    | 4     | Q8WU38      |
| 6          | 463   | 72.1        | 118    | 4     | Q9UL91      |
| 7          | 463   | 72.1        | 494    | 4     | Q96K68      |
| 8          | 461   | 71.8        | 147    | 4     | Q9Y509      |
| 9          | 459.5 | 71.6        | 113    | 4     | Q9UL90      |
| 10         | 459.5 | 71.6        | 116    | 4     | Q9UL93      |
| 11         | 457.5 | 71.3        | 499    | 4     | Q8NSK4      |
| 12         | 456   | 71.0        | 112    | 4     | Q9HCC1      |
| 13         | 453   | 70.6        | 122    | 4     | Q9UL84      |
| 14         | 448.5 | 69.9        | 479    | 11    | Q91WPS      |
| 15         | 439   | 68.4        | 487    | 11    | Q99K44      |
| 16         | 438.5 | 68.3        | 119    | 11    | Q920E7      |

|    |       |      |     |    |        |                    |
|----|-------|------|-----|----|--------|--------------------|
| 17 | 435   | 67.8 | 118 | 4  | Q9UL72 | Q9UL72 homo sapien |
| 18 | 433   | 67.4 | 473 | 11 | Q91Z05 | Q91Z05 mus musculu |
| 19 | 418.5 | 65.2 | 493 | 4  | Q8NCL6 | Q8NCL6 homo sapien |
| 20 | 417.5 | 65.0 | 480 | 11 | Q91XE1 | Q91XE1 mus musculu |
| 21 | 416   | 64.8 | 469 | 11 | Q8R3V9 | Q8R3V9 mus musculu |
| 22 | 413.5 | 64.4 | 131 | 4  | Q9UL88 | Q9UL88 homo sapien |
| 23 | 402.5 | 62.7 | 486 | 11 | Q91Z07 | Q91Z07 mus musculu |
| 24 | 399.5 | 62.2 | 521 | 4  | Q8N4Y9 | Q8N4Y9 homo sapien |
| 25 | 395   | 61.5 | 484 | 11 | Q8VEA0 | Q8VEA0 mus musculu |
| 26 | 394   | 61.4 | 95  | 4  | Q9UL86 | Q9UL86 homo sapien |
| 27 | 391   | 60.9 | 298 | 11 | Q9QYF0 | Q9QYF0 mus musculu |
| 28 | 384.5 | 59.9 | 112 | 4  | Q9GCP3 | Q9GCP3 homo sapien |
| 29 | 384   | 59.8 | 159 | 4  | Q9GQ50 | Q9GQ50 homo sapien |
| 30 | 381   | 59.3 | 437 | 11 | Q9R1A4 | Q9R1A4 mus musculu |
| 31 | 375.5 | 58.5 | 104 | 4  | Q9UL87 | Q9UL87 homo sapien |
| 32 | 369   | 57.5 | 124 | 4  | Q9UL92 | Q9UL92 homo sapien |
| 33 | 368   | 57.3 | 124 | 6  | Q9N0M4 | Q9N0M4 oryctolagus |
| 34 | 365   | 56.9 | 124 | 6  | Q9N0M6 | Q9N0M6 oryctolagus |
| 35 | 359.5 | 56.0 | 125 | 4  | Q9UL95 | Q9UL95 homo sapien |
| 36 | 356   | 55.5 | 500 | 4  | Q9BRV0 | Q9BRV0 homo sapien |
| 37 | 352.5 | 54.9 | 119 | 4  | Q9UL94 | Q9UL94 homo sapien |
| 38 | 351.5 | 54.8 | 484 | 11 | Q9ULA6 | Q9ULA6 mus musculu |
| 39 | 349.5 | 54.4 | 473 | 11 | Q9DL84 | Q9DL84 mus musculu |
| 40 | 347.5 | 54.1 | 117 | 11 | Q9QXE9 | Q9QXE9 mus musculu |
| 41 | 342   | 53.3 | 145 | 11 | Q924P7 | Q924P7 mus musculu |
| 42 | 339   | 52.8 | 116 | 4  | Q9UL89 | Q9UL89 homo sapien |
| 43 | 338   | 52.6 | 145 | 11 | Q924R1 | Q924R1 mus musculu |
| 44 | 338   | 52.6 | 145 | 11 | Q924R4 | Q924R4 mus musculu |
| 45 | 336   | 52.3 | 121 | 11 | Q99NG4 | Q99NG4 mus musculu |

## ALIGNMENTS

### RESULT 1

Q8WU38 ID Q8WU38 PRELIMINARY; PRT; 573 AA.  
AC Q8WU38;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Tonsil;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC021276; AAH21276.1; -  
DR InterPro: IPR007110; IG-1like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; IG\_4.  
DR SMART: SM00406; IG; 1.  
DR PROSITE: PS50835; IG\_LIKE; 2.  
DR PROSITE: PS00290; IG\_MHC; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 573 AA; 62967 MW; PD072344033AC530 CRC64;

Query Match 80.2%; Score 515; DB 4; Length 573;  
Best Local Similarity 79.8%; Pred. No. 4.4e-43;

Matches 99; Conservative 9; Mismatches 14; Indels 2; Gaps 1;

QY 1 EVQLVESGGDLVQPGSRLRSCAASGFTFSNPAWVRQAFGKLEWYAAIGRSGRTFY 60  
DB 20 EVQLVESGGGLVQPGSRLRSCAASGFTFDYAMHWVRQAFGKLEWYSGISWNSIGY 79  
QY 61 ADVSVGRFTISRDNKSLTYLQNSLRRAEDTALYYCAHGSGSYIGYVWGQGTIV 118  
DB 80 ADVSVGRFTISRDNKSLTYLQNSLRRAEDTALYYCAHGSGSYIGYVWGQGTIV 139

RESULT 14  
 ID HV21\_MOUSE STANDARD; PRT; 122 AA.  
 AC P01790;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region M511.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=81054880; PubMed=6776528;  
 RA Robinson E.A., Appella E.;  
 RT "Complete amino acid sequence of a mouse immunoglobulin alpha chain (MOPC 511).";  
 RT Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PHOSPHORYLCHOLINE.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR HSSP; P01789; IMCP.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 114 IG-LIKE.  
 FT NON\_TER 122 122  
 SQ SEQUENCE 122 AA; 13652 MW; 9F4837731EA50207 CRC64;  
 Query Match 65.7%; Score 422; DB 1; Length 122;  
 Best Local Similarity 67.7%; Pred. No. 2.2e-36;  
 Matches 84; Conservative 15; Mismatches 21; Indels 4; Gaps 2;  
 QY 1 EVLVESGGDLVOPGSLRLSCAASGFTFSNPFAMSWVRQAPGKLEWVAIGRSG--TT 58  
 DB 1 EVLVESGGGLVOPGSLRLSCATSGFTFSDFYMEVWRQSPGKLEWVAIRNKANDYTT 60  
 QY 59 FYADSVKGRFTISRDNKNTVYLENNSLRADDTAIYYCAKRGYKYYGMDWGQGTIV 118  
 DB 61 EYSASVKGKRFIVSRDTSQSIYLVQNNALRAEDTAIYYCARYGSSYWF--DVMGAGTTV 118  
 QY 119 TVSS 122  
 DB 119 TVSS 122  
 RESULT 15  
 ID HV18\_MOUSE STANDARD; PRT; 123 AA.  
 AC P01787;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V region TEPIC 15/S107/HPCM1/HPCM2/HPCM3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE (TEPIC 15).  
 RX MEDLINE=76222762; PubMed=819932;  
 RA Rudikoff S., Potter M.;  
 RT "Size differences among immunoglobulin heavy chains from phosphorylcholine-binding proteins.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).  
 RN [2]  
 RP SEQUENCE FROM N.A. (H107).

EX MEDLINE=80199926; PubMed=6769593;  
 RA Early P., Huang H., Davis M., Calame K., Hood L.;  
 RT "An immunoglobulin heavy chain variable region gene is generated from three segments of DNA: VH, D and JH.";  
 RL Cell 19:981-992(1980).  
 RN [3]  
 RP SEQUENCE (S107).  
 RX MEDLINE=76110488; PubMed=813561;  
 RA Rudikoff S., Barstad P., Potter M., Hood L.;  
 RL Unpublished results, cited by:  
 RL Hood L., Campbell J.H., Elgin S.C.R.;  
 RL Annu. Rev. Genet. 9:305-353(1975).  
 RN [4]  
 RP SEQUENCE (HPCM1, HPCM2 AND HPCM3).  
 RX MEDLINE=81197602; PubMed=7231520;  
 RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;  
 RT "IgG antibodies to phosphorylcholine exhibit more diversity than their IgM counterparts.";  
 RL Nature 291:29-34(1981).  
 CC -1- MISCELLANEOUS: ALL THOSE SEQUENCE APPEARS TO BE IDENTICAL.  
 CC -1- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA AND HYBRIDOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A93804; AVMST5.  
 DR HSSP; P01789; IMCP.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Immunoglobulin V region; Hybridoma.  
 FT DOMAIN 1 114 IG-LIKE.  
 FT NON\_TER 123 123  
 SQ SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;  
 Query Match 65.5%; Score 420.5; DB 1; Length 123;  
 Best Local Similarity 68.5%; Pred. No. 3.2e-36;  
 Matches 85; Conservative 13; Mismatches 23; Indels 3; Gaps 2;  
 QY 1 EVLVESGGDLVOPGSLRLSCAASGFTFSNPFAMSWVRQAPGKLEWVAIGRSG--TT 58  
 DB 1 EVLVESGGGLVOPGSLRLSCATSGFTFSDFYMEVWRQSPGKLEWVAIRNKANDYTT 60  
 QY 59 FYADSVKGRFTISRDNKNTVYLENNSLRADDTAIYYCAKRGYKYYGMDWGQGTIV 118  
 DB 61 EYSASVKGKRFIVSRDTSQSIYLVQNNALRAEDTAIYYCA-RDYGSSYWFQVWGAGTTV 119  
 QY 119 TVSS 122  
 DB 120 TVSS 123

Search completed: December 30, 2003, 10:55:55  
 Job time : 7.54102 secs





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Query Match      67.4%; Score 433; DB 1; Length 126;
Best Local Similarity 66.7%; Pred. No. 1.7e-37;
Matches 84; Conservative 15; Mismatches 23; Indels 4; Gaps 1;

OY 1 EVOLVESGDLVOPGSLRLSCAASGFTSNFAMSVWROAPGKLEWVAIGRSCTTYY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVDSGGGLVOPGSLRLSCAASGFTSNFAMSVWROAPGKLEWVAIINDGSDQHY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 ADSVKGKRFITSRDNSKNTYVLENNSLRAEDTAIYYCAKRGKGY----KYYGMDVWGQGT 116
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGKRFITSRDNSKNTYVLENNSLRAEDTAIYYCAKRGKGY----KYYGMDVWGQGT 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 117 TTYTSS 122
    :|||||:
Db 121 PTVTSS 126

RESULT 9
HV3B_HUMAN STANDARD; PRT; 120 AA.
AC P01766;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DB Ig heavy chain V-II region BRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77117674; PubMed=65324;
RA Capra J.D., Hopper J.E.;
RT "Comparative studies on monocytic Igm lambda and Igm kappa from an
RT individual patient. III. The complete amino acid sequence of the VH
RT region of the Igm paraprotein."
RL Immunohematology 13:995-999(1976).
CC -1 MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE
CC SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
CC TYPE.
CC -1 SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR: A02049; M3HUBW.
DR HSSP: P01772; 2F84.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS00835; IG-LIKE; 1.
KW Immunoglobulin V region.
KW DOMAIN 1 111 IG-LIKE.
FT NON_TER 120
FT MOD_RES 114 114
SQ SEQUENCE 120 AA; 13227 MW; D3F0428F7C2E6410 CRC64;

Query Match      67.4%; Score 432.5; DB 1; Length 120;
Best Local Similarity 72.5%; Pred. No. 1.8e-37;
Matches 87; Conservative 10; Mismatches 18; Indels 5; Gaps 2;

OY 1 EVOLVESGDLVOPGSLRLSCAASGFTSNFAMSVWROAPGKLEWVAIGRSCTTYY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVDSGGGLVOPGSLRLSCAASGFTSNFAMSVWROAPGKLEWVAIINDGSDQHY 59
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 ADSVKGKRFITSRDNSKNTYVLENNSLRAEDTAIYYCAKRGKGY----KGYKYYGMDVWGQGT 116
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 ADSVKGKRFITSRDNSKNTYVLENNSLRAEDTAIYYCAKRGKGY----KGYKYYGMDVWGQGT 119
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
HV3B_HUMAN STANDARD; PRT; 114 AA.

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AC P01763;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DB Ig heavy chain V-II region WEA.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Gont F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal Igm
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33."
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1 MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
CC -1 SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR: A02046; M3HUBW.
DR HSSP: P01772; 2F84.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS00835; IG-LIKE; 1.
KW Immunoglobulin V region; Pyroglutone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 114 114 PYROGLUTONE CARBOXYLIC ACID.
FT NON_TER 114
SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;

Query Match      67.1%; Score 431; DB 1; Length 114;
Best Local Similarity 68.9%; Pred. No. 2.4e-37;
Matches 84; Conservative 18; Mismatches 12; Indels 8; Gaps 2;

OY 1 EVOLVESGDLVOPGSLRLSCAASGFTSNFAMSVWROAPGKLEWVAIGRSCTTYY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVDSGGGLVOPGSLRLSCAASGFTSNFAMSVWROAPGKLEWVAIFIGSGCTTYY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 ADSVKGKRFITSRDNSKNTYVLENNSLRAEDTAIYYCAKRGKGYKYYGMDVWGQGT 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGKRFITSRDNSKNTYVLENNSLRAEDTAIYYCAR----GW----LLNMGQGTLT 112
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 121 SS 122
    :|||
Db 113 SS 114

RESULT 11
HV3B_HUMAN STANDARD; PRT; 122 AA.
AC P01769;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DB Ig heavy chain V-II region GA.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human Igm immunoglobulins."
RL Biochemistry 13:2482-2498(1974).

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Query Match 58.1%; Score 437; DB 1; Length 116;  
 Best Local Similarity 70.5%; Pred. No. 6,1e-38;  
 Matches 86; Conservative 9; Mismatches 21; Indels 6; Gaps 1;

QY 1 EVQLVESGGDLVPGGSLRLSCAASGFTFSNFMASWVRQAPGKLEWVAIIGRSCTTFF 60  
 DB 1 EVQLVESGGDLVPGGSLRLSCAASGFPBBLGWTWVRQAPGKLEWVAIKZBGSZBY 60

QY 61 ADSVKGRTISRDNKNTVYLENNSLRAEDTAIYYCAKRGQYKYGMVWGCGTTVT 120  
 DB 61 VDSVKGRTISRDNKNTVYLENNSLRAEDTAIYYCAKRGQYKYGMVWGCGTTVT 114

QY 121 SS 122  
 DB 115 ST 116

RESULT 7  
 HV3A\_HUMAN STANDARD; PRT; 122 AA.

AC P01762;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region TRO.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE (WEI)LOMA PROTEIN TRO.  
 RX MEDLINE=76023781; PubMed=809331;  
 RA Kretzschmar H., Altevogt P., Rudan E., Kortt A., Starescuk K.,  
 RA Hilschmann N.;  
 RT "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.),  
 RT II. The amino acid sequence of the H-chain, alpha-type, subgroup II;  
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).  
 CC -1- SIMILARITY: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02045; A1HUTR.  
 DR HSSP; P01772; 2PB4.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; P:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Pyroliidone carboxylic acid.  
 FT DOMAIN 1 108  
 FT MOD\_RES 1 108  
 FT NON\_TER 122 122  
 FT SEQUENCE 122 AA; 13472 MW; 2E21A11DA04D80F9 CRC64;

Query Match 67.4%; Score 433; DB 1; Length 122;  
 Best Local Similarity 60.7%; Pred. No. 1,6e-37;  
 Matches 74; Conservative 24; Mismatches 24; Indels 0; Gaps 0;

QY 1 EVQLVESGGDLVPGGSLRLSCAASGFTFSNFMASWVRQAPGKLEWVAIIGRSCTTFF 60  
 DB 1 EVQLVESGGDLVPGGSLRLSCAASGFPBBLGWTWVRQAPGKLEWVAIKZBGSZBY 60

QY 61 ADSVKGRTISRDNKNTVYLENNSLRAEDTAIYYCAKRGQYKYGMVWGCGTTVT 120  
 DB 61 ADSVKGRTISRDNKNTVYLENNSLRAEDTAIYYCAKRGQYKYGMVWGCGTTVT 120

QY 121 SS 122  
 DB 121 SS 122

QY 121 SS 122  
 DB 121 SS 122

RESULT 8  
 HV3K\_HUMAN STANDARD; PRT; 126 AA.

AC P01772;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ig heavy chain V-II region KOL.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE, AND DISULFIDE BONDS.  
 RX MEDLINE=83289131; PubMed=6884994;  
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
 RA "Three-dimensional structure determination of antibodies. Primary  
 RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=81072295; PubMed=741755;  
 RA Marquart M., Deisenhofer J., Huber R., Palm W.;  
 RA "Crystallographic refinement and atomic models of the intact  
 RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A  
 RT and 1.0-A resolution.";  
 RL J. Mol. Biol. 141:369-391(1980).  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR; A02055; G1HDKL.  
 DR PDB; 2PB4; 12-JUL-89.  
 DR PDB; 2IG2; 12-JUL-89.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; P:antigen binding activity; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; 3D-structure; Pyroliidone carboxylic acid.  
 FT DOMAIN 1 112  
 FT MOD\_RES 1 112  
 FT DISULFID 22 96  
 FT DISULFID 105 110  
 FT STRAND 3 7  
 FT STRAND 11 12  
 FT TURN 14 15  
 FT TURN 18 25  
 FT STRAND 29 31  
 FT STRAND 34 39  
 FT TURN 41 42  
 FT STRAND 45 51  
 FT TURN 53 54  
 FT STRAND 58 60  
 FT STRAND 62 64  
 FT HELIX 65 67  
 FT STRAND 68 73  
 FT TURN 74 77  
 FT STRAND 78 83  
 FT STRAND 88 90  
 FT HELIX 92 99  
 FT STRAND 106 106  
 FT TURN 107 108  
 FT STRAND 109 109  
 FT STRAND 113 116  
 FT STRAND 120 124  
 FT NON\_TER 126 126  
 FT SEQUENCE 126 AA; 13718 MW; EAD71B52B16F8776 CRC64;

|                                                              |                                                                     |
|--------------------------------------------------------------|---------------------------------------------------------------------|
| DE                                                           | Ig heavy chain V-III region CAM.                                    |
| OS                                                           | Homo sapiens (Human).                                               |
| OC                                                           | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |
| OC                                                           | Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.            |
| OX                                                           | NCBI_TaxID=9606;                                                    |
| RN                                                           | [1]                                                                 |
| RP                                                           | SEQUENCE.                                                           |
| RX                                                           | MEDLINE=81013859; PubMed=6774332;                                   |
| RA                                                           | Lehman D.W., Putnam F.W.;                                           |
| RT                                                           | "Amino acid sequence of the variable region of a human mu chain:    |
| RT                                                           | location of a possible JH segment.";                                |
| RL                                                           | Proc. Natl. Acad. Sci. U.S.A. 77:323-324(1980).                     |
| CC                                                           | -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A  |
| CC                                                           | PATIENT WITH MACROGLOBULINEMIA.                                     |
| CC                                                           | -1- SIMILARITY: Contains 1 immunoglobulin-like domain.              |
| DR                                                           | PIRSP; P01772; 2F84.                                                |
| DR                                                           | GO; GO:0005576; C:extracellular; NAS.                               |
| DR                                                           | GO; GO:0003823; F:antigen binding activity; NAS.                    |
| DR                                                           | GO; GO:0006955; P:immune response; NAS.                             |
| DR                                                           | InterPro; IPR007110; IG-1like.                                      |
| DR                                                           | InterPro; IPR003006; IG-1MC.                                        |
| DR                                                           | InterPro; IPR003596; IG_v.                                          |
| DR                                                           | Pfam; PF00047; Ig_1.                                                |
| DR                                                           | SMART; SM00406; IGV; 1.                                             |
| DR                                                           | PROSITE; PS50835; IG_LIKE; 1.                                       |
| KW                                                           | Immunoglobulin V region; Pyrolydine carboxylic acid.                |
| FT                                                           | DOMAIN 1 112                                                        |
| FT                                                           | MOD_RES 1 1                                                         |
| FT                                                           | NON_TER 1 1                                                         |
| FT                                                           | IG-LIKE.                                                            |
| FT                                                           | PYROLYDINE CARBOXYLIC ACID.                                         |
| SO                                                           | SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;                  |
| Query Match                                                  |                                                                     |
| Best Local Similarity 69.0%; Score 443; DB 1; Length 122;    |                                                                     |
| Matches 86; Conservative 14; Mismatches 21; Indels 2; Gaps 2 |                                                                     |
| OY                                                           | 1 EVLVESGGLDLPQGSRLSCAASGFTFSNFMWSVRAQPKGLEWVAALIGRSSTTFY 60        |
| DB                                                           | 1 QVELTESGGGVVZPERSRLSCAASGFTFSNFMWVRAQPKGLEWVAALISBGBKRY 60        |
| OY                                                           | 61 ADVSVGRFTISRDNSKNTVYLEMNSLRADPTAIYYCARGRGY-KYGGMDVGGTTFY 119     |
| DB                                                           | 61 ABSVVGRTFTISRDNSKNTVLYQMSLRABETAVYCA-RDRPLGYBPAFMYGGTLVT 119     |
| OY                                                           | 120 VSS 122                                                         |
| DB                                                           | 120 VSS 122                                                         |
| RESULT 5                                                     |                                                                     |
| HV3F_HUMAN                                                   |                                                                     |
| ID                                                           | HV3F_HUMAN STANDARD; PRT; 115 AA.                                   |
| AC                                                           | P01767;                                                             |
| DT                                                           | 21-JUL-1986 (Rel. 01, Created)                                      |
| DT                                                           | 21-JUL-1986 (Rel. 01, Last sequence update)                         |
| DT                                                           | 15-SEP-2003 (Rel. 42, Last annotation update)                       |
| DE                                                           | Ig heavy chain V-III region BUI.                                    |
| OS                                                           | Homo sapiens (Human)                                                |
| OC                                                           | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |
| OC                                                           | Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.            |
| OX                                                           | NCBI_TaxID=9606;                                                    |
| RN                                                           | [1]                                                                 |
| RP                                                           | SEQUENCE.                                                           |
| RX                                                           | MEDLINE=78137069; PubMed=416441;                                    |
| RA                                                           | Torano A., Putnam F.W.;                                             |
| RT                                                           | "Complete amino acid sequence of the alpha 2 heavy chain of a human |
| RT                                                           | IgA2 immunoglobulin of the A2m (2) allotype.";                      |
| RL                                                           | Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).                     |
| CC                                                           | -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPB, C  |
| CC                                                           | REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.                       |
| CC                                                           | -1- SIMILARITY: Contains 1 immunoglobulin-like domain.              |
| DR                                                           | PIR; A02050; A2HUBU.                                                |
| DR                                                           | HSSP; P01789; IMCP.                                                 |

| DR                                                            | GO:0005576; C:extracellular; NAS.                                     |
|---------------------------------------------------------------|-----------------------------------------------------------------------|
| DR <td>GO:0003823; F:antigen binding activity; NAS.</td>      | GO:0003823; F:antigen binding activity; NAS.                          |
| DR <td>GO:0006955; P:immune response; NAS.</td>               | GO:0006955; P:immune response; NAS.                                   |
| DR <td>InterPro; IPR007110; IG-like.</td>                     | InterPro; IPR007110; IG-like.                                         |
| DR <td>InterPro; IPR03006; IG-MHC.</td>                       | InterPro; IPR03006; IG-MHC.                                           |
| DR <td>InterPro; IPR03596; IG_v.</td>                         | InterPro; IPR03596; IG_v.                                             |
| DR <td>Pfam; PF00047; Ig; 1.</td>                             | Pfam; PF00047; Ig; 1.                                                 |
| DR <td>SMART; SM00406; IGV; 1.</td>                           | SMART; SM00406; IGV; 1.                                               |
| KM <td>PROSITE; PS50835; IG-LIKE; 1.</td>                     | PROSITE; PS50835; IG-LIKE; 1.                                         |
| KM <td>Immunoglobulin V region.</td>                          | Immunoglobulin V region.                                              |
| FT <td>DOMAIN 1 111 IG-LIKE.</td>                             | DOMAIN 1 111 IG-LIKE.                                                 |
| FT <td>NON TER 115 115</td>                                   | NON TER 115 115                                                       |
| SEQ <td>SEQUENCE 115 AA; 12379 MW; 2088764752DCFA CRC64;</td> | SEQUENCE 115 AA; 12379 MW; 2088764752DCFA CRC64;                      |
| Query Match                                                   |                                                                       |
|                                                               | Best Local Similarity 68.5%; Score 439.5; DB 1; Length 115;           |
|                                                               | Matches 86; Conservative 17; Mismatches 12; Indels 7; Gaps 2          |
| QY                                                            | 1 EVQLVESGGD LVQPGGSLRLS CAAGFTTSNFMAMVRRAPGKGLEWVAIGRSCTFY 60        |
| DB                                                            | 1 EVQLVETGGGLQPGGSLRLS CAAGFTVSSBHSMSWVRAPGALZWSAI-YRGCTTYY 59        |
| QY                                                            | 61 ADVSVGRFTISRDNSKNTYYLEMSLRADETAIYYCAKGRGGYKYYGMDVMGCGTTVV 120      |
| DB                                                            | 60 ADVSVGRFTISRDSDRBTIVLQMSLRADETAVYYCAR-----DLAARLFKGGITTVV 113      |
| QY                                                            | 121 SS 122                                                            |
| DB                                                            | 114 SS 115                                                            |
| RESULT 6                                                      |                                                                       |
| H3T3                                                          | HUMAN                                                                 |
| ID                                                            | HV3T HUMAN STANDARD; PRT; 116 AA.                                     |
| AC                                                            | P01781;                                                               |
| DT                                                            | 21-JUL-1986 (Rel. 01, Created)                                        |
| DT                                                            | 21-JUL-1986 (Rel. 01, Last sequence update)                           |
| DT                                                            | 15-SEP-2003 (Rel. 42, Last annotation update)                         |
| DE                                                            | Ig heavy chain V-III region GALT.                                     |
| OS                                                            | Homo sapiens (Human).                                                 |
| OC                                                            | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;               |
| OC                                                            | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.             |
| OX                                                            | NCBI_TaxId=9606;                                                      |
| RN                                                            | [1]                                                                   |
| RP                                                            | SEQUENCE.                                                             |
| RX                                                            | MEDLINE=75059123; PubMed=4803843;                                     |
| RA                                                            | Watanabe S., Barikol H.U., Horn J., Bertram J., Hilschmann N.;        |
| RT                                                            | "The primary structure of a monoclonal IgM-immunoglobulin             |
| RT                                                            | (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu- |
| RT                                                            | type), subgroup H III. Architecture of the complete IgM-molecule.";   |
| RL                                                            | Hope-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).                  |
| RN                                                            | [2]                                                                   |
| RP                                                            | REVISION TO 28-33.                                                    |
| RA                                                            | Hilschmann N.;                                                        |
| RL                                                            | Submitted (JUN-1975) to the PIR data bank.                            |
| CC                                                            | -I- MISCELLANEOUS; THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S    |
| CC                                                            | MACROGLOBULIN.                                                        |
| CC                                                            | -I- SIMILARITY: Contains 1 immunoglobulin-like domain.                |
| CC                                                            | PIR; A02064; M3HUGL.                                                  |
| DR                                                            | HSSP; P01772; 2F84.                                                   |
| DR                                                            | GO:0005576; C:extracellular; NAS.                                     |
| DR                                                            | GO:0003823; F:antigen binding activity; NAS.                          |
| DR                                                            | GO:0006955; P:immune response; NAS.                                   |
| DR                                                            | InterPro; IPR007110; IG-like.                                         |
| DR                                                            | InterPro; IPR03006; IG-MHC.                                           |
| DR                                                            | InterPro; IPR03596; IG_v.                                             |
| DR                                                            | Pfam; PF00047; Ig; 1.                                                 |
| DR                                                            | SMART; SM00406; IGV; 1.                                               |
| DR                                                            | PROSITE; PS50835; IG-LIKE; 1.                                         |
| KM                                                            | Immunoglobulin V region.                                              |
| FT                                                            | DOMAIN 1 112 IG-LIKE.                                                 |
| FT                                                            | NON TER 116 116                                                       |
| SEQ                                                           | SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;                    |

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SQ SEQUENCE      136 AA; 15071 MW; 2276A9BDBDF7016 CRC64;
Query Match          72.7%; Score 467; DB 1; Length 136;
Best Local Similarity 73.8%; Pred. No. 6,2e-41;
Matches 90; Conservative 11; Mismatches 19; Indels 2; Gaps 1;

QY 1 EVOLVEGGDPLVVGCGSLRLSCAASGFTPSNPAWSWROAPGKGLEVAALIGRSGLTFY 60
   :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 17 DVOLVEGGGLVDPGGRSKLSCAASGTFSSFGHMRORPEKCLEVAVALISGSSTLAHY 76
   :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 61 ADVKGFRTISRDNKNVTYLLENLSLRABEDTAIYIKCAKRGRGGKYKGMDVGGTIVTV 120
   :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 77 ADTYKGFRTISRDPKNTTLFLQMTSLNSDEPTAMYYCAR--MGWNPYAMDMYGSGTSVTY 134
   :|::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 121 SS 122
   ||
Db 135 SS 136

RESULT 2
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE Ig heavy chain V-II region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A..
RX MEDLINE=81101090; PubMed=6450418;
RA Matthyssens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RL heavy chain variable region.";
RT Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outpostation -
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-----
DR EMBL; J00236; AAA53516.1; -.
DR EMBL; M35415; AAA58735.1; -.
DR PIR; A02047; H3HU26.
DR PDB; 1HOU; 23-DEC-99.
DR Genew; HGNC:5545; IGHV@.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR00306; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT CHAIN 1
FT DOMAIN 20 117 IG HEAVY CHAIN V-II REGION VH26.
FT NON_TER 117 IG-LIKE.
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match          70.6%; Score 453; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 1,4e-39;
Matches 84; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
```

|                                                              |                                                                   |                                                           |              |
|--------------------------------------------------------------|-------------------------------------------------------------------|-----------------------------------------------------------|--------------|
| Oy                                                           | 1                                                                 | EVOLVESGGLVPGGSLRLISCAASGTFPSNPNMSWROAPGKLEWVAIIGSGSTTFY  | 60           |
| Db                                                           | 20                                                                | EVOLLEBGGGLVPGGSLRLISCAASGTFPSNPNMSWROAPGKLEWVAISGSGSTTY  | 79           |
| Oy                                                           | 61                                                                | ADSVKGRFTISRDNKNTVYLEMNSLRAEDTAIYYCAK                     | 98           |
| Db                                                           | 80                                                                | GDSVKGRFTISRDNKNTVLYLQNSLRAEDTAIYYCAK                     | 117          |
| RESULT 3                                                     |                                                                   |                                                           |              |
| HV3D HUMAN                                                   |                                                                   |                                                           |              |
| ID                                                           | HV3D HUMAN                                                        | STANDARD;                                                 | PRT; 115 AA. |
| AC                                                           | P01765;                                                           |                                                           |              |
| DT                                                           | 21-JUL-1986 (Rel. 01, Created)                                    |                                                           |              |
| DT                                                           | 21-JUL-1986 (Rel. 01, Last sequence update)                       |                                                           |              |
| DT                                                           | 15-SEP-2003 (Rel. 42, Last annotation update)                     |                                                           |              |
| DE                                                           | IG heavy chain V-II region TIL.                                   |                                                           |              |
| OS                                                           | Homo sapiens (Human).                                             |                                                           |              |
| OC                                                           | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |                                                           |              |
| CC                                                           | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.       |                                                           |              |
| OX                                                           | NCBI_TaxId=9606;                                                  |                                                           |              |
| RN                                                           | [1]                                                               |                                                           |              |
| RP                                                           | SEQUENCE.                                                         |                                                           |              |
| RX                                                           | MEDLINE=78005528; PubMed=409716;                                  |                                                           |              |
| RA                                                           | Wang A.-C., Wang I.Y., Fudenberg H.H.;                            |                                                           |              |
| RT                                                           | "Immunoglobulin structure and genetics. Identity between variable |                                                           |              |
| RL                                                           | regions of a mu and a gamma2 chain."/;                            |                                                           |              |
| J.                                                           | Biol. Chem. 252:7192-7199 (1977).                                 |                                                           |              |
| -1-                                                          | MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS |                                                           |              |
| OF                                                           | IGH AND IGH2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL         |                                                           |              |
| GAMMOPATHY                                                   | ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO             |                                                           |              |
| IDENTICAL.                                                   |                                                                   |                                                           |              |
| -1-                                                          | SMILARITY: Contains 1 immunoglobulin-like domain.                 |                                                           |              |
| CC                                                           | PIR: A02048; H3HUTL.                                              |                                                           |              |
| DR                                                           | HSSP: P01772; 2PB4.                                               |                                                           |              |
| DR                                                           | GO: GO:0005576; C:extracellular; NAS.                             |                                                           |              |
| DR                                                           | GO: GO:0003823; P:antigen binding activity; NAS.                  |                                                           |              |
| DR                                                           | GO: GO:0006955; P:immune response; NAS.                           |                                                           |              |
| DR                                                           | InterPro: IPR007110; IG-1like.                                    |                                                           |              |
| DR                                                           | InterPro: IPR003006; IG_MHC.                                      |                                                           |              |
| DR                                                           | InterPro: IPR003596; IG_V.                                        |                                                           |              |
| DR                                                           | Pfam: PF00047; Ig_1.                                              |                                                           |              |
| DR                                                           | SMART; SM00406; IGV_1.                                            |                                                           |              |
| DR                                                           | PROSITE; PS50835; IG-LIKE; 1.                                     |                                                           |              |
| KW                                                           | Immunoglobulin V region.                                          |                                                           |              |
| DOMAIN                                                       | 1 108                                                             |                                                           |              |
| FT                                                           | NON_TER 115 115                                                   |                                                           |              |
| FT                                                           | SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;                |                                                           |              |
| Query Match 69.4%; Score 445.5; DB 1; Length 115;            |                                                                   |                                                           |              |
| Best Local Similarity 73.0%; Pred. No. 8.1e-39;              |                                                                   |                                                           |              |
| Matches 89; Conservative 9; Mismatches 17; Indels 7; Gaps 2; |                                                                   |                                                           |              |
| Oy                                                           | 1                                                                 | EVOLVESGGLVPGGSLRLISCAASGTFPSNPNMSWROAPGKLEWVAIIGSGSTTFY  | 60           |
| Db                                                           | 1                                                                 | EVOLLEBGGGLVPGGSLRLISCAASGTFPSNPNMSWROAPGKLEWVAISGSGSTTY  | 60           |
| Oy                                                           | 61                                                                | ADSVKGRFTISRDNKNTVYLEMNSLRAEDTAIYYCAKRGGRGVYKYGMVDWGOSTTV | 120          |
| Db                                                           | 61                                                                | ABSVKGRFTISRDNKNTVYLEMNSLRAEDTAIYYCAKRGGRGVYKYGMVDWGOSTTV | 113          |
| Oy                                                           | 121                                                               | SS 122                                                    |              |
| Db                                                           | 114                                                               | SS 115                                                    |              |
| RESULT 4                                                     |                                                                   |                                                           |              |
| HV3G HUMAN                                                   |                                                                   |                                                           |              |
| ID                                                           | HV3G HUMAN                                                        | STANDARD;                                                 | PRT; 122 AA. |
| AC                                                           | P01768;                                                           |                                                           |              |
| DT                                                           | 21-JUL-1986 (Rel. 01, Created)                                    |                                                           |              |
| DT                                                           | 21-JUL-1986 (Rel. 01, Last sequence update)                       |                                                           |              |
| DT                                                           | 15-SEP-2003 (Rel. 42, Last annotation update)                     |                                                           |              |

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OM protein - protein search, using sw model

Run on: December 30, 2003, 10:43:09 ; Search time 6.54102 Seconds  
(without alignments)

877,119 Million cell updates/sec

Title: US-09-674-752-53

Perfect score: 642  
Sequence: 1 EVQLVSGDGLVPGSSSLRL.....GKYRYGMVDWGQITTVSS 122

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 467   | 72.7        | 136    | 1  | HV16_MOUSE  |
| 2          | 463   | 70.6        | 117    | 1  | HV3C_HUMAN  |
| 3          | 445.5 | 69.4        | 115    | 1  | HV3D_HUMAN  |
| 4          | 443   | 69.0        | 122    | 1  | HV3E_HUMAN  |
| 5          | 439.5 | 68.5        | 115    | 1  | HV3F_HUMAN  |
| 6          | 437   | 68.1        | 116    | 1  | HV3I_HUMAN  |
| 7          | 433   | 67.4        | 122    | 1  | HV3K_HUMAN  |
| 8          | 433   | 67.4        | 126    | 1  | HV3L_HUMAN  |
| 9          | 432.5 | 67.1        | 120    | 1  | HV3B_HUMAN  |
| 10         | 431   | 67.1        | 114    | 1  | HV3H_HUMAN  |
| 11         | 428   | 66.7        | 122    | 1  | HV3M_HUMAN  |
| 12         | 427.5 | 66.6        | 121    | 1  | HV3J_HUMAN  |
| 13         | 422   | 65.7        | 119    | 1  | HV3G_MOUSE  |
| 14         | 422   | 65.7        | 122    | 1  | HV2I_MOUSE  |
| 15         | 420.5 | 65.5        | 123    | 1  | HV18_MOUSE  |
| 16         | 420.5 | 65.5        | 123    | 1  | HV25_MOUSE  |
| 17         | 419.5 | 65.3        | 123    | 1  | HV19_MOUSE  |
| 18         | 419.5 | 65.3        | 123    | 1  | HV22_MOUSE  |
| 19         | 419   | 65.3        | 122    | 1  | HV20_MOUSE  |
| 20         | 417.5 | 65.0        | 120    | 1  | HV3U_HUMAN  |
| 21         | 417   | 65.0        | 120    | 1  | HV3V_HUMAN  |
| 22         | 416.5 | 64.9        | 123    | 1  | HV22_MOUSE  |
| 23         | 410   | 63.9        | 111    | 1  | HV35_MOUSE  |
| 24         | 409.5 | 63.8        | 116    | 1  | HV05_CARAU  |
| 25         | 409.5 | 63.8        | 123    | 1  | HV24_MOUSE  |
| 26         | 408.5 | 63.6        | 144    | 1  | HV26_MOUSE  |
| 27         | 406   | 63.2        | 114    | 1  | HV01_CANFA  |
| 28         | 405.5 | 63.2        | 115    | 1  | HV33_MOUSE  |
| 29         | 405.5 | 63.2        | 119    | 1  | HV33_MOUSE  |
| 30         | 405   | 63.1        | 119    | 1  | HV40_MOUSE  |
| 31         | 404   | 62.9        | 119    | 1  | HV37_MOUSE  |
| 32         | 403.5 | 62.9        | 113    | 1  | HV30_MOUSE  |
| 33         | 403.5 | 62.9        | 142    | 1  | HV01_RAT    |

|    |       |      |     |   |            |        |      |         |
|----|-------|------|-----|---|------------|--------|------|---------|
| 34 | 398.5 | 62.1 | 113 | 1 | HV27_MOUSE | P01796 | mus  | musculu |
| 35 | 398.5 | 62.1 | 117 | 1 | HV42_MOUSE | P01812 | mus  | musculu |
| 36 | 397.5 | 61.9 | 118 | 1 | HV39_MOUSE | P01809 | mus  | musculu |
| 37 | 396.5 | 61.8 | 115 | 1 | HV33_MOUSE | P01802 | mus  | musculu |
| 38 | 396   | 61.7 | 119 | 1 | HV3M_HUMAN | P01774 | homo | sapien  |
| 39 | 395.5 | 61.6 | 113 | 1 | HV31_MOUSE | P01800 | mus  | musculu |
| 40 | 394.5 | 61.4 | 116 | 1 | HV3Q_HUMAN | P01778 | homo | sapien  |
| 41 | 394   | 61.4 | 117 | 1 | HV3O_HUMAN | P01776 | homo | sapien  |
| 42 | 393.5 | 61.3 | 119 | 1 | HV3L_HUMAN | P01773 | homo | sapien  |
| 43 | 392.5 | 61.1 | 113 | 1 | HV28_MOUSE | P01797 | mus  | musculu |
| 44 | 389   | 60.6 | 119 | 1 | HV2N_HUMAN | P01775 | homo | sapien  |
| 45 | 388.5 | 60.5 | 113 | 1 | HV29_MOUSE | P01798 | mus  | musculu |

## ALIGNMENTS

RESULT 1  
HV16\_MOUSE STANDARD; PRT; 136 AA.  
AC P01783;  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region MOPC 21 precursor (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81234548; PubMed=6788376;  
RA Botwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NDb family of  
RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
RN [2]  
RP SEQUENCE OF 17-136.  
RX MEDLINE=77100368; PubMed=401950;  
RA Aderugbo K., Milestein C., Secher D.S.;  
RT "Molecular analysis of spontaneous somatic mutants.";  
RL Nature 265:299-304(1977).  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL: J05522; AAD15290.1; -  
DR PIR: E90809; GIM521.  
DR PDB: 1ICG; 03-JUN-95.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_v.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS00835; IG\_LIKE; 1.  
KW Immunoglobulin V region; Signal; 3D-structure.  
DR NON\_TER 1  
FT SIGNAL 1  
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.  
FT DOMAIN 115 119 D SEGMENT.  
FT DOMAIN 120 136 JH4 SEGMENT.  
FT DISULFID 78 112  
FT CONFLICT 75 112  
FT CONFLICT 89 90  
FT CONFLICT 115 115 DN -> ND (IN REF. 2).  
FT CONFLICT 120 120 W -> H (IN REF. 2).  
FT CONFLICT 120 120 Y -> W (IN REF. 2).  
FT NON\_TER 136

C:Accession: S31114  
 R:Raaphorst, F.M.; Timmer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
 Eur. J. Immunol. 22, 247-251, 1992  
 A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement  
 A:Reference number: S31104; MUID:92111633; PMID:1730252  
 A:Accession: S31114  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-123 <PAA>  
 A:Cross-references: EMBL:X62963  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 493.5; DB 2; Length 123;  
 Best Local Similarity 78.0%; Pred. No. 3.3e-37;  
 Matches 96; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVQLVDSGGDLVPGGSLRLSCAASGFTFSNFMASWVRQAPGKLEWVAIGRSGTTFY 60  
 |||||  
 DB 1 EVQLVDSGGDLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISGSGSTYY 60

QY 61 ADSVKGRFTISRDNSTKNTVYLEMNSLRAEDTAIYYCAKGRG- GYKYVGMVWGQGTTFV 119  
 |||||  
 DB 61 ADSVKGRFTISRDNSTKNTVYLEMNSLRAEDTAIYYCAKASLYRFLDEWLFDTWGQGTTLV 120

QY 120 VSS 122  
 |||  
 DB 121 VSS 123

# RESULT 15 S23624

Ig heavy chain V region - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
 C:Accession: S23624  
 R:Olée, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftoe, M.; Kozin, F.; Carson, D.A.;  
 J. Exp. Med. 175, 831-842, 1992  
 A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from  
 A:Reference number: S23623; MUID:92156804; PMID:1740665  
 A:Accession: S23624  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-143 <OLE>  
 A:Cross-references: EMBL:X59703; NID:932012; PIDN:CAA42224.1; PID:932013  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 491.5; DB 2; Length 143;  
 Best Local Similarity 77.0%; Pred. No. 5.8e-37;  
 Matches 94; Conservative 11; Mismatches 12; Indels 5; Gaps 1;

QY 1 EVQLVESGGDLVPGGSLRLSCAASGFTFSNFMASWVRQAPGKLEWVAIGRSGTTFY 60  
 |||||  
 DB 1 EVQLVESGGDLVPGGSLRLSCAASGFTFSNMVWRQAPGKLEWVAISSSSTIYY 60

QY 61 ADSVKGRFTISRDNSTKNTVYLEMNSLRAEDTAIYYCAKGRGGRGKYKYGMDVWGQGTTFV 120  
 |||||  
 DB 61 ADSVKGRFTISRDNSTKNTVYLEMNSLRAEDTAIYYCARSG----YRGDYWGQGTTLVTV 115

QY 121 SS 122  
 |||  
 DB 116 SS 117

Search completed: December 30, 2003, 11:03:20  
 Job time : 11.6946 secs









GenCore version 5.1.6  
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OM protein - protein search, using BW model

Run on: December 30, 2003, 10:47:09 ; Search time 11.6946 Seconds  
(without alignments)  
1003.251 Million cell updates/sec

Title: US-09-674-752-53

Perfect score: 642  
Sequence: 1 EVQLVESGGDLVQPGSRLT.....GKYKGMVDVWGQTTVTSS 122

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:.\*  
1: p1r1:.\*  
2: p1r2:.\*  
3: p1r3:.\*  
4: p1r4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 547.5 | 85.3        | 160    | 2 S05271 | Ig heavy chain pre |
| 2          | 521   | 81.2        | 147    | 2 I37780 | Ig variable region |
| 3          | 514.5 | 80.1        | 138    | 2 S31666 | Ig heavy chain V r |
| 4          | 510.5 | 79.5        | 119    | 2 S31107 | Ig heavy chain - h |
| 5          | 509   | 79.3        | 120    | 2 S48798 | Ig heavy chain V r |
| 6          | 507.5 | 79.0        | 119    | 2 C36005 | Ig heavy chain V r |
| 7          | 500.5 | 78.0        | 119    | 2 S31108 | Ig heavy chain - h |
| 8          | 500.5 | 78.0        | 127    | 2 S38489 | Ig heavy chain - h |
| 9          | 499.5 | 77.8        | 140    | 2 S31588 | Ig heavy chain V r |
| 10         | 499   | 77.7        | 122    | 2 B36005 | Ig heavy chain V r |
| 11         | 498.5 | 77.6        | 119    | 2 D36005 | Ig heavy chain V r |
| 12         | 497.5 | 77.5        | 123    | 2 S26794 | Ig heavy chain V r |
| 13         | 494.5 | 77.0        | 140    | 2 S31686 | Ig heavy chain V r |
| 14         | 493.5 | 76.9        | 123    | 2 S31114 | Ig heavy chain - h |
| 15         | 491.5 | 76.6        | 120    | 2 S23624 | Ig heavy chain V r |
| 16         | 490   | 76.3        | 120    | 2 S49590 | Ig heavy chain V r |
| 17         | 488.5 | 76.1        | 121    | 2 I55673 | Ig heavy chain - h |
| 18         | 487   | 75.9        | 128    | 2 S48797 | Ig heavy chain V r |
| 19         | 485.5 | 75.6        | 134    | 2 S31599 | Ig heavy chain V r |
| 20         | 484.5 | 75.5        | 140    | 2 A30532 | Ig heavy chain V r |
| 21         | 484   | 75.4        | 122    | 2 PC2398 | anti-tetanus toxin |
| 22         | 482   | 75.1        | 112    | 2 PH1647 | Ig heavy chain V r |
| 23         | 480.5 | 74.8        | 123    | 2 S38493 | Ig heavy chain - h |
| 24         | 479.5 | 74.7        | 121    | 2 S31113 | Ig heavy chain - h |
| 25         | 479.5 | 74.7        | 125    | 2 S30531 | Ig heavy chain V r |
| 26         | 478   | 74.5        | 124    | 2 S20782 | Ig heavy chain V r |
| 27         | 476.5 | 74.2        | 109    | 2 PH1649 | Ig heavy chain V r |
| 28         | 474   | 73.8        | 120    | 2 S44111 | Ig heavy chain V-D |
| 29         | 473   | 73.7        | 135    | 2 I37778 | Ig variable region |

|    |       |      |     |          |                    |
|----|-------|------|-----|----------|--------------------|
| 30 | 470.5 | 73.3 | 134 | 2 S31679 | Ig heavy chain V r |
| 31 | 470   | 73.2 | 128 | 2 S31595 | Ig heavy chain V r |
| 32 | 469.5 | 73.1 | 117 | 2 S78486 | Ig heavy chain V r |
| 33 | 469   | 73.1 | 140 | 2 S70442 | Ig heavy chain pre |
| 34 | 469   | 73.1 | 141 | 2 S31669 | Ig heavy chain V r |
| 35 | 467   | 72.7 | 108 | 2 PH1648 | Ig heavy chain V r |
| 36 | 467   | 72.7 | 128 | 2 S26790 | Ig heavy chain V r |
| 37 | 467   | 72.7 | 136 | 1 G1MS21 | Ig heavy chain pre |
| 38 | 466.5 | 72.7 | 121 | 2 S19666 | Ig heavy chain V r |
| 39 | 465   | 72.4 | 139 | 2 S38808 | Ig heavy chain - m |
| 40 | 464.5 | 72.4 | 127 | 2 S19878 | Ig heavy chain V r |
| 41 | 464.5 | 72.3 | 139 | 2 S31674 | Ig heavy chain V r |
| 42 | 462.5 | 72.0 | 121 | 2 S31104 | Ig heavy chain (eu |
| 43 | 462.5 | 72.0 | 121 | 2 S31106 | Ig heavy chain - h |
| 44 | 462   | 72.0 | 145 | 2 S11239 | Ig heavy chain V r |
| 45 | 461.5 | 71.9 | 119 | 2 F36005 | Ig heavy chain V r |

## ALIGNMENTS

## RESULT 1

S05271  
Ig heavy chain precursor - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Aug-1996

C/Accession: S05271, S04602

R/Kishimoto, T.  
Submitted to the EMBL Data Library, March 1989

A/Reference number: S05270

A/Accession: S05271

A/Molecule type: mRNA

A/Residues: 1-160 <KIS1>

A/cross-references: EMBL:X14584

R/Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.  
Nucleic Acids Res. 17, 4385, 1989

A/Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of

A/Reference number: S04601; MUID:89296497; PMID:2500644

A/Accession: S04602

A/Molecule type: mRNA

A/Residues: 1-144 <KIS2>

A/cross-references: EMBL:X14584

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/1-19/Domain: signal sequence #status predicted <Sig>

F/20-160/Product: Ig heavy chain (fragment) #status predicted <Mat>

F/34-117/Domain: immunoglobulin homology <Imm>

## Query Match

Best Local Similarity 85.3%; Score 547.5; DB 2; Length 160;

Matches 105; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

|    |     |                                                               |
|----|-----|---------------------------------------------------------------|
| QY | 1   | EVQLVESGGDLVQPGSRLTSCAASGFTFSNFRAMSWVRQAPGKLEWVAALIGSRSTTY 60 |
| DB | 20  | EVQLVESGGDLVQPGSRLTSCAASGFTFSNFRAMSWVRQAPGKLEWVAALIGSRSTTY 79 |
| QY | 61  | ASVSKGRFTISRDNKNTYYLENSLRADDTAIYYCAK---RGRGKYKGMVDVWGQTT 117  |
| DB | 80  | ASVSKGRFTISRDNKNTYYLENSLRADDTAIYYCAKAVRQVSYTYGMDVWGQTT 139    |
| QY | 118 | VTWSS 122                                                     |
| DB | 140 | VTWSS 144                                                     |

## RESULT 2

I37780  
Ig variable region (VDJ) (clone T20-11) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 23-Jul-1999

C/Accession: I37780; S25474

R/Demaision, C.; Chaetegner, P.; These, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994



CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Howell, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: PD-2630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: BOR  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..120  
PCT-US93-10555-12

Query Match 79.5%; Score 474.5; DB 5; Length 120;  
Best Local Similarity 79.2%; Pred. No. 8e-42;  
Matches 95; Conservative 7; Mismatches 11; Indels 7; Gaps 1;

QY 2 VOLVOSGAEVKKPGSSVVKVSCKASGTFSSHAISWVROAPGQGLEMMGDIIPILGTGNYA 61  
DB 1 VOLVOSGAEVKKPGSSVVKVSCKASGTFSSHAISWVROAPGQGLEMMGDIIPILGTGNYA 60

QY 62 OKFGQRTITADESTAYMELSTLTSEDTAVYYC-----ELDFYIMQGTMVYSS 114  
DB 61 OKFGQRTITADESTAYMELSTLTSEDTAVYYC-----ELDFYIMQGTMVYSS 120

RESULT 13  
PCT-US93-10555-13  
Sequence 13, Application PC/TUS9310555  
GENERAL INFORMATION:  
APPLICANT: SILVERMAN, GREGG J.  
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF  
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH  
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Judas & Lubitz  
STREET: 1880 Century Park East - Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10555  
FILING DATE: 29-OCT-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Howell, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: PD-2630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: KAS  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..120  
PCT-US93-10555-13

Query Match 79.5%; Score 474.5; DB 5; Length 120;  
Best Local Similarity 78.3%; Pred. No. 8e-42;  
Matches 94; Conservative 7; Mismatches 12; Indels 7; Gaps 1;

QY 2 VOLVOSGAEVKKPGSSVVKVSCKASGTFSSHAISWVROAPGQGLEMMGDIIPILGTGNYA 61  
DB 1 VOLVOSGAEVKKPGSSVVKVSCKASGTFSSHAISWVROAPGQGLEMMGDIIPILGTGNYA 60

QY 62 OKFGQRTITADESTAYMELSTLTSEDTAVYYCELDW-----FYIMQGTMVYSS 114  
DB 61 OKFGQRTITADESTAYMELSTLTSEDTAVYYCAKEGYGDYGRPFDFWQGLTVYSS 120

RESULT 14  
US-08-378-939-10  
Sequence 10, Application US/08378939  
Patent No. 5876961  
GENERAL INFORMATION:  
APPLICANT: CROWE, JAMES SCOTT  
APPLICANT: LEWIS, ALAN PETER  
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ  
STREET: 555 THIRTEENTH ST. N.W.  
CITY: WASHINGTON  
STATE: D. C.  
COUNTRY: U.S.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,939  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/952640  
FILING DATE: 01-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: ERNST, BARBARA G  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1808-118  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-378-939-10

Query Match 79.0%; Score 471.5; DB 2; Length 476;  
Best Local Similarity 72.4%; Pred. No. 8.4e-41;  
Matches 92; Conservative 11; Mismatches 11; Indels 13; Gaps 1;

QY 1 VOLVOSGAEVKKPGSSVVKVSCKASGTFSSHAISWVROAPGQGLEMMGDIIPILGTGNYA 60  
DB 20 QMVOVSGAEVKKPGSSVVKVSCKASGTFSSHAISWVROAPGQGLEMMGDIIPILGTPTV 79

TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH  
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East - Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/428,197  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10555  
FILING DATE: 29-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Howells, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: PD-2630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: BOR  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..120  
US-08-428-197-12  
Query Match 79.5%; Score 474.5; DB 2; Length 120;  
Best Local Similarity 79.2%; Pred. No. 8e-42;  
Matches 95; Conservative 7; Mismatches 11; Indels 7; Gaps 1;  
QY 2 VOLVSGAEVKKKPGSSVKVSCKASGTFSSSHAIISWVROAPGQGLEWMGDIIPILGTGNYA 61  
DB 1 VOLVSGAEVKKKPGSSVKVSCKASGTFSSSHAIISWVROAPGQGLEWMGDIIPILGTGNYA 60  
QY 62 OKFGQRTITADESTAYMELSTLTSEDYAVYYCELDWFIWGGTMTVSS 114  
DB 61 OKFGQRTITADESTAYMELSTLTSEDYAVYYCELDWFIWGGTMTVSS 120  
RESULT 11  
US-08-428-197-13  
Sequence 13, Application US/08428197  
Patent No. 5891438  
GENERAL INFORMATION:  
APPLICANT: SILVERMAN, GREGG J.  
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF  
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH  
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East - Suite 500  
CITY: Los Angeles  
STATE: California

COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/428,197  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10555  
FILING DATE: 29-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Howells, Stacy L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: PD-2630  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: KAS  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..120  
US-08-428-197-13  
Query Match 79.5%; Score 474.5; DB 2; Length 120;  
Best Local Similarity 78.3%; Pred. No. 8e-42;  
Matches 94; Conservative 7; Mismatches 12; Indels 7; Gaps 1;  
QY 2 VOLVSGAEVKKKPGSSVKVSCKASGTFSSSHAIISWVROAPGQGLEWMGDIIPILGTGNYA 61  
DB 1 VOLVSGAEVKKKPGSSVKVSCKASGTFSSSHAIISWVROAPGQGLEWMGDIIPILGTGNYA 60  
QY 62 OKFGQRTITADESTAYMELSTLTSEDYAVYYCELDWFIWGGTMTVSS 114  
DB 61 OKFGQRTITADESTAYMELSTLTSEDYAVYYCELDWFIWGGTMTVSS 120  
RESULT 12  
PCT-US93-10555-12  
Sequence 12, Application PC/TUS9310555  
GENERAL INFORMATION:  
APPLICANT: SILVERMAN, GREGG J.  
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF  
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH  
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East - Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10555  
FILING DATE: 29-OCT-1993

Db 61 AOKFQGRLLTTADESTAYMELSLRSEDYAVYVCAGSHITYELYYMDVWGQGTMT 120  
QY 112 VSS 114  
121 VSS 123

RESULT 8  
US-08-232-081B-41

Sequence 41, Application US/08232081B  
Patent No. 5886152

## GENERAL INFORMATION:

APPLICANT: NAKATANI, TOMOYUKI  
APPLICANT: GOMI, HIDEYUKI  
APPLICANT: WIDENES, JOHN  
APPLICANT: NOGUCHI, HIROSHI  
TITLE OF INVENTION: HUMANIZED B-B10  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,081B  
FILING DATE:  
CLASSIFICATION: 424

## ATTORNEY/AGENT INFORMATION:

NAME: SVENSSON, LEONARD R  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 20-3484  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050

## INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide

US-08-232-081B-41

Query Match 79.8%; Score 476.5; DB 2; Length 121;  
Best Local Similarity 77.7%; Pred. No. 5,1e-42;  
Matches 94; Conservative 8; Mismatches 12; Indels 7; Gaps 1;

QY 1 QVQLVSGAEVKKPKSSVKVSCVSAAGTFSNHAISWROAPQGLEMMGDIPIIGTGY 60  
Db 1 EHVLVSGAEVKKPKSSVKVSCVSAAGTFSNHAISWROAPQGLEMMGDIPIIGTGY 60  
QY 61 AOKFQGRVITTADESTAYMELSLTSEDTAVYYC-----FTYWGQGTMTVTS 113  
Db 61 AOKFQGRVITTADESTAYMELSLTSEDTAVYYC-----FTYWGQGTMTVTS 113  
QY 114 S 114  
Db 121 S 121

## RESULT 9

US-08-983-607-50  
Sequence 50, Application US/08983607  
Patent No. 6140470  
GENERAL INFORMATION:  
APPLICANT: Alan Garen

APPLICANT: Xiaohong Cai  
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-  
TITLE OF INVENTION: bodies  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Department of Molecular Biophysics  
and Biochemistry, Yale University  
STREET: 266 Whitney Avenue  
CITY: New Haven  
STATE: Connecticut  
COUNTRY: United States of America  
ZIP: 06520-8114

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" 1.44 Mb diskette  
COMPUTER: IBM PC  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Word Processing  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/983,607  
FILING DATE: April 27, 1998

## CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/IB96/01032  
FILING DATE: June 28, 1996

## ATTORNEY/AGENT INFORMATION:

NAME: Mary M. Klineky  
REGISTRATION NUMBER: 32423  
REFERENCE/DOCKET NUMBER: OCR-679  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 203-773-9544  
TELEFAX: 203-773-1183

## INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:  
LENGTH: 119 residues  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: polypeptide

ORIGINAL SOURCE:  
ORGANISM: Homo sapiens (melanoma patient  
ORGANISM: immunized with autologous tumor cells)  
INDIVIDUAL ISOLATE: peripheral blood lympho-  
INDIVIDUAL ISOLATE: cytes  
IMMEDIATE SOURCE:  
LIBRARY: VH antibodies obtained from fuses  
LIBRARY: fusion phage construct  
CLONE: 2-71

## FEATURES:

NAME/KEY: heavy chain  
US-08-983-607-50

Query Match 79.5%; Score 474.5; DB 3; Length 119;  
Best Local Similarity 83.9%; Pred. No. 8e-42;  
Matches 94; Conservative 4; Mismatches 9; Indels 5; Gaps 1;

QY 8 GAEVKKPKSSVYVSCVSAAGTFSNHAISWROAPQGLEMMGDIPIIGTGYAOKFGGR 67  
Db 8 GLEVKKPKSSVYVSCVSAAGTFSNHAISWROAPQGLEMMGDIPIIGTGYAOKFGGR 67  
QY 68 VITTADESTAYMELSLTSEDTAVYYC-----ELDFYIWGQGTMTVTS 114  
Db 68 VITTADESTAYMELSLRSEDYAVYVCAGGGRYDAFDWGGTTLVTS 119

## RESULT 10

US-08-428-197-12  
Sequence 12, Application US/08428197  
Patent No. 5891438  
GENERAL INFORMATION:  
APPLICANT: SILVERMAN, GREGG J.  
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF